

```
Db 2384 CGGCACAAGCATGAGGCCCGCGAGCTGGCCACTCCGCCCATACGCCGCATCATGCTGAA 2325
Qy 3469 ctcttggtccggagaccccaaggcagacactgcatctctcggagctggtgagatccctggg 3528
Db 2324 CTGCTGTCGGGAGACCCCAAGCGGAGACTGTCATTTCTCGGAGCTGCTGGAGATCCTGGG 2265
Qy 3529 ggccttgctccaggcaggggctcgaagaggaagaggtctgcatggtcccccgcgcag 3588
Db 2264 GGACCTGCTCCAGCGGCGAGGGCTGCAAGAGGAAGAGGAGGTCTGCTGATGCCCCCGCGAG 2205
Qy 3589 ctctcagagctcagaagagggcagctctctcgcaggtgtccaccatggccctacacatcgc 3648
Db 2204 CTCTCAGAGCTCAGAAGAGGGCAGCTTCTGCGAGGTGTCCACCATGGCCCTACACATCGC 2145
Qy 3649 ccaggctgacgctgagacagcccgcaagcctgacgagccacagcctgagccgcaggta 3708
Db 2144 CCAGGCTGACGCTGAGGACAGCCCGCAAGCCTGACGCCACAGCCTGGCCCGCAGGTA 2085
Qy 3709 ttcaactgggtgctcttctcccggtgctggtggtggtggtggtggtggtggtggtggtggt 3768
Db 2084 TTACAAGTGGGTCTCTTTTCCCGGTGCTGCTGGCCAGAGGGCTGACAGCCGCTGTTTCTC 2025
Qy 3769 caggatgaagacatttgaggaattcccatgacaccccaagacacacaaaggctctgtgga 3828
Db 2024 CAGGATGAAGACATTTGAGGAATTTCCCATATGACCCCAACGACCTACAAAAGGCTCTCTGGA 1965
Qy 3829 caaccagacagcagtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 3869
Db 1964 CAACCAGACAGACATGGGATGTGCTGGCTCGGAGGAGT 1924

RESULT 11
US-08-795-430-2
: Sequence 2, Application US/08795430
: Patent No. 6130071
: GENERAL INFORMATION:
: APPLICANT: Allitalo, Karl
: APPLICANT: Joukov, Vladimir
: TITLE OF INVENTION: Vascular Endothelial Growth Factor C (VEGF-C)
: TITLE OF INVENTION: Protein and Gene, Mutants Thereof, and Uses Thereof
: NUMBER OF SEQUENCES: 57
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
: STREET: 6300 Sears Tower, 233 South Wacker Drive
: CITY: Chicago
: STATE: Illinois
: COUNTRY: United States of America
: ZIP: 60606-6402
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/795,430
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/FI96/00427
: FILING DATE: 01-AUG-1996
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/671,573
: FILING DATE: 28-JUN-1996
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/601,132
: FILING DATE: 14-FEB-1996
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/585,895
: FILING DATE: 12-JAN-1996
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/510,133
: FILING DATE: 01-AUG-1995
: PRIOR APPLICATION DATA:
```

```
: APPLICATION NUMBER: 08/340,011
: FILING DATE: 14-NOV-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Gass, David A.
: REGISTRATION NUMBER: 38,153
: REFERENCE/DOCKET NUMBER: 28967/33691
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312/474-6300
: TELEFAX: 312/474-0448
: TELEX: 25-3856
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 216 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
US-08-795-430-2

Query Match 5.3% Score 216; DB 3; Length 216;
Best Local Similarity 100.0%; Pred. No. 5.1e-89;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3896 caagaagcgcgttcagctgtaaaagacctggtccagaatgtgctgtgaccagggcacac 3955
Db 1 CAAGAAAGCGCTTTCAGCTGTTAAAGCACCTGGCCAGAAATGTGCTGTGACAGGGCACAC 60
Qy 3956 cctgactcccaaggaggcggcggcggcggcggcggcggcggcggcggcggcggcggcggc 4015
Db 61 CCTGACTCCCAAGGGAGGGCGGGCGGCTGAGCGGGGGGGGGGGGGGGGGGGGGGGGGGG 120
Qy 4016 tacaacagcagatggtggagcgtgctcgagccaagcagagagagacactgctcccgctct 4075
Db 121 TACAACAGCAGTATGCGGAGGCTGTGCGAGCCCAACGAGAGGACCACTGCTCCCCGCTCT 180
Qy 4076 gccgcgctgactttcttcacagacacagctactaa 4111
Db 181 GCCCGCGTCACTTTCTTCACAGACAACAGCTACTAA 216

RESULT 12
US-08-222-616-5
: Sequence 5, Application US/08222616
: Patent No. 5635177
: GENERAL INFORMATION:
: APPLICANT: Bennett, Brian D.
: APPLICANT: Goeddel, David
: APPLICANT: Lee, James M.
: APPLICANT: Matthews, William
: APPLICANT: Tsai, Siao Ping
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST
: NUMBER OF INVENTION: ANTIBODIES
: NUMBER OF SEQUENCES: 42
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 460 Point San Bruno Blvd
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: patin (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/222,616
: FILING DATE: 4-APR-1994
: CLASSIFICATION: 530
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/US93/00586
```

;; FILING DATE: 22-JAN-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/826935
;; FILING DATE: 22-JAN-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Lee, Wendy M.
;; REGISTRATION NUMBER:
;; REFERENCE/DOCKET INFORMATION:
;; TELEPHONE: 415/225-1994
;; TELEFAX: 415/952-9881
;; TELEX: 910/371-7168
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 160 bases
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
US-08-222-616-5

Query Match 1.8%; Score 76; DB 1; Length 160;
Best Local Similarity 100.0%; Pred. No. 3.3e-25;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3141 ggaacattctgtcgcgaagcgcgtgtgaaagatctgtgaccttggccttgcccg 3200
Db 30 GGAACATTCTGCTGCGGAAGCGACGTGTGAAGATCTGTGACCTTGGCCCTTGCCCGG 89
QY 3201 acatctacaaagacc 3216
Db 90 ACATCTACAAAGACCC 105

RESULT 13
PCT-US95-04228-5
;; Sequence 5, Application PC/TUS9504228
;; GENERAL INFORMATION:
;; APPLICANT: Genentech, Inc.
;; APPLICANT: Bennett, Brian D.
;; APPLICANT: Goeddel, David
;; APPLICANT: Lee, James M.
;; APPLICANT: Matthews, William
;; APPLICANT: Tsai, Siao ping
;; APPLICANT: Wood, William I.
;; TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES
;; NUMBER OF SEQUENCES: 45
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Genentech, Inc.
;; STREET: 460 Point San Bruno Blvd
;; CITY: South San Francisco
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04228
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/222616
FILING DATE: 04-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Wendy M. Lee
REGISTRATION NUMBER: 00.000
REFERENCE/DOCKET NUMBER: 821P3PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881

;; TELEX: 910/371-7168
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 160 bases
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
PCT-US95-04228-5

Query Match 1.8%; Score 76; DB 5; Length 160;
Best Local Similarity 100.0%; Pred. No. 3.3e-25;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3141 ggaacattctgtcgcgaagcgcgtgtgaaagatctgtgaccttggccttgcccg 3200
Db 30 GGAACATTCTGCTGCGGAAGCGACGTGTGAAGATCTGTGACCTTGGCCCTTGCCCGG 89
QY 3201 acatctacaaagacc 3216
Db 90 ACATCTACAAAGACCC 105

RESULT 14
US-08-340-011-7
;; Sequence 7, Application US/08340011
;; Patent No. 5776755
;; GENERAL INFORMATION:
;; APPLICANT: Alitalo, et al.
;; TITLE OF INVENTION: FLT4, A NOVEL RECEPTOR TYROSIN KINASE
;; NUMBER OF SEQUENCES: 20
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
;; STREET: 6300 Sears Tower, 233 South Wacker Drive
;; CITY: Chicago
;; STATE: Illinois
;; COUNTRY: United States of America
;; ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/340.011
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/959,951
FILING DATE: 09-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Thomas C.
REGISTRATION NUMBER: 36,989
REFERENCE/DOCKET NUMBER: 32267
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 70 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
US-08-340-011-7

Query Match 1.4%; Score 56; DB 1; Length 70;
Best Local Similarity 100.0%; Pred. No. 4.4e-16;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 20 atgcagcggggcgccgctgctgcctgcactgtgctctgcctgcctgcctgga 75


```
Db 15 ATGCAGCGGGCGCGCTGTGCTCGGACTGTGCTCTGCCTGGGACTCTCTCGGA 70
|||||
RESULT 15
US-08-901-710-7
: Sequence 7, Application US/08901710
: Patent No. 6107046
: GENERAL INFORMATION:
: APPLICANT: Alitalo, Kari
: APPLICANT: Aprelikova, Olga
: APPLICANT: Pajusola, Katri
: APPLICANT: Korhonen, Elina
: APPLICANT: Korhonen, Jaana
: APPLICANT: Kaipainen, Arja
: APPLICANT: Matikainen, Marja-Terttu
: TITLE OF INVENTION: FLT4, A RECEPTOR TYROSINE KINASE, AND USES
: TITLE OF INVENTION: THEREOF
: NUMBER OF SEQUENCES: 20
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
: STREET: 6300 Sears Tower, 233 South Wacker Drive
: CITY: Chicago
: STATE: Illinois
: COUNTRY: United States of America
: ZIP: 60606-6402
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/901,710
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/340,011
: FILING DATE: 14-NOV-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/257,754
: FILING DATE: 09-JUL-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/959,951
: FILING DATE: 09-OCT-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: Gass, David A.
: REGISTRATION NUMBER: 38,153
: REFERENCE/DOCKET NUMBER: 28113/33824
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312/474-6300
: TELEFAX: 312/474-0448
: TELEX: 25-3856
: INFORMATION FOR SEQ ID NO: 7:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 70 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
US-08-901-710-7

Query Match 1.4% Score 56: DB 3: Length 70;
Best Local Similarity 100.0%; Pred. No. 4.4e-16;
Matches 56: Conservative 0: Mismatches 0: Indels 0: Gaps 0;

Qy 20 atgcagggcgcgctgtgctgcgactgtgctctgcctgggactctctgga 75
|||||
Db 15 ATGCAGCGGGCGCGCTGTGCTCGGACTGTGCTCTGCCTGGGACTCTCTCGGA 70
|||||
RESULT 16
US-08-510-133A-2

Query Match 1.4% Score 56: DB 4: Length 70;
Best Local Similarity 100.0%; Pred. No. 4.4e-16;
Matches 56: Conservative 0: Mismatches 0: Indels 0: Gaps 0;

Qy 20 atgcagggcgcgcgctgtgctgcgactgtgctctgcctgggactctctgga 75
|||||
Db 15 ATGCAGCGGGCGCGCTGTGCTCGGACTGTGCTCTGCCTGGGACTCTCTCGGA 70
|||||
RESULT 17
US-08-585-895-2
: Sequence 2, Application US/08585895
: Patent No. 6245530
: GENERAL INFORMATION:
: APPLICANT: Alitalo, Kari
: APPLICANT: Joukov, Vladimir
: TITLE OF INVENTION: Receptor Ligand
: NUMBER OF SEQUENCES: 35
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
: STREET: 6300 Sears Tower, 233 South Wacker Drive
: CITY: Chicago
: STATE: Illinois
: COUNTRY: United States of America
: ZIP: 60606-6402
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
```

```
: Sequence 2, Application US/08510133A
: Patent No. 6221839
: GENERAL INFORMATION:
: APPLICANT: Alitalo, Kari
: APPLICANT: Joukov, Vladimir
: TITLE OF INVENTION: Receptor Ligand
: NUMBER OF SEQUENCES: 35
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
: STREET: 6300 Sears Tower, 233 South Wacker Drive
: CITY: Chicago
: STATE: Illinois
: COUNTRY: United States of America
: ZIP: 60606-6402
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/510,133A
: FILING DATE: 01-Aug-1995
: CLASSIFICATION: <Unknown>
: ATTORNEY/AGENT INFORMATION:
: NAME: Gass, David A.
: REGISTRATION NUMBER: 38,153
: REFERENCE/DOCKET NUMBER: 28113/32863
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312/474-6300
: TELEFAX: 312/474-0448
: TELEX: 25-3856
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 70 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-08-510-133A-2

Query Match 1.4% Score 56: DB 4: Length 70;
Best Local Similarity 100.0%; Pred. No. 4.4e-16;
Matches 56: Conservative 0: Mismatches 0: Indels 0: Gaps 0;

Qy 20 atgcagggcgcgcgctgtgctgcgactgtgctctgcctgggactctctgga 75
|||||
Db 15 ATGCAGCGGGCGCGCTGTGCTCGGACTGTGCTCTGCCTGGGACTCTCTCGGA 70
|||||
RESULT 17
US-08-585-895-2
: Sequence 2, Application US/08585895
: Patent No. 6245530
: GENERAL INFORMATION:
: APPLICANT: Alitalo, Kari
: APPLICANT: Joukov, Vladimir
: TITLE OF INVENTION: Receptor Ligand
: NUMBER OF SEQUENCES: 35
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
: STREET: 6300 Sears Tower, 233 South Wacker Drive
: CITY: Chicago
: STATE: Illinois
: COUNTRY: United States of America
: ZIP: 60606-6402
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
```

```

: APPLICATION NUMBER: US/08/585,895
: FILING DATE:
: CLASSIFICATION: 514
: ATTORNEY/AGENT INFORMATION:
: NAME: Gass, David A.
: REGISTRATION NUMBER: 38,153
: REFERENCE/DOCKET NUMBER: 28113/33072
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312/474-6300
: TELEFAX: 312/474-0448
: TELEX: 25-3856
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 70 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: US-08-585-895-2

Query Match 1.4% Score 56: DB 4: Length 70;
Best Local Similarity 100.0%; Pred. No. 4.4e-16;
Matches 56: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

Qy 20 atgcagcggggcgcgcgtgtgcctgcgactgtggctctgcctgggactcctgga 75
|||||
Db 15 ATGCAGCGGGCGCGCCTGTGCTCGGACTGTGGCTCTGCCTGGGACTCTCTGGA 70

RESULT 18
US-08-176-620A-3
: Sequence 3, Application US/08176620A
: Patent No. 5595904
: GENERAL INFORMATION:
: APPLICANT: Boulton, Teri G.
: APPLICANT: Cobb, Melanie H.
: APPLICANT: Yancopoulos, George D.
: APPLICANT: Nye, Steven
: APPLICANT: Panayotatos, Nikos
: TITLE OF INVENTION: A Family of Map2 Protein Kinases
: NUMBER OF SEQUENCES: 21
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Pennie & Edmonds
: STREET: 1155 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: U.S.A.
: ZIP: 10036
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/176,620A
: FILING DATE: 03-JAN-1994
: CLASSIFICATION: 800
: ATTORNEY/AGENT INFORMATION:
: NAME: Mirock, S. Leslie
: REGISTRATION NUMBER: 18,872
: REFERENCE/DOCKET NUMBER: 6526-123
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 790-9090
: TELEFAX: (212) 869-8864/9741
: TELEX: 66141 PENNIE
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1467 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: unknown
: MOLECULE TYPE: DNA (genomic)

```

US-08-461-985-3
; Sequence 3, Application US/08461985
; Patent No. 5872006
; GENERAL INFORMATION:
; APPLICANT: Boulton, Teri G.
; APPLICANT: Cobb, Melanie H.
; APPLICANT: Yancopoulos, George D.
; APPLICANT: Nye, Steven
; APPLICANT: Panayotatos, Nikos
; TITLE OF INVENTION: A Family of Map2 Protein Kinases
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461.985
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/176,620
; FILING DATE: 03-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 6526-123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1467 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1245
US-08-461-985-3

Query Match 0.6% Score 26; DB 2: Length 1467;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3173 agatctgtgactttggccttgcccg 3198
|||||
Db 655 AAGATCTGTGACTTTGGCCTTGCCCG 680

RESULT 21
US-08-458-887-3
; Sequence 3, Application US/08458887
; Patent No. 5914261
; GENERAL INFORMATION:
; APPLICANT: Boulton, Teri G. et al.
; TITLE OF INVENTION: A FAMILY OF MAP2 PROTEIN KINASES
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York

COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458.887
FILING DATE: 02-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,544
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6526-049
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1467 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1245
US-08-458-887-3

Query Match 0.6% Score 26; DB 2: Length 1467;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3173 agatctgtgactttggccttgcccg 3198
|||||
Db 655 AAGATCTGTGACTTTGGCCTTGCCCG 680

RESULT 22
US-08-932-787B-3
; Sequence 3, Application US/08932787B
; Patent No. 6277963
; GENERAL INFORMATION:
; APPLICANT: Boulton et al.
; TITLE OF INVENTION: ANTIBODIES DIRECTED TOWARD EXTRACELLULAR SIGNAL-RELATED
; FILE REFERENCE: REG 430-A-1
; CURRENT APPLICATION NUMBER: US/08/932.787B
; CURRENT FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 08/469,547
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: 08/178,488
; PRIOR FILING DATE: 1994-01-07
; PRIOR APPLICATION NUMBER: 07/701,544
; PRIOR FILING DATE: 1991-05-16
; PRIOR APPLICATION NUMBER: 07/532,004
; PRIOR FILING DATE: 1990-06-01
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 1467
; TYPE: DNA
; ORGANISM: RAT
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1245)
; OTHER INFORMATION: ERK2 cdna

US-08-932-787B-3

Query Match 0.6%; Score 26; DB 4; Length 1467;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3173 aagatctgtgactttggccttgcccg 3198
|||||
Db 655 aagatctgtgactttggccttgcccg 680

RESULT 23

US-08-932-012C-3
; Sequence 3, Application US/08932012C
; Patent No. 6257035
; GENERAL INFORMATION:
; APPLICANT: Boulton et al.
; TITLE OF INVENTION: A FAMILY OF MAP2 PROTEIN KINASES
; FILE REFERENCE: REG 430-Y-1
; CURRENT APPLICATION NUMBER: US/08/932,012C
; CURRENT FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 08/462,874
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: 08/178,488
; PRIOR FILING DATE: 1994-01-07
; PRIOR APPLICATION NUMBER: 07/701,544
; PRIOR FILING DATE: 1991-05-16
; PRIOR APPLICATION NUMBER: 07/532,004
; PRIOR FILING DATE: 1990-06-01
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 1467
; TYPE: DNA
; ORGANISM: RAT
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1245)
; OTHER INFORMATION: ERK2 CDNA
US-08-932-012C-3

Query Match 0.6%; Score 26; DB 4; Length 1467;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3173 aagatctgtgactttggccttgcccg 3198
|||||
Db 655 aagatctgtgactttggccttgcccg 680

RESULT 24

US-08-888-818C-3
; Sequence 3, Application US/08888818C
; Patent No. 6303358
; GENERAL INFORMATION:
; APPLICANT: Boulton et al.
; TITLE OF INVENTION: A FAMILY OF MAP2 PROTEIN KINASES
; FILE REFERENCE: REG 430-Y-1
; CURRENT APPLICATION NUMBER: US/08/888,818C
; CURRENT FILING DATE: 1997-07-07
; PRIOR APPLICATION NUMBER: 08/478,985
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/178,488
; PRIOR FILING DATE: 1994-01-07
; PRIOR APPLICATION NUMBER: 07/701,544
; PRIOR FILING DATE: 1991-05-16
; PRIOR APPLICATION NUMBER: 07/532,004
; PRIOR FILING DATE: 1990-06-01
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3

; LENGTH: 1467
; TYPE: DNA
; ORGANISM: RAT
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1245)
; OTHER INFORMATION: ERK2 CDNA
US-08-888-818C-3

Query Match 0.6%; Score 26; DB 4; Length 1467;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3173 aagatctgtgactttggccttgcccg 3198
|||||
Db 655 aagatctgtgactttggccttgcccg 680

RESULT 25

US-08-469-537A-19
; Sequence 19, Application US/08469537A
; Patent No. 5843749
; GENERAL INFORMATION:
; APPLICANT: Maisonplierre, et al.
; TITLE OF INVENTION: EHK AND ROR TYROSINE
; TITLE OF INVENTION: KINASES
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Regeneron Pharmaceuticals, Inc.
; STREET: 777 Old Saw Mill River Road
; CITY: Tarrytown
; STATE: NY
; COUNTRY: U.S.A.
; ZIP: 10591
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,537A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/406,247
; FILING DATE: 17-MAR-1995
; APPLICATION NUMBER: USSN 08/144,992
; FILING DATE: 28-OCT-1993
; APPLICATION NUMBER: USSN 07/736,559
; FILING DATE: 26-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Kempler, Ph.D., Gail M
; REGISTRATION NUMBER: 32,143
; REFERENCE/DOCKET NUMBER: REG 070C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 914-345-7400
; TELEFAX: 914-345-7721
; TELEX:
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 159 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..159
US-08-469-537A-19

Query Match 0.6%; Score 23; DB 2; Length 159;

Best Local Similarity 100.0%; Pred. No. 0.46; Mismatches 0; Indels 0; Gaps 0;
Matches 23; Conservative 0;

Qy 3167 gtggtgaagatctgtgactttgg 3189
|||||
Db 22 GTGGTGAAGATCTGTGACTTTGG 44

RESULT 26

US-07-912-122-3
: Sequence 3, Application US/07912122
: Patent No. 6228609
: GENERAL INFORMATION:
: APPLICANT: YANG, Zhi
: TITLE OF INVENTION: NOVEL FLK-2 AND ANALOGS
: NUMBER OF SEQUENCES: 6
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Bertram I. Rowland
: STREET: 4 Embarcadero Center, Suite 3400
: CITY: San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94111

COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/912,122
: FILING DATE: 19920709
: CLASSIFICATION: 435

: ATTORNEY/AGENT INFORMATION:
: NAME: Rowland, Bertram I.
: REGISTRATION NUMBER: 20,015
: REFERENCE/DOCKET NUMBER: A-55931/BIR
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415)789-1989
: TELEFAX: (415) 398-3249
: INFORMATION FOR SEQ ID NO: 3:

: SEQUENCE CHARACTERISTICS:
: LENGTH: 1894 base pairs
: TYPE: NUCLEIC ACID
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 31..1473
US-07-912-122-3

Query Match 0.6%; Score 23; DB 4; Length 1894;
Best Local Similarity 100.0%; Pred. No. 0.42; Mismatches 0; Indels 0; Gaps 0;
Matches 23; Conservative 0;

Qy 3167 gtggtgaagatctgtgactttgg 3189
|||||
Db 976 GTGGTGAAGATCTGTGACTTTGG 998

RESULT 27

PCT-US93-06404-3
: Sequence 3, Application PC/TUS9306404
: GENERAL INFORMATION:

: APPLICANT: YANG, Zhi
: TITLE OF INVENTION: NOVEL FLK-2 AND ANALOGS
: NUMBER OF SEQUENCES: 6
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Bertram I. Rowland
: STREET: 4 Embarcadero Center, Suite 3400
: CITY: San Francisco
: STATE: California

: COUNTRY: USA
: ZIP: 94111
COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US93/06404
: FILING DATE: 19930707
: CLASSIFICATION:

: ATTORNEY/AGENT INFORMATION:
: NAME: Rowland, Bertram I.
: REGISTRATION NUMBER: 20,015
: REFERENCE/DOCKET NUMBER: FP-55931/BIR
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415)789-1989
: TELEFAX: (415) 398-3249
: INFORMATION FOR SEQ ID NO: 3:

: SEQUENCE CHARACTERISTICS:
: LENGTH: 1894 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 31..1473
PCT-US93-06404-3

Query Match 0.6%; Score 23; DB 5; Length 1894;
Best Local Similarity 100.0%; Pred. No. 0.42; Mismatches 0; Indels 0; Gaps 0;
Matches 23; Conservative 0;

Qy 3167 gtggtgaagatctgtgactttgg 3189
|||||
Db 976 GTGGTGAAGATCTGTGACTTTGG 998

RESULT 28

US-07-813-593-1
: Sequence 1, Application US/07813593
: Patent No. 5185438
: GENERAL INFORMATION:

: APPLICANT: Lemischka, Ihor R.
: TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
: NUMBER OF SEQUENCES: 4
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: IMCLONE SYSTEMS INCORPORATED
: STREET: 180 VARICK STREET
: CITY: NEW YORK
: STATE: NEW YORK
: COUNTRY: U.S.A.
: ZIP: 10014

COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/813,593
: FILING DATE: 19920415
: CLASSIFICATION: 435

: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/793,065
: FILING DATE: 15-NOV-1991
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/728,913
: FILING DATE: 28-JUN-1991
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/679,666

```

; FILING DATE: 02-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Feit, Irving N.
; REGISTRATION NUMBER: 28,601
; REFERENCE/DOCKET NUMBER: LEM-3-PPP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-645-1405
; TELEFAX: 212-645-2054
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3453 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 31..3009
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 31..3006
; US-07-813-593-1

Query Match 0.6%; Score 23; DB 1; Length 3453:
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0:

Qy 3167 gtcgtgaagatctgtgactttgg 3189
|||||
Db 2509 gtcgtgaagatctgtgactttgg 2531

RESULT 29
US-07-977-451-1
; Sequence 1, Application US/07977451
; Patent No. 5270458
; GENERAL INFORMATION:
; APPLICANT: Lemischka, Ihor R.
; TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
; TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ImClone Systems Incorporated
; STREET: 180 Varick Street
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10014
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/977,451
; FILING DATE: 19921119
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US UNASSIGNED
; FILING DATE: 12-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/906,397
; FILING DATE: 26-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US PCT/US92/05401
; FILING DATE: 26-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: TW 81102961
; FILING DATE: 15-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US PCT/US92/02750
; FILING DATE: 02-APR-1992
```

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/813,593
; FILING DATE: 24-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/793,065
; FILING DATE: 15-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/728,913
; FILING DATE: 28-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/679,666
; FILING DATE: 02-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Feit, Irving N.
; REGISTRATION NUMBER: 28,601
; REFERENCE/DOCKET NUMBER: LEM-3-7P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-645-1405
; TELEFAX: 212-645-2054
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3453 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-Terminal
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 112..3006
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 31..111
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 31..3009
; US-07-977-451-1

Query Match 0.6%; Score 23; DB 1; Length 3453:
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0:

Qy 3167 gtcgtgaagatctgtgactttgg 3189
|||||
Db 2509 gtcgtgaagatctgtgactttgg 2531

RESULT 30
US-07-946-507-1
; Sequence 1, Application US/07946507
; Patent No. 5283354
; GENERAL INFORMATION:
; APPLICANT: Lemischka, Ihor R.
; TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
; TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMCLONE SYSTEMS INCORPORATED
; STREET: 180 VARICK STREET
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10014
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; APPLICATION NUMBER: US/07/946,507
; FILING DATE: 19921119
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US UNASSIGNED
; FILING DATE: 12-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/906,397
; FILING DATE: 26-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US PCT/US92/05401
; FILING DATE: 26-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: TW 81102961
; FILING DATE: 15-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US PCT/US92/02750
; FILING DATE: 02-APR-1992
```

; FILING DATE: 19920917
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA: US/07/813,593
; FILING DATE: 24-DEC-1991
; PRIOR APPLICATION DATA: US/07/793,065
; FILING DATE: 15-NOV-1991
; PRIOR APPLICATION DATA: US/07/728,913
; FILING DATE: 28-JUN-1991
; PRIOR APPLICATION DATA: US/07/679,666
; FILING DATE: 02-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Felt, Irving N.
; REGISTRATION NUMBER: 28,601
; REFERENCE/DOCKET NUMBER: LEM-3-PPP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-645-1405
; TELEFAX: 212-645-2054
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3453 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 31..3009
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 31..3006
US-07-946-507-1

Query Match 0.6%; Score 23; DB 1; Length 3453;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3167 gtggtgaagatctgtgactttgg 3189
|||||
Db 2509 GTGCTGAAGATCTGTGACTTTGG 2531

RESULT 31
US-08-252-517-1
; Sequence 1, Application US/08252517
; Patent No. 5548065
; GENERAL INFORMATION:
; APPLICANT: Lemischka, Ihor R.
; TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Imclone Systems Incorporated
; STREET: 180 Varick Street
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10014
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/252,517
; FILING DATE: 31-OCT-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,451

; FILING DATE: 19-NOV-1992
; PRIOR APPLICATION DATA: US 07/906,397
; FILING DATE: 26-JUN-1992
; PRIOR APPLICATION DATA: US PCT/US92/05401
; FILING DATE: 26-JUN-1992
; PRIOR APPLICATION DATA: TW 81102961
; FILING DATE: 15-APR-1992
; PRIOR APPLICATION DATA: US PCT/US92/02750
; FILING DATE: 02-APR-1992
; PRIOR APPLICATION DATA: US 07/813,593
; FILING DATE: 24-DEC-1991
; PRIOR APPLICATION DATA: US 07/793,065
; FILING DATE: 15-NOV-1991
; PRIOR APPLICATION DATA: US 07/728,913
; FILING DATE: 28-JUN-1991
; PRIOR APPLICATION DATA: US 07/679,666
; FILING DATE: 02-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Felt, Irving N.
; REGISTRATION NUMBER: 28,601
; REFERENCE/DOCKET NUMBER: LEM-3-7P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-645-1405
; TELEFAX: 212-645-2054
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3453 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 112..3006
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 31..111
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 31..3009
US-08-252-517-1

Query Match 0.6%; Score 23; DB 1; Length 3453;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3167 gtggtgaagatctgtgactttgg 3189
|||||
Db 2509 GTGCTGAAGATCTGTGACTTTGG 2531

RESULT 32
US-07-906-397A-1
; Sequence 1, Application US/07906397A
; Patent No. 5621090
; GENERAL INFORMATION:
; APPLICANT: Lemischka, Ihor R.
; TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
; TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:

ADDRESSEE: IMCLONE SYSTEMS INCORPORATED
STREET: 180 VARICK STREET
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 10014
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/906.397A
FILING DATE: 19920626
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/813,593
FILING DATE: 24-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/793,065
FILING DATE: 15-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/728,913
FILING DATE: 28-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/679,666
FILING DATE: 02-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Felt, Irving N.
REGISTRATION NUMBER: 28,601
REFERENCE/DOCKET NUMBER: LEM-3-PPPPPP
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3453 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
FEATURE:
NAME/KEY: CDS
LOCATION: 31..3009
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 31..3006
US-07-906-397A-1

Query Match 0.6%; Score 23; DB 1; Length 3453;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3167 gtggtgaagatctgtgactttgg 3189
|||||
Db 2509 GTGGTGAAGATCTGTGACTTTGG 2531

RESULT 33
US-08-601-891-1
Sequence 1, Application US/08601891
Patent No. 5747651
GENERAL INFORMATION:
APPLICANT: Lemischka, Ihor R.
TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: InClone Systems Incorporated

STREET: 180 Varick Street
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10014
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/601,891
FILING DATE: 15-FEB-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,451
FILING DATE: 19-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/906,397
FILING DATE: 26-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US92/05401
FILING DATE: 26-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: TW 81102961
FILING DATE: 15-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US92/02750
FILING DATE: 02-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/813,593
FILING DATE: 24-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/793,065
FILING DATE: 15-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/728,913
FILING DATE: 28-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/679,666
FILING DATE: 02-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Felt, Irving N.
REGISTRATION NUMBER: 28,601
REFERENCE/DOCKET NUMBER: LEM-3-7P
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3453 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cdna
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 112..3006
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 31..111
FEATURE:
NAME/KEY: CDS
LOCATION: 31..3009
US-08-601-891-1

Query Match 0.6%; Score 23; DB 1; Length 3453;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3167 gtggtgaagatctgtgactttgg 3189
|||||
Db 2509 GTGGTGAAGATCTGTGACTTTGG 2531

RESULT 34

US-09-021-324-1
: Sequence 1, Application US/09021324
: Patent No. 5912133
: GENERAL INFORMATION:
: APPLICANT: Lemischka, Ihor R.
: TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
: TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
: NUMBER OF SEQUENCES: 10
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: InClone Systems Incorporated
: STREET: 180 Varlick Street
: CITY: New York
: STATE: New York
: COUNTRY: U.S.A.
: ZIP: 10014
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/021,324
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/07/977,451
: FILING DATE: 1992-11-19
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/906,397
: FILING DATE: 26-JUN-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US PCT/US92/05401
: FILING DATE: 26-JUN-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: TW 81102961
: FILING DATE: 15-APR-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US PCT/US92/02750
: FILING DATE: 02-APR-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/813,593
: FILING DATE: 24-DEC-1991
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/793,065
: FILING DATE: 15-NOV-1991
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/728,913
: FILING DATE: 28-JUN-1991
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/679,666
: FILING DATE: 02-APR-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Feit, Irving N.
: REGISTRATION NUMBER: 28,601
: REFERENCE/DOCKET NUMBER: LEM-3-7P
: TELEPHONE: 212-645-1405
: TELEFAX: 212-645-2054
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3453 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: HYPOTHETICAL: NO

: ANTI-SENSE: NO
: FRAGMENT TYPE: N-terminal
: FEATURE:
: NAME/KEY: mat_peptide
: LOCATION: 112..3006
: FEATURE:
: NAME/KEY: sig_peptide
: LOCATION: 31..111
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 31..3009
: US-09-021-324-1

Query Match 0.6%; Score 23; DB 2; Length 3453;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3167 gtggtgaagatctgtgactttgg 3189
|||||
Db 2509 GTGGTGAAGATCTGTGACTTTGG 2531

RESULT 35
PCT-US92-02750-1
: Sequence 1, Application PC/TUS9202750
: GENERAL INFORMATION:
: APPLICANT: LEMISCHKA, IHOR R.
: TITLE OF INVENTION: Totipotent Hematopoietic Stem Cell
: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: INCLONE SYSTEMS INCORPORATED
: STREET: 180 VARICK STREET
: CITY: NEW YORK
: STATE: NEW YORK
: COUNTRY: US
: ZIP: 10014
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US92/02750
: FILING DATE: 19920402
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: FEIT, IRVING N.
: REGISTRATION NUMBER: 28,601
: REFERENCE/DOCKET NUMBER: LEM-3-PPPPT
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 212-645-1405
: TELEFAX: 212-645-2054
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3453 base pairs
: TYPE: NUCLEIC ACID
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 31..3009
: FEATURE:
: NAME/KEY: mat_peptide
: LOCATION: 31..3006
: PCT-US92-02750-1

Query Match 0.6%; Score 23; DB 5; Length 3453;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3167 gtcgtgaagatctgtgactttgg 3189
|||||
Db 2509 GTGGTGAAGATCTGTGACTTTGG 2531

RESULT 36

PCT-US92-05401-1
; Sequence 1, Application PC/TUS9205401
; GENERAL INFORMATION:
; APPLICANT: Lemischka, Ihor R.
; TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
; TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMCLONE SYSTEMS INCORPORATED
; STREET: 180 VARICK STREET
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10014

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05401
; FILING DATE: 19920626
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Feit, Irving N.
; REGISTRATION NUMBER: 28,601
; REFERENCE/DOCKET NUMBER: LEM-3-PPPPPT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-645-1405
; TELEFAX: 212-645-2054
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3453 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 31..3009

FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 31..3006
PCT-US92-05401-1

Query Match 0.6%; Score 23; DB 5; Length 3453;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3167 gtcgtgaagatctgtgactttgg 3189
|||||
Db 2509 GTGGTGAAGATCTGTGACTTTGG 2531

RESULT 37

PCT-US92-09893-1
; Sequence 1, Application PC/TUS9209893
; GENERAL INFORMATION:
; APPLICANT: Lemischka, Ihor R.
; TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
; TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ImClone Systems Incorporated
; STREET: 180 Varick Street

CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10014
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/09893
; FILING DATE: 19921116
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Feit, Irving N.
; REGISTRATION NUMBER: 28,601
; REFERENCE/DOCKET NUMBER: LEM-3-7PT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-645-1405
; TELEFAX: 212-645-2054
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3453 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 112..3006
; NAME/KEY: sig_peptide
; LOCATION: 31..111
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 31..3009

PCT-US92-09893-1

Query Match 0.6%; Score 23; DB 5; Length 3453;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3167 gtcgtgaagatctgtgactttgg 3189
|||||
Db 2509 GTGGTGAAGATCTGTGACTTTGG 2531

RESULT 38

US-08-222-299-1
; Sequence 11, Application US/08122795B
; Patent No. 5635385
; GENERAL INFORMATION:
; APPLICANT: Lance H. Leopold
; APPLICANT: Scott K. Shore
; APPLICANT: Moolle V. R. Reddy
; APPLICANT: E. Premkumar Reddy
; TITLE OF INVENTION: MULTI-UNIT RIBOZYME
; TITLE OF INVENTION: INHIBITION OF ONCOGENE EXPRESSION
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seidel, Gonda, Lavorgna
; STREET: Two Penn Center Plaza, Suite 1800
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 Inch, 720 Kb

COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA: US/08/122,795B
FILING DATE: 15 September 1993
PRIORITY APPLICATION DATA: 122,795
FILING DATE: 15 September 1993
NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 6056-192
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
TELEX: No. 563538E
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 Nucleotides
TYPE: nucleic acid
STRANDEDNESS: single stranded
Sequence 1, Application US/08222299
Patent No. 5635388
GENERAL INFORMATION:
APPLICANT: Bennett, Brian D.
APPLICANT: Broz, Susan D.
APPLICANT: Matthews, William
APPLICANT: Zeigler, Francis C.
TITLE OF INVENTION: AGONIST ANTIBODIES AGAINST THE FLK2/FLT3 RECEPTOR AND USES THEREOF
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
FILING DATE: 15 September 1993
PRIORITY APPLICATION DATA: 122,795
FILING DATE: 15 September 1993
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 879
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/952-9881
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3521 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-222-299-1

Query Match 0.6%; Score 23; DB 1; Length 3521;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3167 gtggtgaagatctgtgactttgg 3189

Db 2560 GTGTTGAAGATCTGTGACTTTGG 2582
RESULT 39
US-08-434-878-1
Sequence 1, Application US/08434878
Patent No. 5957865
GENERAL INFORMATION:
APPLICANT: Bennett, Brian D.
APPLICANT: Broz, Susan D.
APPLICANT: Matthews, William
APPLICANT: Zeigler, Francis C.
TITLE OF INVENTION: AGONIST ANTIBODIES AGAINST THE FLK2/FLT3 RECEPTOR AND USES THEREOF
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
FILING DATE: 15 September 1993
PRIORITY APPLICATION DATA: 434
FILING DATE: 15 September 1993
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 879
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/952-9881
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3521 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-434-878-1

Query Match 0.6%; Score 23; DB 2; Length 3521;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3167 gtggtgaagatctgtgactttgg 3189
Db 2560 GTGTTGAAGATCTGTGACTTTGG 2582

RESULT 40
PCT-US95-03718-1
Sequence 1, Application PC/TUS9503718
GENERAL INFORMATION:
APPLICANT: GENENTECH, INC.
TITLE OF INVENTION: AGONIST ANTIBODIES AGAINST THE FLK2/FLT3 RECEPTOR AND USES THEREOF
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA

ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genetech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03718
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Wendy M. Lee
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 879PCT
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3521 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US95-03718-1

Query Match 0.6%; Score 23; DB 5; Length 3521;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3167 gtggtgaagatctgtgactttgg 3189
|||||
Db 2560 GTGCTGAAGATCTGTGACTTTGG 2582

RESULT 41
US-08-180-195-35
Sequence 35, Application US/08180195
Patent No. 5567584
GENERAL INFORMATION:
APPLICANT: Sledziewski Ph.D., Andrzej Z
APPLICANT: Bell, Lillian A.
APPLICANT: Kindsvogel Ph.D., Wayne R.
TITLE OF INVENTION: METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS
TITLE OF INVENTION: AND BIOLOGICALLY ACTIVE DIMERIZED POLYPEPTIDE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/180,195
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/634,510
FILING DATE:
APPLICATION NUMBER: US 07/146,877
FILING DATE: 22-JAN-1988
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/347,291
FILING DATE: 02-MAY-1989
ATTORNEY/AGENT INFORMATION:
NAME: Makl J.D., David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 990008.446C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
TELEFAX: 206-682-6031
TELEX: 3723836
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 4054 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: N
ANTI-SENSE: N
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: p-alpha-17B
FEATURE:
NAME/KEY: CDS
LOCATION: 205..3471
OTHER INFORMATION:
US-08-180-195-35

Query Match 0.6%; Score 23; DB 1; Length 4054;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3170 gtgaagatctgtgactttggcct 3192
|||||
Db 2698 GTGAAGATCTGTGACTTTGGCCT 2720

RESULT 42
US-08-477-329-35
Sequence 35, Application US/08477329
Patent No. 5750375
GENERAL INFORMATION:
APPLICANT: Sledziewski Ph.D., Andrzej Z
APPLICANT: Bell, Lillian A.
APPLICANT: Kindsvogel Ph.D., Wayne R.
TITLE OF INVENTION: METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS AND BIOLOGI
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,329
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Makl, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 990008.446C6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
TELEFAX: 206-682-6031
TELEX: 3723836

INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 4054 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: N
ANTI-SENSE: N
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: p-alpha-17B
FEATURE:
NAME/KEY: CDS
LOCATION: 205..3471
OTHER INFORMATION:
US-08-477-329-35

Query Match 0.6%; Score 23; DB 1; Length 4054;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3170 gtgaagatctgtgactttggcct 3192
|||||
Db 2698 GTGAAGATCTGTGACTTTGGCCT 2720

RESULT 43

US-08-475-458-35
Sequence 35, Application US/08475458
Patent No. 5843725
GENERAL INFORMATION:
APPLICANT: Sledziewski Ph.D., Andrzej Z
APPLICANT: Bell, Lillian A.
APPLICANT: Kindsvogel Ph.D., Wayne R.
TITLE OF INVENTION: METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS AND BIOLOGICAL
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,458
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 990008.446D5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
TELEFAX: 206-682-6031
TELEX: 3723836
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 4054 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: N
ANTI-SENSE: N
ORIGINAL SOURCE:

ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: p-alpha-17B
FEATURE:
NAME/KEY: CDS
LOCATION: 205..3471
OTHER INFORMATION:
US-08-475-458-35

Query Match 0.6%; Score 23; DB 2; Length 4054;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3170 gtgaagatctgtgactttggcct 3192
|||||
Db 2698 GTGAAGATCTGTGACTTTGGCCT 2720

RESULT 44

US-08-980-400-35
Sequence 35, Application US/08980400
Patent No. 6018026
GENERAL INFORMATION:
APPLICANT: Sledziewski Ph.D., Andrzej Z
APPLICANT: Bell, Lillian A.
APPLICANT: Kindsvogel Ph.D., Wayne R.
TITLE OF INVENTION: METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS AND BIOLOGIC
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/980,400
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/477,329
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 990008.446C6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
TELEFAX: 206-682-6031
TELEX: 3723836
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 4054 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: N
ANTI-SENSE: N
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: p-alpha-17B
FEATURE:
NAME/KEY: CDS
LOCATION: 205..3471
OTHER INFORMATION:

US-08-980-400-35

Query Match 0.6%; Score 23; DB 3; Length 4054;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3170 gtgaagatctgtgactttggcct 3192
|||||
Db 2698 GTGAAGATCTGTGACTTTGGCCT 2720

RESULT 45

US-09-583-459A-35
; Sequence 35, Application US/09583459A
; Patent No. 6291212
; GENERAL INFORMATION:
; APPLICANT: Sledziwski Ph.D., Andrzej Z
; APPLICANT: Bell, Lillian A.
; APPLICANT: Kindsvogel Ph.D., Wayne R.
; TITLE OF INVENTION: METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS
; TITLE OF INVENTION: AND BIOLOGICALLY ACTIVE DIMERIZED POLYPEPTIDE
; TITLE OF INVENTION: FUSIONS
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/583,459A
; FILING DATE: 30-MAY-2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,510
; FILING DATE: 27-DEC-1990
; APPLICATION NUMBER: US 07/146,877
; FILING DATE: 22-JAN-1988
; APPLICATION NUMBER: US 07/347,291
; FILING DATE: 02-MAY-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki J.D., David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 990008.446C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; TELEFAX: 206-682-6031
; TELEX: 3723836
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4054 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: N
; ANTI-SENSE: N
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: p-alpha-17B
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 205..3471
; OTHER INFORMATION:
; IS-99-03-459A-35

Query Match 0.6%; Score 23; DB 4; Length 4054;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3170 gtgaagatctgtgactttggcct 3192
|||||
Db 2698 GTGAAGATCTGTGACTTTGGCCT 2720

Search completed: July 15, 2002, 22:53:39
Job time: 22152 sec

' . '

Qy 4021 cagcgagataggagctgtcgagccaagcagagagagaccactgctcccgctgtgccg 4080
Db 4021 cagcgagataggagctgtcgagccaagcagagagagaccactgctcccgctgtgccg 4080
Qy 4081 cgtgactttcttcacagacaagctactaa 4111
Db 4081 cgtgactttcttcacagacaagctactaa 4111
RESULT 2
ID AAA37816
XX AAA37816 standard; cDNA; 4795 BP.
AC AAA37816;
XX
DT 15-JAN-2001 (first entry)
XX
DE Human Flt4 receptor tyrosine kinase long form coding sequence.
XX
KW Human; Flt4 receptor tyrosine kinase; antibody; extracellular domain;
KW lymphatic vessel detection; lymphatic tissue; lymph node tissue;
KW endothelial venule; diagnosis; lymphoma; long form; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 20..4111
FT FTT /*tag= a
FT PTT /product= Flt4 receptor tyrosine kinase long form
XX
PN US6107046-A.
XX
PD 22-AUG-2000.
XX
PE 28-JUL-1997; 97US-0901710.
XX
PR 09-OCT-1992; 92US-0959951.
PR 09-JUN-1994; 94US-0257754.
PR 14-NOV-1994; 94US-0340011.
XX
XX (ORIN) ORION CORP.
PA (LUDW-) LUDWIG INST CANCER RES.
XX
XX Alitalo K, Aprelikova O, Armstrong E, Korhonen J, Kaipainen A;
P1 Matikainen M, Pajusola K;
XX
XX WPI: 2000-571323/53.
DR P-PSDB: AAY90366.
XX
XX Antibody to extracellular domain of or to an epitope unique to a
PT vertebrate Flt4 receptor tyrosine kinase protein useful for diagnosing
PT lymphoma and imaging lymphatic vessels or high endothelial venules in
PT tissue .
XX
PS Disclosure: Column 55-66: 66pp; English.
XX
XX This sequence encodes the human Flt4 receptor tyrosine kinase long
XX form protein. The invention relates to an antibody (I) specific to the
CC extracellular domain of or to an epitope unique to a vertebrate Flt4
CC receptor tyrosine kinase protein (II). A composition comprising (I) is
CC useful for detecting lymphatic vessels, lymphatic tissue comprising lymph
CC node tissue or high endothelial venules in an organism preferably mammal
CC especially human. The method comprises administering the composition and
CC detecting (I) bound to lymphatic vessels, lymphatic tissue or high
CC endothelial venules. (I) is also useful for screening a biological sample
CC for the presence of (II) or diagnosing a disease state. The diagnosing
CC method of the disease state preferably lymphoma comprises obtaining a
CC tissue sample on a vertebrate organism suspected of being in a diseased
CC state characterised by in Flt4 expression in lymphatic cells or high
CC endothelial venules and screening the diseased state utilising (I).
CC (I) is also useful for imaging lymphatic vessels or high endothelial
CC venules in a tissue by contacting the tissue with (I) and imaging the
CC vessels by detecting (I) bound to the tissues.

XX SQ Sequence 4795 BP; 977 A; 1490 C; 1494 G; 834 T; 0 other;
Query Match 100.0%; Score 4111; DB 21; Length 4795;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ccacgcgcagcggccggagatgcagcggggcgccgcgcgtgtgctcgcgactgtggctctg 60
Db 1 ccacgcgcagcggccggagatgcagcggggcgccgcgcgtgtgctcgcgactgtggctctg 60
Qy 61 cctgggaactcctgcagcggcctggtgagtctactcatgaccccccccgaccttgaaat 120
Db 61 cctgggaactcctgcagcggcctggtgagtctactcatgaccccccccgaccttgaaat 120
Qy 121 cagcgaggagtcacacgctcatcgacacccggtgcagacccctgtccatctcctgcaggggaca 180
Db 121 cagcgaggagtcacacgctcatcgacacccggtgcagacccctgtccatctcctgcaggggaca 180
Qy 181 gacccccctcagtgggccttgccagagagctcaggaggcgccaccccgagagacaagga 240
Db 181 gacccccctcagtgggccttgccagagagctcaggaggcgccaccccgagagacaagga 240
Qy 241 cagcgaggacacgggggtggtgcgagactcgcaggggcacagacgcgagcccttactgcaa 300
Db 241 cagcgaggacacgggggtggtgcgagactcgcaggggcacagacgcgagcccttactgcaa 300
Qy 301 ggtgtgtcgtcgcagcagagtacatgccaaacacagcagcagctacgtctgtactacaa 360
Db 301 ggtgtgtcgtcgcagcagagtacatgccaaacacagcagcagctacgtctgtactacaa 360
Qy 361 gtacatcaaggacgcagtcagaggcaccacgcgcgcgcagctcctacgtgtctcgtgagaga 420
Db 361 gtacatcaaggacgcagtcagaggcaccacgcgcgcgcagctcctacgtgtctcgtgagaga 420
Qy 421 ctttgagcagccattcatcaacaagcctgcacgcctcttgggtcaacaggaagacgcgat 480
Db 421 ctttgagcagccattcatcaacaagcctgcacgcctcttgggtcaacaggaagacgcgat 480
Qy 481 gtgggtgcctctgtgtgttccatccccggcctcaatgtcacgctgcgtcgcgaagctc 540
Db 481 gtgggtgcctctgtgtgttccatccccggcctcaatgtcacgctgcgtcgcgaagctc 540
Qy 541 ggtgtgtggccagcagcggcagagagtggtgtgggatgacccggcggtcgtcgtgtc 600
Db 541 ggtgtgtggccagcagcggcagagagtggtgtgggatgacccggcggtcgtcgtgtc 600
Qy 601 cagccactcgtcgcagatgccctgtacctgcagtcgagaccacacctgggagaccaggga 660
Db 601 cagccactcgtcgcagatgccctgtacctgcagtcgagaccacacctgggagaccaggga 660
Qy 661 ctctcttccaaaccccttctgtgtgcacatccacagcaacgagctctaagacatccagct 720
Db 661 ctctcttccaaaccccttctgtgtgcacatccacagcaacgagctctaagacatccagct 720
Qy 721 gtgccccagaaatcgtcgtgagagctgctggttaggggagaaagctgtcctgaactgaccgt 780
Db 721 gtgccccagaaatcgtcgtgagagctgctggttaggggagaaagctgtcctgaactgaccgt 780
Qy 781 gtgggctgagtttaactcaggtgtcacctttgactgggactaccagggaagcaggcaga 840
Db 781 gtgggctgagtttaactcaggtgtcacctttgactgggactaccagggaagcaggcaga 840
Qy 841 gcgggggtaagtgggtgcccgagcgcgtccccagcagaccacacagaactctcccagcat 900
Db 841 gcgggggtaagtgggtgcccgagcgcgtccccagcagaccacacagaactctcccagcat 900
Qy 901 cctgacatccacaacgctcagccagcacacacctgggctcgtatgtgtcaagccacaacaa 960
Db 901 cctgacatccacaacgctcagccagcacacacctgggctcgtatgtgtcaagccacaacaa 960
Qy 961 cggcaccagcagcttttcgggagagaccgggttcattgtgtcagaaatcccccttcacag 1020

QY 3181 tgactttggccttgcccgagacatctacaaagaccctgactagtcctccgcaaggcagtgac 3240
|||||
Db 3181 tgactttggccttgcccgagacatctacaaagaccctgactagtcctccgcaaggcagtgac 3240
QY 3241 cggctgcccctgaagtgtatggccctgaaagcatcttcgcagaaggtgtacaccacgca 3300
|||||
Db 3241 cggctgcccctgaagtgtatggccctgaaagcatcttcgcagaaggtgtacaccacgca 3300
QY 3301 gagtgacgtgtatggccttgccctgagagatcttctctgagagatcttctctgagggcctcccc 3360
|||||
Db 3301 gagtgacgtgtatggccttgccctgagagatcttctctgagagatcttctctgagggcctcccc 3360
QY 3361 gtaccctgggtgtcagatcaatgagaggtctctgcccagcgctgagagacgacacagat 3420
|||||
Db 3361 gtaccctgggtgtcagatcaatgagaggtctctgcccagcgctgagagacgacacagat 3420
QY 3421 gaggggcccccggagctggccactccgcacatcgcgcgcatcatgtctgaaactgtgtcccg 3480
|||||
Db 3421 gaggggcccccggagctggccactccgcacatcgcgcgcatcatgtctgaaactgtgtcccg 3480
QY 3481 aaaccccaaggcagacactgcatcttcgagagctggtggagatccctggggagacactgctcca 3540
|||||
Db 3481 agaccccaaggcagacactgcatcttcgagagctggtggagatccctggggagacactgctcca 3540
QY 3541 gggcaggggcctgcaagagaaagagaggtctgtcagtgcccgccgcagctctcagagctc 3600
|||||
Db 3541 gggcaggggcctgcaagagaaagagaggtctgtcagtgcccgccgcagctctcagagctc 3600
QY 3601 agaagagggcagcttctcaggtgtccaccatggccctacacatcgcgccaggtctgacgc 3660
|||||
Db 3601 agaagagggcagcttctcaggtgtccaccatggccctacacatcgcgccaggtctgacgc 3660
QY 3661 taagacacccgcagcagctcagcgcacacagcctggccgaggtattacaactggct 3720
|||||
Db 3661 taagacacccgcagcagctcagcgcacacagcctggccgaggtattacaactggct 3720
QY 3721 gtctttcccggtgctgcccagaggggctgagaccgtgtctctccaggatgaagac 3780
|||||
Db 3721 gtctttcccggtgctgcccagaggggctgagaccgtgtctctccaggatgaagac 3780
QY 3781 atttgagggaattcccatgaccaccaagcactacaaaaggctctgtggacaaccagacaga 3840
|||||
Db 3781 atttgagggaattcccatgaccaccaagcactacaaaaggctctgtggacaaccagacaga 3840
QY 3841 caagtggatggtgctgacctcgagaggtttgagcagatagagacgagcatagacaaga 3900
|||||
Db 3841 caagtggatggtgctgacctcgagaggtttgagcagatagagacgagcatagacaaga 3900
QY 3901 aagcgcttcagctgtaaaggacctggccagaaatgtggctgtgaccagggcacacctga 3960
|||||
Db 3901 aagcgcttcagctgtaaaggacctggccagaaatgtggctgtgaccagggcacacctga 3960
QY 3961 ctcccaaggagggcgccgctgagcggggggcccgagagggccagaggtattttacaa 4020
|||||
Db 3961 ctcccaaggagggcgccgctgagcggggggcccgagagggccagaggtattttacaa 4020
QY 4021 cagcgagatggggagctgtcgagaccaaagcagagagagaccactgctccccgtctgcccq 4080
|||||
Db 4021 cagcgagatggggagctgtcgagaccaaagcagagagagaccactgctccccgtctgcccq 4080
QY 4081 cgtgactttcttccacagacaacagctactaa 4111
|||||
Db 4081 cgtgactttcttccacagacaacagctactaa 4111

RESULT 3
AA252334
ID AA252334 standard; cDNA: 4795 BP.
AC AA252334;
XX
XX
DT 17-AUG-2000 (first entry)

XX Human tyrosine kinase receptor Flt4-long form cDNA.
DE
XX
KW Human; receptor tyrosine kinase; RTK; Flt4; fms-like tyrosine kinase 4;
VEGFR-3; vascular endothelial growth factor receptor-3; chromosome 5q35;
cytostatic; tumour imaging; anti-tumour therapy; treatment; diagnosis;
neoplastic disease; lymphoma; carcinoma; breast; squamous cell; melanoma;
sarcoma; malignancy; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
CDS 20..4111
FT /*tag= a
ET /product= "Flt4 receptor-long form"
XX
PN WO200021560-A1.
XX
PD 20-APR-2000.
XX
PF 08-OCT-1999; 99WO-US23525.
XX
PR 09-OCT-1998; 98US-0169079.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX (UYHE-) UNIV HELSINKI LICENSING LTD OY.
XX
PI Alitalo K, Kaipainen A, Valtola R, Jussila L;
XX
DR WPI: 2000-317850/27.
DR P-PSDB: AAY70747.
XX
PT Treating neoplastic diseases such as lymphoma, carcinomas, melanomas
and sarcomas, involves administering a compound capable of inhibiting
binding of ligand proteins to fms-like tyrosine kinase-4 receptor -
XX
PS Disclosure: Page 120-127; 148pp; English.
XX
CC The patent discloses a method to treat neoplastic disease characterised
by expression of fms-like tyrosine kinase 4 (Flt4) receptor (also
referred as vascular endothelial growth factor receptor-3, VEGFR-3) in
endothelial cells of blood vessels adjacent to malignant neoplasm. The
method involves administering a compound that inhibits binding of a
ligand to Flt4 thereby inhibiting Flt4 mediated proliferation of vascular
endothelial cells. The compound is useful for treating neoplastic disease
such as breast carcinomas, squamous cell carcinomas, lymphomas, melanomas
and sarcomas. Flt4 receptor tyrosine kinase binding compounds can be used
for manufacturing medicament useful for diagnostic screening, imaging and
treatment of malignancies characterised by Flt4-expressing blood cells.
The present sequence is a cDNA encoding the long form of Flt4 receptor
from an oligo-dT primed human erythroleukaemia cell line (HEL) cDNA
library in bacteriophage lambda gt11. The Flt4 gene maps to chromosomal
region 5q35 and is expressed as 5.8 kb and 4.5 kb mRNAs which differ in
their 3' sequences and are differentially expressed in HEL and DAMI cell
lines. Flt4 belongs to a subfamily of class III receptor tyrosine kinases
(RTKs). It is used as a target for tumour imaging and anti-tumour
therapy.
XX
SQ Sequence 4795 BP; 977 A; 1490 C; 1494 G; 834 T; 0 other;

Query Match 100.0%; Score 4111; DB 21; Length 4795;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 caacgcgacggccggagatgcagcgggcgccgcgcgcgtgtgctgcactgtgacctg 60
|||||
Db 1 caacgcgacggccggagatgcagcgggcgccgcgcgcgtgtgctgcactgtgacctg 60
QY 61 cctgggactcttgacggcctggtgagtgctactccatgaccccccgacctgaacat 120
|||||
Db 61 cctgggactcttgacggcctggtgagtgctactccatgaccccccgacctgaacat 120

Oy	121	cacgaggagtcacacgctcaatcagacaccggtgacagcctgtccatctctctcagggaca	180
Db	121	caagaggagtcacacgctcatcgacaccggtgacagcctgtccatctctcagggaca	180
Oy	181	gcaccctcctcagatggcttggccraggagctcagagggcgccajccaccgagagacaaga	240
Db	181	gcaccctcctcagatggcttggccraggagctcagagggcgccajccaccgagagacaaga	240
Oy	241	cagcagagcacaggggtgtggtcgagactgycgagggcacagagccagagccctactlcaa	300
Db	241	cagcagagcacaggggtgtggtcgagactgycgagggcacagagccagagccctactlcaa	300
Oy	301	gggtgtgctgtgcacaggtacatgccaacgacacagcgagctacgtctgtctactacaa	360
Db	301	gggtgtgctgtgcacaggtacatgccaacgacacagcgagctacgtctgtctactacaa	360
Oy	361	gtacataaagcagcatcgaggggacacacgcccaccagctcctacgtattcgtgagaga	420
Db	361	gtacataaagcagcatcgaggggacacacgcccaccagctcctacgtattcgtgagaga	420
Oy	421	ctttgagcagccattcatcaacaagcctgacacgctcttggccaacagaaagagcgccat	480
Db	421	ctttgagcagccattcatcaacaagcctgacacgctcttggccaacagaaagagcgccat	480
Oy	481	gtgggtgcccgtgtggtgttccatccccggcctcaatgtcacgctgcgctcgcgaaagctc	540
Db	481	gtgggtgcccgtgtggtgttccatccccggcctcaatgtcacgctgcgctcgcgaaagctc	540
Oy	541	gggtgctgtggccagcggcagagagtggtgtggtgagatgacccggcgggagctctcgtgc	600
Db	541	gggtgctgtggccagcggcagagagtggtgtggtgagatgacccggcgggagctctcgtgc	600
Oy	601	cacgcactgtgcacgaatgcccgttaccctgcagctgcgagaccactctgggagaccagga	660
Db	601	cacgcactgtgcacgaatgcccgttaccctgcagctgcgagaccactctgggagaccagga	660
Oy	661	cttctcttccaaacctctcctggtgcacatcacagggcaacagagctctatgacatccagct	720
Db	661	cttctcttccaaacctctcctggtgcacatcacagggcaacagagctctatgacatccagct	720
Oy	721	gttgcccaggaatctgctgtagagctgctggtaggggagagagcttggtctggaactgcacgt	780
Db	721	gttgcccaggaatctgctgtagagctgctggtaggggagagagcttggtctggaactgcacgt	780
Oy	781	gtgggtctgagtttaactcaggtgtcacctttgacttgggactaccagggagagcaggcaga	840
Db	781	gtgggtctgagtttaactcaggtgtcacctttgacttgggactaccagggagagcaggcaga	840
Oy	841	gcggggttaagtgggttcccgagcgacgcttcccgagcagaccaccaacagaactctccagcat	900
Db	841	gcggggttaagtgggttcccgagcgacgcttcccgagcagaccaccaacagaactctccagcat	900
Oy	901	cttgaccatccacaagctcagccagcacgacctgggctcgatgtgtgcaagggccaacaa	960
Db	901	cttgaccatccacaagctcagccagcacgacctgggctcgatgtgtgcaagggccaacaa	960
Oy	961	cggcatccagcgatttcgggagagcagcaggtctatgtgcatgaaalcccttccatcag	1020
Db	961	cggcatccagcgatttcgggagagcagcaggtctatgtgcatgaaalcccttccatcag	1020
Oy	1021	cgtcgagtggtctcaaaaggaccatctggagggccacgagagctcgttgaagct	1080
Db	1021	cgtcgagtggtctcaaaaggaccatctggagggccacgagagctcgttgaagct	1080
Oy	1081	gcccgtagagctggcagctaccctcccgagcttccagtggtacaaagatggaagggc	1140
Db	1081	gcccgtagagctggcagctaccctcccgagcttccagtggtacaaagatggaagggc	1140
Oy	1141	actgtccggggccacagtcacatgcccctggctcgtcagagaggtgcacagagggccagcac	1200
Db	1141	actgtccggggccacagtcacatgcccctggctcgtcagagaggtgcacagagggccagcac	1200
Oy	1201	aggcactacacctgcacctgtggaactccgctgctgagcctgagggcgcaacatccagct	1260

Db	1201	aggcaactacaccctcgcccttggaactccgtgctgctggaagcgcaacatcagcct	1260
Qy	1261	ggagctggtgtaaatgcccccagatataagaagagagcctcctccccagcat	1320
Db	1261	ggagctgggtgtaatgcccccagatataagaagagagcctcctccccagcat	1320
Qy	1321	ctactcgcgtacacgcgcagagccctcacctgcacgcgctacgggggtgcacctgacct	1380
Db	1321	ctactcgcgtacacgcgcagagccctcacctgcacgcgctacgggggtgcacctgacct	1380
Qy	1381	cagcatccagtggcactggcggccctggacaacctgcaagaatggtttgccagcgtagtct	1440
Db	1381	cagcatccagtggcactggcggccctggacaacctgcaagaatggtttgccagcgtagtct	1440
Qy	1441	ccgcgcgcgcagacagcaagacacctcatgccacagtccgtgactgagggcggtgcaccac	1500
Db	1441	ccgcgcgcgcagacagcaagacacctcatgccacagtccgtgactgagggcggtgcaccac	1500
Qy	1501	gcaggatggcgtgaacccccatcgagagcctggacacctggacccgagtttgtggagggaaa	1560
Db	1501	gcaggatggcgtgaacccccatcgagagcctggacacctggacccgagtttgtggagggaaa	1560
Qy	1561	gaataagactgtgagcaagtgtgatccagaatgccacgttgtctgcatgtacaaagt	1620
Db	1561	gaataagactgtgagcaagtgtgatccagaatgccacgttgtctgcatgtacaaagt	1620
Qy	1621	tgtggtctccaaagttggccagagatgagcggtcatctactcttatgtgcaccaacct	1680
Db	1621	tgtggtctccaaagttggccagagatgagcggtcatctactcttatgtgcaccaacct	1680
Qy	1681	ccgcgcgcgttcaccatcgaaatccaaagcattcgaggagctactagaggccagccggt	1740
Db	1681	ccgcgcgcgttcaccatcgaaatccaaagcattcgaggagctactagaggccagccggt	1740
Qy	1741	gctcctgagctgcgaagccgaacagctacaagtacgaagatctgcgctagtcaccgcctcaa	1800
Db	1741	gctcctgagctgcgaagccgaacagctacaagtacgaagatctgcgctagtcaccgcctcaa	1800
Qy	1801	cctgtccacgctgcagatgcgcaggggaacccgctctgtctgcagctcgaagaacgtgca	1860
Db	1801	cctgtccacgctgcagatgcgcaggggaacccgctctgtctgcagctcgaagaacgtgca	1860
Qy	1861	ctgtttgcgacccctctggcccgagctggaggaggtggcacctggggcgccacgc	1920
Db	1861	ctgtttgcgacccctctggcccgagctggaggaggtggcacctggggcgccacgc	1920
Qy	1921	caagctcagcctgagtatcccccggttcgcccgcagacagggcgcaactatgtgtcgga	1980
Db	1921	caagctcagcctgagtatcccccggttcgcccgcagacagggcgcaactatgtgtcgga	1980
Qy	1981	agtcgaagacgcgcagccatgacaagcacitgccacaagaagtacctgtcggltgcaggc	2040
Db	1981	agtcgaagacgcgcagccatgacaagcacitgccacaagaagtacctgtcggltgcaggc	2040
Qy	2041	cctggaagccctctggctcacgcagaaacttgaccacacctctgttggaacgtlgagcagctc	2100
Db	2041	cctggaagccctctggctcacgcagaaacttgaccacacctctgttggaacgtlgagcagctc	2100
Qy	2101	gctggagatcgagtgtgtgtggccggagcgcaacgcgccagcatctgtgtgtacaaaga	2160
Db	2101	gctggagatcgagtgtgtgtggccggagcgcaacgcgccagcatctgtgtgtacaaaga	2160
Qy	2161	cgagagctgtgaggaaagcttgagctgcacttggcgagctccaacagaagcgtgag	2220
Db	2161	cgagagctgtgaggaaagcttgagctgcacttggcgagctccaacagaagcgtgag	2220
Qy	2221	catccagcgctgcgcgagagagatgcggagcagctatctgtgcagcggtgtgcaacgcgcaa	2280
Db	2221	catccagcgctgcgcgagagagatgcggagcagctatctgtgcagcggtgtgcaacgcgcaa	2280
Qy	2281	ggctcgcgtcaactcctccgcagcgtggccgtggaaagctccgaggaagaagggcagcat	2340

Db 2281 ggactcgctcaactctctccgcagcgtggccgtggaagctccgaggaataaggcagca 2340
Qy 2341 gaagatcgatgacctgtgcgtaccgagctcatcgtctctctctctcgtggtcctctct 2400
Db 2341 gggatcgatgacctgtgcgtaccgagctcatcgtctctctctctcgtggtcctctct 2400
Qy 2401 cctcatctctgtaaatgagagggccgcccacacgacacatacaagaggggtacctgtc 2460
Db 2401 cctcatctctgtaaatgagagggccgcccacacgacacatacaagaggggtacctgtc 2460
Qy 2461 calcatcatggaccctcgaggaggtgctctctgagaggaatgcgaatacctgtctctaca 2520
Db 2461 calcatcatggaccctcgaggaggtgctctctgagaggaatgcgaatacctgtctctaca 2520
Qy 2521 tgcacagcagtggaattcccccgagagcggtgcacctgggagagtgctcggctacgg 2580
Db 2521 tgcacagcagtggaattcccccgagagcggtgcacctgggagagtgctcggctacgg 2580
Qy 2581 cgctctcggggaagtggtggaagctctcgtctcttgagcatcccaagggcagcagctgtga 2640
Db 2581 cgctctcggggaagtggtggaagctctcgtctcttgagcatcccaagggcagcagctgtga 2640
Qy 2641 caccgtggccgtgaaatgctgaaagagggcgccacgagcagcagcagcgcgcgtgat 2700
Db 2641 caccgtggccgtgaaatgctgaaagagggcgccacgagcagcagcagcgcgcgtgat 2700
Qy 2701 gtcggagctcaagatcctcatctacatcggcgaaccacctcaacgtggtcaacctctcgg 2760
Db 2701 gtcggagctcaagatcctcatctacatcggcgaaccacctcaacgtggtcaacctctcgg 2760
Qy 2761 ggcgtacacaaagccagggccctctcatggtgatcgtggaggtctctgcaatcagggaa 2820
Db 2761 ggcgtacacaaagccagggccctctcatggtgatcgtggaggtctctgcaatcagggaa 2820
Qy 2821 cctctccaaactctcgtcgccaaagcgagcctctcagccctcgccgaggaagtctcc 2880
Db 2821 cctctccaaactctcgtcgccaaagcgagcctctcagccctcgccgaggaagtctcc 2880
Qy 2881 cgagcagcgagcgtctccgagcctatggtgagctctccagagctggaatggaagatct 2940
Db 2881 cgagcagcgagcgtctccgagcctatggtgagctctccagagctggaatggaagatct 2940
Qy 2941 gggagcagcagcagggctctctcgccggttctcgaaagaccagagggcgagcgagggcg 3000
Db 2941 gggagcagcagcagggctctctcgccggttctcgaaagaccagagggcgagcgagggcg 3000
Qy 3001 ggcctctccagacaaagagctgaggaacctgtggtgagcccgctgacctatggaagatct 3060
Db 3001 ggcctctccagacaaagagctgaggaacctgtggtgagcccgctgacctatggaagatct 3060
Qy 3061 tgcctgtacagcttccaggtggccagagggatggaggttctgtggtctccgaaagtgc 3120
Db 3061 tgcctgtacagcttccaggtggccagagggatggaggttctgtggtctccgaaagtgc 3120
Qy 3121 ccacagagactggctgctcggaacattctgctgctggaaagcgagctggtggaagatctg 3180
Db 3121 ccacagagactggctgctcggaacattctgctgctggaaagcgagctggtggaagatctg 3180
Qy 3181 tgactttggccttgcgcgggacatctacaaagacctgactacgttcgcaagggcgagtcg 3240
Db 3181 tgactttggccttgcgcgggacatctacaaagacctgactacgttcgcaagggcgagtcg 3240
Qy 3241 ccggctgccccctgaagtggatggccctgaaagcatcttcgacaaggtgtacaccacgca 3300
Db 3241 ccggctgccccctgaagtggatggccctgaaagcatcttcgacaaggtgtacaccacgca 3300
Qy 3301 gagtgcgtgtggttctcttgggtgtctctctgggagatcttctctctggggccctcccc 3360
Db 3301 gagtgcgtgtggttctcttgggtgtctctctgggagatcttctctctggggccctcccc 3360
Qy 3361 gtaccctgggggtgcagatacaatgagaggttctccagcggctgagagacggcacaaggat 3420
Db 3361 gtaccctgggggtgcagatacaatgagaggttctccagcggctgagagacggcacaaggat 3420

Qy 3421 gagggcccgagctggccactcccgccatagccgcacatctgtgaaactgctggtccgg 3480
Db 3421 gagggcccgagctggccactcccgccatagccgcacatctgtgaaactgctggtccgg 3480
Qy 3481 agaccccaagcgagacacctctcggagctggtgagatcctgggggagacctgctcca 3540
Db 3481 agaccccaagcgagacacctctcggagctggtgagatcctgggggagacctgctcca 3540
Qy 3541 gggcagggcctgcaagaggaagaggtctgcatggcccgcgagctctcagagctc 3600
Db 3541 gggcagggcctgcaagaggaagaggtctgcatggcccgcgagctctcagagctc 3600
Qy 3601 agaagagggcagctctcgcaggtgtccaccatggccctacaca tgcgccaggctgcagc 3660
Db 3601 agaagagggcagctctcgcaggtgtccaccatggccctacaca tgcgccaggctgcagc 3660
Qy 3661 tgagagacggccgcaaacctgcagcgcacagcctggcccgaggtattacaactgggt 3720
Db 3661 tgagagacggccgcaaacctgcagcgcacagcctggcccgaggtattacaactgggt 3720
Qy 3721 gtcctttccgggtgcctggccagagggctgagaccccgctggttccctccagatgaagac 3780
Db 3721 gtcctttccgggtgcctggccagagggctgagaccccgctggttccctccagatgaagac 3780
Qy 3781 attgaggaattcccatgaccccaacgacctacaaaggtctctgagacaaccagacaga 3840
Db 3781 attgaggaattcccatgaccccaacgacctacaaaggtctctgagacaaccagacaga 3840
Qy 3841 cagtggatggtgctggtcgtcgagaggtttgagcagatagagagcaggtggttttaca 3900
Db 3841 cagtggatggtgctggtcgtcgagaggtttgagcagatagagagcaggtggttttaca 3900
Qy 3901 aagcgcttcagctgtaaaggacctggccagaaatggtgctgtgaccagggcacacctga 3960
Db 3901 aagcgcttcagctgtaaaggacctggccagaaatggtgctgtgaccagggcacacctga 3960
Qy 3961 ctcccaagggagcgcgcgccctgagcggggcccgagagccaggtggttttaca 4020
Db 3961 ctcccaagggagcgcgcgccctgagcggggcccgagagccaggtggttttaca 4020
Qy 4021 cagcagtatggggagctgctcgagcgaagcgaagcagagaccactgctccccgctgccc 4080
Db 4021 cagcagtatggggagctgctcgagcgaagcgaagcagagaccactgctccccgctgccc 4080
Qy 4081 cgtgactttcttcacagacaacagctactaa 4111
Db 4081 cgtgactttcttcacagacaacagctactaa 4111

RESULT 4

AAC68952

ID AAC68952 standard; cDNA; 4111 BP.

XX AAC68952;

XX 27-FEB-2001 (first entry)

XX Human Flt4/VEGFR-3 coding sequence.

XX Human; gene therapy; lymphatic disorder; hereditary lymphoedema; Flt4;
KW vascular endothelial growth factor receptor-3; VEGFR-3; VEGF-D;
KW fms-like tyrosine kinase 4; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT 20..4111

FT /*tag= a

FT /product= "Human Flt4/VEGFR-3"

XX CA2283470-A1.

XX

Db 1501 gcaaggatgcggtgaaccccatcgagagcctggacacctggacccagtttctgtggaaggaaa 1560

Qy 1561 gaataagactgtagcaagctggtgatccagaatgccaactgcttgccatgtacaagtg 1620

Db 1561 gaataagactgtagcaagctggtgatccagaatgccaactgcttgccatgtacaagtg 1620

Qy 1621 tctggtctccaacaagttggccagagatagcggctcatctacttctatgtacaacct 1680

Db 1621 tctggtctccaacaagttggccagagatagcggctcatctacttctatgtacaacct 1680

Qy 1681 ccccgagcgtctcaccatcgaaatccaaagccatccgaggagctactagagggccagccgt 1740

Db 1681 ccccgagcgtctcaccatcgaaatccaaagccatccgaggagctactagagggccagccgt 1740

Qy 1741 gctcctgagctgccaagcgcaagctacaagtacagagatctgctgtgtaccgctcaa 1800

Db 1741 gctcctgagctgccaagcgcaagctacaagtacagagatctgctgtgtaccgctcaa 1800

Qy 1801 cctgtccaagctgacgatgcgcacgggaaccgctctctgctcgactgcaagaacgtgca 1860

Db 1801 cctgtccaagctgacgatgcgcacgggaaccgctctctgctcgactgcaagaacgtgca 1860

Qy 1861 tctgttgcgaacccctctggccgcagcctggaggaggtggcacctggggcgccacgc 1920

Db 1861 tctgttgcgaacccctctggccgcagcctggaggaggtggcacctggggcgccacgc 1920

Qy 1921 caagctcaagctgagtatcccccgctgcgcgccagacaggggccatactgtgtgca 1980

Db 1921 caagctcaagctgagtatcccccgctgcgcgccagacaggggccatactgtgtgca 1980

Qy 1981 agtgcgaagccggcgacgcaatgacaagcacltgcacaagaagtacctgctggtgcagc 2040

Db 1981 agtgcgaagccggcgacgcaatgacaagcacltgcacaagaagtacctgctggtgcagc 2040

Qy 2041 cctggaagccctcggtctcaagcagaacttgaccgacctccttggtaacgctgagcgactc 2100

Db 2041 cctggaagccctcggtctcaagcagaacttgaccgacctccttggtaacgctgagcgactc 2100

Qy 2101 gctggaagatgcagtgcttggtagccgagcgacgcgccagcatcgtgtgtacaaaqa 2160

Db 2101 gctggaagatgcagtgcttggtagccgagcgacgcgccagcatcgtgtgtacaaaqa 2160

Qy 2161 cgaagagctgctggaagaaagtctggatcgacttggcgagctccaacgaagctgag 2220

Db 2161 cgaagagctgctggaagaaagtctggatcgacttggcgagctccaacgaagctgag 2220

Qy 2221 catccaagcgtgctgcgagagagatgcgggaagctatctgtgcagcgtgtgcaacgccea 2280

Db 2221 catccaagcgtgctgcgagagagatgcgggaagctatctgtgcagcgtgtgcaacgccea 2280

Qy 2281 gggctcgctcaactctccgcagcgtgccgtggaagctccgaggataaaggcagcat 2340

Db 2281 gggctcgctcaactctccgcagcgtgccgtggaagctccgaggataaaggcagcat 2340

Qy 2341 ggagatcgtgatlcttctgctggtaccggcgtcatcgctgtcttcttctgggtcctcctct 2400

Db 2341 ggagatcgtgatlcttctgctggtaccggcgtcatcgctgtcttcttctgggtcctcctct 2400

Qy 2401 cctcatcttctgtaacatgagagggccggccacgcagacatacaagaagggtaacctgtc 2460

Db 2401 cctcatcttctgtaacatgagagggccggccacgcagacatacaagaagggtaacctgtc 2460

Qy 2461 catcatcatggaccggggaggtgcctctggaggagcaatgcgaataaccttctactaga 2520

Db 2461 catcatacaggaccggggaggtgcctctggaggagcaatgcgaataaccttctactaga 2520

Qy 2521 tgcagagccagtgaggaaatcccccgagagcgctgcacctggggagagtgctcggctacqg 2580

Db 2521 tgcagagccagtgaggaaatcccccgagagcgctgcacctggggagagtgctcggctacqg 2580

Qy 2581 cgccttcgggaaggtggtggaagcctccgcttctcgycatccacaagggcagcayctgta 2640

Db 2581 cgccttcgggaaggtggtggaagcctccgcttctcggcataccacaagggcagcayctgta 2640

Qy 2641 caccgtggccgtgaaaaatgctgaaagaggcgccacggcgagcaccgcgctgat 2700

Db 2641 caccgtggccgtgaaaaatgctgaaagaggcgccacggcgagcaccgcgctgat 2700

Qy 2701 gtcgagatcgaagtccctcattccatcggcaaacacacctcaacgtgttcaacctcctcgg 2760

Db 2701 gtcgagatcgaagtccctcattccatcggcaaacacacctcaacgtgttcaacctcctcgg 2760

Qy 2761 ggcgtgcaccaagcgcgaggggccctctcatggtatcgtgagttcttcaagtagcgcaa 2820

Db 2761 ggcgtgcaccaagcgcgaggggccctctcatggtatcgtgagttcttcaagtagcgcaa 2820

Qy 2821 cctctccaacttctctgctgcgcgcaagcggaacgcttcaagccctctgcgggaaagtctcc 2880

Db 2821 cctctccaacttctctgctgcgcgcaagcggaacgcttcaagccctctgcgggaaagtctcc 2880

Qy 2881 cgagcagcgcgagcgttccgcgcatggtgagctcgcgaagcttggatcggagcgcc 2940

Db 2881 cgagcagcgcgagcgttccgcgcatggtgagctcgcgaagcttggatcggagcgcc 2940

Qy 2941 ggggagcagcgacagggctctcttcgcgcttctcgaagaccggaggcgagcg 3000

Db 2941 ggggagcagcgacagggctctcttcgcgcttctcgaagaccggaggcgagcg 3000

Qy 3001 ggcctctccagaccagaagctgaggaacctgtggtgagccgctlgacatggaaagtct 3060

Db 3001 ggcctctccagaccagaagctgaggaacctgtggtgagccgctlgacatggaaagtct 3060

Qy 3061 tctctgctacagcttccaggtggccagaggtgaggttccctggcttcccgaagtgcac 3120

Db 3061 tctctgctacagcttccaggtggccagaggtgaggttccctggcttcccgaagtgcac 3120

Qy 3121 ccacagagacctggctgtctcggaacatctctgctgctggaagcgacgtggtaagatctg 3180

Db 3121 ccacagagacctggctgtctcggaacatctctgctgctggaagcgacgtggtaagatctg 3180

Qy 3181 tgactttggccttcccgggacatctacaagacctgactacgcccgaagggcgagtcg 3240

Db 3181 tgactttggccttcccgggacatctacaagacctgactacgcccgaagggcgagtcg 3240

Qy 3241 ccggctgccccgaagtggatgggccccgaagcaatcttcgaagaagtgtcacacacgca 3300

Db 3241 ccggctgccccgaagtggatgggccccgaagcaatcttcgaagaagtgtcacacacgca 3300

Qy 3301 gagtgaactgtgttcccttgggggtctctctggaagatcttctctgagggtccccc 3360

Db 3301 gagtgaactgtgttcccttgggggtctctctggaagatcttctctgagggtccccc 3360

Qy 3361 gtaccctgggtgcagatcaatgagaggttctgcccagcgctgagagacgcacaaggat 3420

Db 3361 gtaccctgggtgcagatcaatgagaggttctgcccagcgctgagagacgcacaaggat 3420

Qy 3421 gagggccccgagctggccactcccgcatacgcgcgcatcatgtgaaactcgtggtccgg 3480

Db 3421 gagggccccgagctggccactcccgcatacgcgcgcatcatgtgaaactcgtggtccgg 3480

Qy 3481 aaaccccaagcgagacctgcatcttcggagctggtgagatccttggggacctgtctcca 3540

Db 3481 aaaccccaagcgagacctgcatcttcggagctggtgagatccttggggacctgtctcca 3540

Qy 3541 gggcaggggctgcaagaggaagaggttctgcatggccccgcgcagctctcagagctc 3600

Db 3541 gggcaggggctgcaagaggaagaggttctgcatggccccgcgcagctctcagagctc 3600

Qy 3601 agaagaggcgacttctcgaggtgtccacatggccctcacatcgccccaggtgcagcg 3660

Db 3601 agaagaggcgacttctcgaggtgtccacatggccctcacatcgccccaggtgcagcg 3660

Qy 3661 tgaagacagccgcgaagcctgcagcgccacagcctggcccgaggtattacaactgggt 3720

Db 3661 tgaagacagccgcgaagcctgcagcgccacagcctggcccgaggtattacaactgggt 3720

2881 caagcagcgcgaacgcttccgcgcacatggtggagctccaccaggctggatcagagacaccc 2940
|||||
2881 cgagcagcgcgcagccttccgcgcacatggtggagctccaccaggctggatcagagcgcgc 2940
|||||
2941 qggagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 3000
|||||
2941 qggagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 3000
|||||
3001 gacttctccagacacgaagctgaggaacctgtggtgagcccgctgacacatggaagatct 3060
|||||
3001 gacttctccagacacgaagctgaggaacctgtggtgagcccgctgacacatggaagatct 3060
|||||
3061 tctctgactacaacttccaggtgagcagagagatgagttcctgcttcccgaaagtgcac 3120
|||||
3061 tctctgactacaacttccaggtgagcagagagatgagttcctgcttcccgaaagtgcac 3120
|||||
3121 ccacagagacctggctgcgggaacatctctgctgcgaaagcagctgggtgaaadatctg 3180
|||||
3121 ccacagagacctggctgcgggaacatctctgctgcgaaagcagctgggtgaaadatctg 3180
|||||
3181 tgacttggccttgcggggagacatctacaaagacacctgactacgtcccaagggcaqtgc 3240
|||||
3181 tgacttggccttgcggggagacatctacaaagacacctgactacgtcccaagggcaqtgc 3240
|||||
3241 ccggctgcggcctgaagtgagtgagcgcctcgaaagcagcttccgacaagcagcagcagc 3300
|||||
3241 ccggctgcggcctgaagtgagtgagcgcctcgaaagcagcttccgacaagcagcagcagc 3300
|||||
3301 gaggtaagctgtggtcttcttctctctctctctctctctctctctctctctctctctct 3360
|||||
3301 gaggtaagctgtggtcttct 3360
|||||
3361 ctacctgggggtgcagatacaatgagaggttctgcagcggctgagagcagcagcagagat 3420
|||||
3361 ctacctgggggtgcagatacaatgagaggttctgcagcggctgagagcagcagcagagat 3420
|||||
3421 gaggcccccggagctggccacatcccgccatcacgcgcgcatctgtaactgctggtccgg 3480
|||||
3421 gaggcccccggagctggccacatcccgccatcacgcgcgcatctgtaactgctggtccgg 3480
|||||
3481 agaccccaaggcagacactgcattctcggagctggtgagatctctcggggggaacctgtcca 3540
|||||
3481 agaccccaaggcagacactgcattctcggagctggtgagatctctcggggggaacctgtcca 3540
|||||
3541 gggcaggggcttcgaaggaagagaggtctgcatggcccgccagctctcagagctc 3600
|||||
3541 gggcaggggcttcgaaggaagagaggtctgcatggcccgccagctctcagagctc 3600
|||||
3601 aagaagggcagcttctcgcaggtgtccaccatggccctacacatcgcgccagctgcagc 3660
|||||
3601 aagaagggcagcttctcgcaggtgtccaccatggccctacacatcgcgccagctgcagc 3660
|||||
3661 taagagagccgcgaagcctgcagcagccacagacgctgcccgaagatattacaactgggt 3720
|||||
3661 taagagagccgcgaagcctgcagcagccacagacgctgcccgaagatattacaactgggt 3720
|||||
3721 gtccttcccggtgcttgccagaggggctgagaccgctggttctccagagataaagac 3780
|||||
3721 gtccttcccggtgcttgccagaggggctgagaccgctggttctccagagataaagac 3780
|||||
3781 attgaggaattccccatgacccccacacacacacacacacacacacacacacacacacacac 3840
|||||
3781 attgaggaattccccatgacccccacacacacacacacacacacacacacacacacacacac 3840
|||||
3841 cagtgaggtggtgctggcctcggaagagtttaagcagatagagacagcagcagcatagacaaga 3900
|||||
3841 cagtgaggtggtgctggcctcggaagagtttaagcagatagagacagcagcagcatagacaaga 3900
|||||
3901 aagcggcttcag 3912
|||||
3901 aagcggcttcag 3912
|||||

RESULT 6
AAZ52333
ID AAZ52333 standard; cDNA; 4195 BP.
XX
AC AAZ52333;
XX
DT 17-AUG-2000 (first entry)
XX
DE Human tyrosine kinase receptor Flt4-short form cDNA.
XX
KW Human; receptor tyrosine kinase; RTK; Flt4; fms-like tyrosine kinase 4;
VEGFR-3; vascular endothelial growth factor receptor-3; chromosome 5q35;
cytostatic; tumour imaging; anti-tumour therapy; treatment; diagnosis;
neoplastic disease; lymphoma; carcinoma; breast; squamous cell; melanoma;
sarcoma; malignancy; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
CDS 20..3916
FT /*tag= a
FT /product= "Flt4 receptor-short form"
FT /note= "The start codon is surrounded by typical
consensus kozak sequence"
FT 20..79
FT sig_peptide /*tag= b
FT /note= "Directs protein to endoplasmic reticulum"
FT 80..3913
FT mat_peptide /*tag= c
FT /product= "Mature Flt4 receptor-short form"
XX
PN WO200021560-A1.
XX
PD 20-APR-2000.
XX
PF 08-OCT-1999; 99WO-US23525.
XX
PR 09-OCT-1998; 98US-0169079.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
PA (UYHE-) UNIV HELSINKI LICENSING LTD OY.
XX
PI Alitaio K, Kaipainen A, Valltoia R, Jussila L;
XX
DR WPI: 2000-317850/27.
DR P-PSDB; RAY70746.
XX
PT Treating neoplastic diseases such as lymphoma, carcinomas, melanomas
and sarcomas, involves administering a compound capable of inhibiting
binding of ligand proteins to fms-like tyrosine kinase-4 receptor .
XX
PS Example 14; Page 109-115; 148pp; English.
XX
CC The patent discloses a method to treat neoplastic disease characterised
by expression of fms-like tyrosine kinase 4 (Flt4) receptor (also
referred as vascular endothelial growth factor receptor-3, VEGFR-3) in
endothelial cells of blood vessels adjacent to malignant neoplasm. The
method involves administering a compound that inhibits binding of a
ligand to Flt4 thereby inhibiting Flt4 mediated proliferation of vascular
endothelial cells. The compound is useful for treating neoplastic disease
such as breast carcinomas, squamous cell carcinomas, lymphomas, melanomas
and sarcomas. Flt4 receptor tyrosine kinase binding compounds can be used
for manufacturing medicament useful for diagnostic screening, imaging and
treatment of malignancies characterised by Flt4-expressing blood cells.
CC The present sequence is a cDNA encoding the short form of Flt4 receptor
from an oligo-dr primed human erythroleukaemia cell line (HEL) cDNA
library in bacteriophage lambda g11. The Flt4 gene maps to chromosomal
region 5q35 and is expressed as 5.8 kb and 4.5 kb mRNAs which differ in
their 3' sequences and are differentially expressed in HEL and DAMI cell
lines. Flt4 belongs to a subfamily of class III receptor tyrosine kinases
(RTKs). It is used as a target for tumour imaging and anti-tumour
therapy.
CC

[illegible]

Db 2041 cctggaagccctcggctcacgcagaaacttgaccgacctctcctggtgaacgtgagcactc 2100
Qy 2101 gctggagatgagatgcttggctggccggagcgacagcgccccagatcgtgctggtacaaaga 2160
Db 2101 gctggagatgagatgcttggctggccggagcgacagcgccccagatcgtggtgacaaaga 2160
Qy 2161 cgagagggctgctggaggaagaagctcgagtgacgttggcgacttccaccagaagctgag 2220
Db 2161 cgagagggctgctggaggaagaagctcgagtgacgttggcgacttccaccagaagctgag 2220
Qy 2221 catccaacgctgcgcggaggaggatgcgggacgctatctgtgcagcgtggtgcaacgccaa 2280
Db 2221 catccagcgcgtgcgcggaggaggatgcgggacgctatctgtgcagcgtggtgcaacgccaa 2280
Qy 2281 gggctgcatcaactcctccgcagcgtgacgttggaagagctccagagataaggcagcat 2340
Db 2281 gggctgcatcaactcctccgcagcgtgacgttggaagagctccagagataaggcagcat 2340
Qy 2341 aaaaatcgtgatacctctgctggtaccggcgctcatcgctgcttcttctggttccrctcct 2400
Db 2341 gggatcgtgatacctctgctggtaccggcgctcatcgctgcttcttctggttccrctcct 2400
Qy 2401 cctcatctctgatacatgagaggagccggcccaacgacagacatcaagacgggctaacctgtc 2460
Db 2401 cctcatctctgatacatgagaggagccggcccaacgacagacatcaagacgggctaacctgtc 2460
Qy 2461 catcatcgtgaccccgaggaggtgcctctctggaagagcaatgcgaataacctgtctcaca 2520
Db 2461 catcatcgtgaccccgaggagggtgcctctctggaagagcaatgcgaataacctgtctcaca 2520
Qy 2521 tgcacgcagctgggaattccccccgagagcgctgcacctggggagtgctcgcgtacgg 2580
Db 2521 tgcacgcagctgggaattccccccgagagcgctgcacctggggagtgctcgcgtacgg 2580
Qy 2581 cgccttcgggaaggtggtggaagctccgcgttcctgggcatccacaaggcgacagctgtga 2640
Db 2581 cgccttcgggaaggtggtggaagctccgcgttcctgggcatccacaaggcgacagctgtga 2640
Qy 2641 caccgtggccgtgaaatgctgaaagaggcgccacgagcgacgacccgcgcgtgat 2700
Db 2641 caccgtggccgtgaaatgctgaaagaggcgccacgagcgacgacccgcgcgtgat 2700
Qy 2701 gtcgagctcaagatcctcatctcaatcgcgcgaacacacctcaacgtggtcgaacctctcgg 2760
Db 2701 gtcgagctcaagatcctcatctcaatcgcgcgaacacacctcaacgtggtcgaacctctcgg 2760
Qy 2761 ggcgtgcaccagccgcagggcccccctcatggtgatcgtgagttcttcaagatcagcga 2820
Db 2761 ggcgtgcaccagccgcagggggcccccctcatggtgatcgtgagttcttcaagatcagcga 2820
Qy 2821 cctctcccaactctctgcgcgaagcgggacgccttcagccrctgcgcggaagaagctcc 2880
Db 2821 cctctcccaactctctgcgcgaagcgggacgccttcagccrctgcgcggaagaagctcc 2880
Qy 2881 cgagcagcgaggacgcttcgcgcgcattggtgagctgcagggcttggtatcgagcgcc 2940
Db 2881 cgagcagcgaggacgcttcgcgcgcattggtgagctgcagggcttggtatcgagcgcc 2940
Qy 2941 ggggagagcagacagggcttcctcttcgcgcggttcttcaaaacccgagggcgagcgagcg 3000
Db 2941 ggggagagcagacaggggttcctcttcgcgcggttcttcaaaacccgagggcgagcgagcg 3000
Qy 3001 ggcctctccagaccaaagatgaggacgttggtgagcccgctgcaccatggaagatct 3060
Db 3001 ggcctctccagaccaaagatgaggacgttggtgagcccgctgcaccatggaagatct 3060
Qy 3061 tctctgtacagcttccaggctgcgcagaggatggagttccttggtctcccgaaaagtgc 3120
Db 3061 tctctgtacagcttccaggctgcgcagaggatggagttccttggtctcccgaaaagtgc 3120
Qy 3121 ccacagagacctgctgctcggaacattctgctgcgaaagcagcgtggtggaagatctg 3180
Db 3121 ccacagagacctgctgctcggaacattctgctgcgaaagcagcgtggtggaagatctg 3180

Qy 3181 tgaatttggccttgcccgggacatctacaaagaccctgactacgctccgcaaggcgactgc 3240
Db 3181 tgaatttggccttgcccgggacatctacaaagaccctgactacgctccgcaaggcgactgc 3240
Qy 3241 ccgctgcgccctgaagtggatggccctgaaagcatcttcgacaaggtgtacaccacgca 3300
Db 3241 ccgctgcgccctgaagtggatggccctgaaagcatcttcgacaaggtgtacaccacgca 3300
Qy 3301 gagtgaagctgtggttcctttggggtgctctctctggtggaatcttctctggtgggctcccc 3360
Db 3301 gagtgaagctgtggttcctttggggtgctctctctggtggaatcttctctggtgggctcccc 3360
Qy 3361 gtacccctggggtgcagatcaatgagggttctgcacggctgagagcggtgacaaagat 3420
Db 3361 gtacccctggggtgcagatcaatgagggttctgcacggctgagagcggtgacaaagat 3420
Qy 3421 gagggcccgagctggccactcccgccatcagccgcgcatcgtgtaactgctggttcctgg 3480
Db 3421 gagggcccgagctggccactcccgccatcagccgcgcatcgtgtaactgctggttcctgg 3480
Qy 3481 agacccaaagcgagacctgcattctcggagctggttgagatcctctggtgggacctgtcca 3540
Db 3481 agacccaaagcgagacctgcattctcggagctggttgagatcctctggtgggacctgtcca 3540
Qy 3541 gggcaggggctcgaagagaaagaggaggtctgcattgqccccgcgcagctctcagagctc 3600
Db 3541 gggcaggggctcgaagagaaagaggaggtctgcattgqccccgcgcagctctcagagctc 3600
Qy 3601 agaagaggagcttctcgcaggtgtccacatggtcccatggtccctacacatcgcccaggctgacgc 3660
Db 3601 agaagaggagcttctcgcaggtgtccacatggtcccatggtccctacacatcgcccaggctgacgc 3660
Qy 3661 tgaagacagcccgccaagcctgcagcgccacagcctgagcagctggcgccaactgggt 3720
Db 3661 tgaagacagcccgccaagcctgcagcgccacagcctgagcagctggcgccaactgggt 3720
Qy 3721 gtcctttcccggtgcttgccagagggtgagaccgtggttctcctccagatgaagac 3780
Db 3721 gtcctttcccggtgcttgccagagggtgagaccgtggttctcctccagatgaagac 3780
Qy 3781 atttgagaaattccccatgaccccaagcactacaaaggctctgtggaaccaaccagacaga 3840
Db 3781 atttgagaaattccccatgaccccaagcactacaaaggctctgtggaaccaaccagacaga 3840
Qy 3841 cagtggagatgctgcctcgagaggtttgaacacatgagagcagcgcatagacaga 3900
Db 3841 cagtggagatgctgcctcgagaggtttgaacacatgagagcagcgcatagacaga 3900
Qy 3901 aagcggttccag 3912
Db 3901 aagcggttccag 3912

RESULT 7
AAT03090
ID AAT03090 standard; DNA; 4425 BP.
XX
AC AAT03090;
XX
DT 14-FEB-1996 (first entry)
XX
DE Protein tyrosine-kinase SAL-S1 gene.
XX
KW Protein tyrosine-kinase; pTK; SAL-S1; agonist; cell growth;
XX differentiation; ss.
XX Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 30..3927
FT /*tag= a
FT sig_peptide 30..102

FT mat_peptide /*tag= b 103..3924
FT /*tag= c
XX
PN W09527061-A1.
XX
PD 12-OCT-1995.
XX
PF 04-APR-1995; 95WO-US04228.
XX
PR 04-APR-1994; 94US-0222616.
XX
PA (GETH) GENENTECH INC.
XX
PI Bennett BD, Goeddel D, Lee JM, Matthews W, Tsai SP;
Wood WJ;
XX
DR WPI; 1995-366160/47.
XX
DR P-PSDB; AAR85937.
XX
XX
XX Agonist antibodies which activate specific protein tyrosine
PT kinases) - also activate chimeric proteins of kinase extracellular
PT domain and ig constant domain, useful for studying, and therapeutic
PT modulation of, cell growth and differentiation
XX
PS Disclosure; Fig 15A-F; 125pp; English.
XX
XX
CC DNA probes based on protein tyrosine-kinase (pTK) sequences were used
CC to screen cDNA libraries to identify novel pTK genes. The SAL-S1
CC gene (see also AAT03101) was isolated from several megakaryocytic cell
CC libraries. The gene can be used to produce recombinant SAL-S1 or its
CC fragments, to detect related genes, and to design drugs, peptides
CC or antisense nucleotides that modulate pTK activity.
XX
XX Sequence 4425 BP; 939 A; 1348 C; 1361 G; 777 T; 0 other;

Query Match 95.2%; Score 3912; DB 16; Length 4425;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3912; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 cxaacgcagcgcgcgagagatcagcggggccgcgcgtgctgacctgactgtgactctg 60
Db |||||
OY 12 ccaacgcagcgcgcgagatcagcggggccgcgcgtgctgacctgactgtgactctg 71
Db |||||
OY 61 cctggagctccctgagcgcctgagtgagtgactcctacatgacccccgcacctgaacat 120
Db |||||
OY 72 cctggagctccctgagcgcctgagtgagtgactcctacatgacccccgcacctgaacat 131
OY 121 cacqagagagtcacacgtcatcgcacaccggtgacagcctgtcctctcctgcaqgqaca 180
Db |||||
OY 132 cacqagagagtcacacgtcatcgcacaccggtgacagcctgtcctctcctgcaqgqaca 191
OY 181 gacccccctcagtgaggcttgccagagctcagagcgccagccacccagagacaaaga 240
Db |||||
OY 192 gacccccctcagtgaggcttgccagagctcagagcgccagccacccagagacaaaga 251
OY 241 cagcagagacacgggggtggtgctgcagactgcagagggcacagcgcagccctactgcaa 300
Db |||||
OY 252 cagcagagacacgggggtggtgctgcagactgcagagggcacagcgcagccctactgcaa 311
OY 301 ggtgtgtcgtgctgcagaggtacatgccaacgacacagcagcagctcgtctgactacaa 360
Db |||||
OY 312 ggtgtgtcgtgctgcagaggtacatgccaacgacacagcagcagctcgtctgactacaa 371
OY 361 gtacatcaaggcacgcacatcagaggcaccacgcgcgcagcctcctcgtctgaaaga 420
Db |||||
OY 372 gtacatcaaggcacgcacatcagaggcaccacgcgcgcagcctcctcgtctgaaaga 431
OY 421 ctttgagcagccatcatcaacaacgtgacacgctcttggtcaacagaaagacgcccac 480
Db |||||
OY 432 ctttgagcagccatcatcaacaacgtgacacgctcttggtcaacagaaagacgcccac 491

OY 481 gtgggtgccctgtctgtgtgtccatccccggcctcaatgtcacgctgcgctcgcaaaagctc 540
Db |||||
OY 492 gtgggtgccctgtctgtgtgtccatccccggcctcaatgtcacgctgcgctcgcaaaagctc 551
OY 541 ggtctgtggccagacgcggcagaggtggtgtgagtgacgcggcgagcaltgctcgtgtc 600
Db |||||
OY 552 ggtctgtggccagacgcggcagaggtggtgtgagtgacgcggcgagcaltgctcgtgtc 611
OY 601 cagccactgctgcacgagtccctgtacctgtacctgtacctgtcautgagaccacctggggagaccagga 660
Db |||||
OY 612 cagccactgctgcacgagtccctgtacctgtacctgtacctgtcautgagaccacctggggagaccagga 671
OY 661 cttctttccaaaccccttctctgtgtgcacatcacaggcaacgagctctatgacatccagct 720
Db |||||
OY 672 cttctttccaaaccccttctctgtgtgcacatcacaggcaacgagctctatgacatccagct 731
OY 721 gttgcccagggaagtgcgtggagctgctggtaggggagaagctggtcttgaactgcacct 780
Db |||||
OY 732 gttgcccagggaagtgcgtggagctgctggtaggggagaagctggtcttgaactgcacct 791
OY 781 gttgggtgagtttaactcaggtgtcaactttgactgggactaccaggggaagcaggcaga 840
Db |||||
OY 792 gttgggtgagtttaactcaggtgtcaactttgactgggactaccaggggaagcaggcaga 851
OY 841 gcggggtaaagtgggtgcccagacgcctcccagacacccacacagaaactctccagat 900
Db |||||
OY 852 gcggggtaaagtgggtgcccagacgcctcccagacacccacacagaaactctccagat 911
OY 901 cctgacctacacacgtcagccagcagcagctgggctcgatgtgtgcaaggccacaa 960
Db |||||
OY 912 cctgacctacacacgtcagccagcagcagctgggctcgatgtgtgcaaggccacaa 971
OY 961 cggcatccagcagatttcgggagagacccagaggtcatgtgcatgaaatcccttccatcag 1020
Db |||||
OY 972 cggcatccagcagatttcgggagagacccagaggtcatgtgcatgaaatcccttccatcag 1031
OY 1021 cgtcgagtggtcctaaaggaccatccttgaggccacgcagcagagcagctggtgaaagct 1080
Db |||||
OY 1032 cgtcgagtggtcctaaaggaccatccttgaggccacgcagcagcagcagctggtgaaagct 1091
OY 1081 gccctggaagctgacagcgtaccctccgcgcgcagltccagtggtacaaaggatgaaaggc 1140
Db |||||
OY 1092 gccctggaagctgacagcgtaccctccgcgcgcagltccagtggtacaaaggatgaaaggc 1151
OY 1141 actgtccgggcgcacacagtcacatgccctggtgtcctcaagaggtgacagagccagcagc 1200
Db |||||
OY 1152 actgtccgggcgcacacagtcacatgccctggtgtcctcaagaggtgacagagccagcagc 1211
OY 1201 aggcacctacacctcgccctgtggaactccgctgctggcctgagggcgcaacatcagcct 1260
Db |||||
OY 1212 aggcacctacacctcgccctgtggaactccgctgctggcctgagggcgcaacatcagcct 1271
OY 1261 ggaagctggtgtaagtgtccccccagatacatgaaagagagcctctctcccccagcat 1320
Db |||||
OY 1272 ggaagctggtgtaagtgtccccccagatacatgaaagagagcctctctcccccagcat 1331
OY 1321 ctactcgcgtcacagcgcagcagccctcactcgcagcctacgcgggtgcccctgcctct 1380
Db |||||
OY 1332 ctactcgcgtcacagcgcagcagccctcactcgcagcctacgcgggtgcccctgcctct 1391
OY 1381 cagcatccagtggcactggcgcgccttgacacctgcaagatgtttgcccagcgtactct 1440
Db |||||
OY 1392 cagcatccagtggcactggcgcgccttgacacctgcaagatgtttgcccagcgtactct 1451
OY 1441 ccggcgcgcgagcagcagaagacctcatgcacagtgccgtgactggagggcggtgaccac 1500
Db |||||
OY 1452 ccggcgcgcgagcagcagaagacctcatgcacagtgccgtgactggagggcggtgaccac 1511
OY 1501 gcaggaatgcctgaaacccatcagagagcctgacacctggaccctggttggaggggaaa 1560
Db |||||
OY 1512 gcaggaatgcctgaaacccatcagagagcctggaacctggaccctggttggaggggaaa 1571
OY 1561 gaataagactgtgagcagctggtgatccagaatgccaaagctgtctgcatgtaacaagt 1620

Db	4304	gtaccctgggggtgcagatcaatgagaggtctctgcccagcgctgagagagcgccacaaggat	4363
Qy	3421	gagggcccgagagctggccactcccccataccgcatcatctgaactgctggtccgg	3480
Db	4364	gagggcccgagctggccactcccccataccgcatcatctgaactgctggtccgg	4423
Qy	3481	agaccccaagggagagacctgcatctcggagctgggtggagatcctggggagacctgctca	3540
Db	4424	agaccccaagggagagacctgcatctcggagctgggtggagatcctggggagacctgctca	4483
Qy	3541	ggcgaggggctcgaagagaaagagaggtctctcatggcccgcgcagctctcagagctc	3600
Db	4484	ggcgaggggctcgaagagaaagagaggtctctcatggcccgcgcagctctcagagctc	4543
Qy	3601	agaagaggcgagctctcgcaggtgtccaccatggccctacacatcgcgcagctgacgc	3660
Db	4544	agaagaggcgagctctcgcaggtgtccaccatggccctacacatcgcgcagctgacgc	4603
Qy	3661	tgagagagcccgcccaagctcgagcgccacagcctggccgcaggtattacaactgggt	3720
Db	4604	tgagagagcccgcccaagctcgagcgccacagcctggccgcaggtattacaactgggt	4663
Qy	3721	gtccttcccggtgctcgtgccagaggggtgagaccctgggttctctccaggatgaagac	3780
Db	4664	gtccttcccggtgctcgtgccagaggggtgagaccctgggttctctccaggatgaagac	4723
Qy	3781	atttgaggaaatcccatgaccccaacagacctacaaaggctctgtggacaaccagacaa	3840
Db	4724	atttgaggaaatcccatgaccccaacagacctacaaaggctctgtggacaaccagacaa	4783
Qy	3841	caatggagatgctgagctcgagagatttgagcagatagagagcagacatagacaa	3900
Db	4784	caatggagatgctgagctcgagagatttgagcagatagagagcagacatagacaa	4843
Qy	3901	aagcgcttcag	3912
Db	4844	aagcgcttcag	4855

RESULT 9

AAT12068	
IN	AAT12068 standard; DNA; 4195 BP.
XX	
AC	AAT12068;
XX	
DT	08-APR-1996 (first entry)
XX	
DE	FLT4 receptor tyrosine kinase DNA.
XX	
KW	FLT4; receptor tyrosine kinase; probe; metastasis; lymphoma;
KW	lymphangioma; immunological disease; cancer; diagnosis; therapy; ss.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	Location/Qualifiers
CDS	20..3976
FT	/*tag= a
XX	
PN	W09533772-A1.
XX	
PD	14-DEC-1995.
XX	
PF	09-JUN-1995: 95WO-FI00337.
XX	
PR	09-JUN-1994: 94US-0257754.
XX	
PA	(ALIT/) ALITALO K.
PA	(KAIP/) KAIPAINEN A.
PA	(KARN/) KARNANI P.
PA	(KORH/) KORHONEN J.
PA	(MATI/) MATIKAINEN M.
PA	(MUST/) MUSTONEN T.
PA	(PAJU/) PAJUSOLA K.

XX	Alitalo K, Kaipainen A, Karnani P, Korhonen J, Matikainen M;
PI	Mustonen T, Pajusola K;
XX	
DR	WPI: 1996-040189/04.
DR	P-PSDB; AAR90528.
XX	
PT	Antibodies against FLT4 receptor tyrosine kinase, hybridomas and
PT	nucleic acid probes - used to diagnose and treat e.g. metastatic
PT	cancers, involving alterations to lymphatic vessels.
XX	
PS	Claim 9; Page 27-33; 54pp; English.
XX	
CC	A DNA sequence (AAT12068) coding for FLT4 receptor tyrosine kinase
CC	(AAR90528) is used as a probe that specifically binds/hybridizes to
CC	DNA encoding human FLT4. Such probes are used to detect FLT4, a
CC	novel marker for lymphatic vessels and some high endothelial
CC	venules, in biological tissue for use in diagnosis and therapy of
CC	e.g. inflammatory, infectious and immunological diseases, metastatic
CC	lymph nodes and lymphangiomas.
XX	
SQ	Sequence 4195 BP: 889 A; 1278 C; 1305 G; 723 T; 0 other;

Query Match 93.9%; Score 3861; DB 17; Length 4195;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 3911; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	ccacgcgacgcccggagatgcagcggcgccgcgctgtgctgcgactgtgctctg	60
Db	1	ccacgcgacgcccggagatgcagcggcgccgcgctgtgctgcgactgtgctctg	60
Qy	61	ctctggactccttggacggcctggtagtggtctactccatgaccccccgacctgaacat	120
Db	61	ctctggactccttggacggcctggtagtggtctactccatgaccccccgacctgaacat	120
Qy	121	cacgagaggtcacagctcatcgacacgggtgacagcctgtccatctctcgaggagaca	180
Db	121	cacgagaggtcacagctcatcgacacgggtgacagcctgtccatctctcgaggagaca	180
Qy	181	gcacccccctcagtgaggcttggccaggagctcagaggcgccagccacggagacaagga	240
Db	181	gcacccccctcagtgaggcttggccaggagctcagaggcgccagccacggagacaagga	240
Qy	241	cagcagagacacgggggtggtgcgagactgcgagggcacagacagcagccctactgcaa	300
Db	241	cagcagagacacgggggtggtgcgagactgcgagggcacagacagcagccctactgcaa	300
Qy	301	ggtgttctgtcgcagaggtacatgccaaacgacacagcagcagctcgtctgtactacaa	360
Db	301	ggtgttctgtcgcagaggtacatgccaaacgacacagcagcagctcgtctgtactacaa	360
Qy	361	gtacatcaaggcacgcgcagcagggcaccacgcccgcagctcctcgtctgtgagaga	420
Db	361	gtacatcaaggcacgcgcagcagggcaccacgcccgcagctcctcgtctgtgagaga	420
Qy	421	ctttgagcagcattcatcaaacgctgacacgctcttgggtcaacagagaagacgccaat	480
Db	421	ctttgagcagcattcatcaaacgctgacacgctcttgggtcaacagagaagacgccaat	480
Qy	481	gtgggtgcccctgtctggtgtccatccccggcctcaatgtcacgctgcgtcgcaagctc	540
Db	481	gtgggtgcccctgtctggtgtccatccccggcctcaatgtcacgctgcgtcgcaagctc	540
Qy	541	ggtgctgtggccagacggcgagaggtggtgggatgacccggcgggcgatcgtctgtc	600
Db	541	ggtgctgtggccagacggcgagaggtggtgggatgacccggcgggcgatcgtctgtc	600
Qy	601	cacgcacctgtgcagcatgccctgtacctgcagtcgagacaccacctggggagacacaga	660
Db	601	cacgcacctgtgcagcatgccctgtacctgcagtcgagacaccacctggggagacacaga	660
Qy	661	cttctcttccaccccttctctggtgcacatcacaggcaacgagctctatgacatccagct	720

Db	661	 cttcccttccaaaccccttccctggtgcacatcacagggcaacgagcctctatgaaatlccagct	720
Qy	721	qllqcccaagaaagtccgtggagctctcgttaqgaggaagatlggtcctgaactgcaccgt	780
Db	721	qllycccaagaaagtcgtggagctctcgttaqgaggaagatlggtcctgaactgcaccgt	780
Qy	781	qlqggctggagtttaactcaggtgtcacctttagactggagctaccacggagagagccaga	840
Db	781	qltgggtlgaatttaactcaggtgtcacctttagactggagctaccacggagagcaqcaga	840
Qy	841	qcgggttaagttgggtlqccagagcgagcgtctccacagaccacacacaqaacttccagcat	900
Db	841	gcgggttaagtggggtggccgagcgagctctccagcagaccacacagaaacttccagcat	900
Qy	901	cclygacatccacaacgtcagcagcagcagactggctgtgtgcaagggccaacaa	960
Db	901	cclygacatccacaacgtcagcagcagcagactggctgtgtgcaagggccaacaa	960
Qy	961	cggatccagcagatttcgagagagcagcaggtctattgcatgaaatcccttccatcag	1020
Db	961	cggatccagcagatttcgagagagcagcaggtctattgcatgaaatcccttccatcag	1020
Qy	1021	cgtcagtggtctaaagagccatcctggagccacggagcagcagctgtgtgaagct	1080
Db	1021	cgtcagtggtctaaagagccatcctggagccacggagcagcagctgtgtgaagct	1080
Qy	1081	ggccgtggaagctggcaagcgtaccccccgcgcaggttcagtggttacaaagatggaaagcc	1140
Db	1081	ggccgtggaagctggcaagcgtaccccccgcgcaggttcagtggttacaaagatggaaagcc	1140
Qy	1141	actgtccggcgccacagltccacatlgccctggctgtctcaagaggtgacagagccagcac	1200
Db	1141	actgtccggcgccacagltccacatlgccctggctgtctcaagaggtgacagagccagcac	1200
Qy	1201	aygcactacacccctgcgccttggaaactccgcgtgtcgtggcgtgagggcgacaactcagcct	1260
Db	1201	aygcactacacccctgcgccttggaaactccgcgtgtcgtggcgtgagggcgacaactcagcct	1260
Qy	1261	ggagctgggtgtgaaatgtcccccccagatacatagaaaggagggcctcctcccccagcat	1320
Db	1261	ggagctgggtgtgaaatgtcccccccagatacatagaaaggagggcctcctcccccagcat	1320
Qy	1321	ctactcgcgtccacagccgcgcagggcctcacttgcacggcctcaggggtgcacctgtcctct	1380
Db	1321	ctactcgcgtccacagccgcgcagggcctcacttgcacggcctcaggggtgcacctgtcctct	1380
Qy	1381	cagcatccagtggcactggcgcccttgacacccctgcacagatgttgcaccagctagctct	1440
Db	1381	cagcatccagtggcactggcgcccttgacacccctgcacagatgttgcaccagctagctct	1440
Qy	1441	ccggcgccgcagcagcaagacctcatgccagtgccgttgactggagggcggtgacccac	1500
Db	1441	ccggcgccgcagcagcaagacctcatgccagtgccgttgactggagggcggtgacccac	1500
Qy	1501	gcagagtcggtgaaccccatcgaaagctggacacctggaccagtttgtgagaggaata	1560
Db	1501	gcagagtcggtgaaccccatcgaaagctggacacctggaccagtttgtgagaggaata	1560
Qy	1561	gaataagacttgtgagcaagctggtgatccagaaatgccaaactgtctgtgcattgtacaagt	1620
Db	1561	gaataagacttgtgagcaagctggtgatccagaaatgccaaactgtctgtgcattgtacaagt	1620
Qy	1621	tggtgtccacaacaaaggtgggcagagatgagcggtctatcttctatgtgacaccat	1680
Db	1621	tggtgtccacaacaaaggtgggcagagatgagcggtctatcttctatgtgacaccat	1680
Qy	1681	ccccgagcgtctcaccatcgaaatccaaagcattccgagagctactagagggcgagccggt	1740
Db	1681	ccccgagcgtctcaccatcgaaatccaaagcattccgagagctactagagggcgagccggt	1740
Qy	1741	gctcctgagctgccaaagccagcagctacaagtatcgagcatctgcgctgtgtaccgcctcaa	1800

Db	1741	gctcctgagctgcgccaagccgacagctacaagtacgagatctgcgctgggtaccgcctcaa	1800
Qy	1801	cctgtccacgtgcacgatgcgcagcgggaacccgcttctgctgactgcagaacgtyca	1860
Db	1801	cctgtccacgtgcacgatgcgcagcgggaacccgcttctgctgactgcagaacgtyca	1860
Qy	1861	tctgtttccacacccctctggtgcgcgcagcctcgagagagtgccactggggcgccacgc	1920
Db	1861	tctgtttccacacccctctggtgcgcgcagcctcgagagagtgccactggggcgccacgc	1920
Qy	1921	cacgctcagccttgatgatcccccggtgcgcgcgcagcacgagggccactatgltgcga	1980
Db	1921	cacgctcagccttgatgatcccccggtgcgcgcgcagcacgagggccactatgltgcga	1980
Qy	1981	agtgcgaagccggcgagccatgacaagcactgcccacaagaagtacctgtcgtgltgcaggc	2040
Db	1981	agtgcgaagccggcgagccatgacaagcactgcccacaagaagtacctgtcgtgltgcaggc	2040
Qy	2041	ccttggaagcccttcggctcacgcagaacttgccagacctctctggltgaacgtlgagcagctc	2100
Db	2041	ccttggaagcccttcggctcacgcagaacttgccagacctctctggltgaacgtlgagcagctc	2100
Qy	2101	gctggagatgcagtgtcttggtggccgagcgacgcgcccagcatctgtgtgtgltacaaga	2160
Db	2101	gctggagatgcagtgtcttggtggccgagcgacgcgcccagcatctgtgtgtgltacaaga	2160
Qy	2161	cgagagcctctgagagaaactctggagtcacttgccgactcgaacacgaagagctlgag	2220
Db	2161	cgagagcctctgagagaaactctggagtcacttgccgactcgaacacgaagagctlgag	2220
Qy	2221	catacagcgtgcgcgagagagatgcgggacgctatctgtgcagcgtgtgcaacgcgcaa	2280
Db	2221	catacagcgtgcgcgagagagatgcgggacgctatctgtgcagcgtgtgcaacgcgcaa	2280
Qy	2281	ggcctgcgtcaactctcgcgcagcgtgccctgaaagctccagagataagggcagcat	2340
Db	2281	ggcctgcgtcaactctcgcgcagcgtgccctgaaagctccagagataagggcagcat	2340
Qy	2341	ggagatcgtgatcctgtcgtgtaccggctcactcgtctcttctctgggtccctccct	2400
Db	2341	ggagatcgtgatcctgtcgtgtaccggctcactcgtctcttctctgggtccctccct	2400
Qy	2401	cctcatctctgttaacatgagagggccgcccacgcagacatcaagacgggctacctgtc	2460
Db	2401	cctcatctctgttaacatgagagggccgcccacgcagacatcaagacgggctacctgtc	2460
Qy	2461	catcatcatggaccccgggagtgccctctggagagcaatgcgaaatccctgtcctacga	2520
Db	2461	catcatcatggaccccgggagtgccctctggagagcaatgcgaaatccctgtcctacga	2520
Qy	2521	tgcacgcagtlgggaatcccccgagagcggtgcaccttggggagagtgctcggctacgg	2580
Db	2521	tgcacgcagtlgggaatcccccgagagcggtgcaccttggggagagtgctcggctacgg	2580
Qy	2581	cgctctcggaagtggtggaagcctccgcttctggcatcccaagggcgagcagctgtga	2640
Db	2581	cgctctcggaagtggtggaagcctccgcttctggcatcccaagggcgagcagctgtga	2640
Qy	2641	cacgtggccgtgaaatgctgaaagggggccacgcccagcagaccctcaacgtggltcaacccctccctcgg	2700
Db	2641	cacgtggccgtgaaatgctgaaagggggccacgcccagcagaccctcaacgtggltcaacccctccctcgg	2700
Qy	2701	gtcggagctcaagatcctcatccatcggaacccctcatggtgaltctgcaagtctcgaagtacggcaa	2760
Db	2701	gtcggagctcaagatcctcatccatcggaacccctcatggtgaltctgcaagtctcgaagtacggcaa	2760
Qy	2761	ggcctgcaccaagccgagggccctcatggtgaltctgcaagtctcgaagtacggcaa	2820
Db	2761	ggcctgcaccaagccgagggccctcatggtgaltctgcaagtctcgaagtacggcaa	2820
Qy	2821	cctctcacaactcctgcgcgcgaagcggagcctctcaagccctcgcgcggagagctctcc	2880
Db	2821	cctctcacaactcctgcgcgcgaagcggagcctctcaagccctcgcgcggagagctctcc	2880

%0	Sequence 4450 BP: 968 A: 1352 C: 1349 G: 781 T: 0 other.:									
	Query Match	69.3%:	Score 2847:	DB 21:	Length 4450:					
	Best local Similarity	99.5%:	Pred. No. 0:							
	Matches 3797:	Conservative	0:	Mismatches	19:	Indels	0:	Gaps		
Qy	97	catgacccccccagcttgaacatcacaggagaggtcacaacgtcatcagacacccagtgacag	156							
Db	99	catgacccccccagucttgaaatcacucggaggaggttcacacgtcatcagacacccagtgacag	158							
Qy	157	ccatgtcatctctgcaggggacagacacccctcctgagtgggctctggccagagactcagga	216							
Db	159	ccgtgtccatctctgcaggggacagacacccctcctgagtgggctctggccagagactcagga	218							
Qy	217	ggcgccagccaccgagagacaaggacacgaggggttggtcgagagactcagggg	276							
Db	219	ggcgccagccaccgagagacaaggacagcgaggggttggtcgagagactcagggg	278							
Qy	277	cacagacgcaggccctactgcgaaggtgttgctgctgcacaggttatcatgctcaacagcac	336							
Db	279	cacagacgcaggccctactgcgaaggtgttgctgctgcacaggttatcatgctcaacagcac	338							
Qy	337	aggcagctacgtctgtctactacaagtacatcaaggcacgcatcaggggacacacgcgcgc	396							
Db	339	aggcagctacgtctgtctactacaagtacatcaaggcacgcatcaggggacacacgcgcgc	398							
Qy	397	cagctcctacgtctcgttgagagactttgacagacatctcatcaacagactgcacgct	456							
Db	399	cagctcctacgtctcgttgagagactttgacagacatctcatcaacagactgcacgct	458							
Qy	457	ctttagttcaacaggaagacgcctatgtgggtgcctctgtctgtgttccatcccgccgtccaa	516							
Db	459	ctttagttcaacaggaagacgcctatgtgggtgcctctgtctgtgttccatcccgccgtccaa	518							
Qy	517	tgtaacgtctgcctgcacaaagcttcggtgtgtgtgcacacagggcagaggttggtgtggga	576							
Db	519	tgtaacgtctgcctgcacaaagcttcggtgtgtgtgcacacagggcagaggttggtgtggga	578							
Qy	577	tgaacgcgtggggcatgctcgtgttccacgcacactgctgtacacgalycccttgtaacttgcagtg	636							
Db	579	tgaacgcgtggggcatgctcgtgttccacgcacactgctgtacacgalycccttgtaacttgcagtg	638							
Qy	637	cgaatacaccttggggaaccaggagcttcttttccaaaccttctctgtgtgacacatcacagg	696							
Db	639	cgaatacaccttggggaaccaggagcttcttttccaaaccttctctgtgtgacacatcacagg	698							
Qy	697	caacagctctctatgacatccagctgtgtgccacggaagtcgctggagctgctggttagggga	756							
Db	699	caacagctctctatgacatccagctgtgtgccacggaagtcgctggagctgctggttagggga	758							
Qy	757	gaagctgtggtcctgaactgcaacgtgttgggcttgagtttaactcaggtgtcacctttgactgt	816							
Db	759	gaagctgtggtcctgaactgcaacgtgttgggcttgagtttaactcaggtgtcacctttgactgt	818							
Qy	817	ggacttcccaggaaacaggaacagcgaggttaagtgggtgcccagcagacgtcccagca	876							
Db	819	ggacttcccaggaaacaggaacagcgaggttaagtgggtgcccagcagacgtcccagca	878							
Qy	877	gacccacacagaactcttcagcatcctgaccatccacaaagtccagccagcagacctggg	936							
Db	879	gacccacacagaactcttcagcatcctgaccatccacaaagtccagccagcagacctggg	938							
Qy	937	ctcgtatgtgtgaaaggcaaacaggacatccaggatctcgggagagacacccaggtcat	996							
Db	939	ctcgtatgtgtgaaaggcaaacaggacatccaggatctcgggagagacacccaggtcat	998							
Qy	997	tgtgcatgaaaaatcccttcatcagctcgagtggtctcaaaaggaccatcccttgagggcccac	1056							
Db	999	tgtgcatgaaaaatcccttcatcagctcgagtggtctcaaaaggaccatcccttgagggcccac	1058							
Qy	1057	ggcaggagacagctggttgaaactgccctgaaactggtgacgttccagccagccaggtt	1116							

D	b	1059	ggcaggagacgactggtgaagctgccgtggaagctggcagcgtaccccccgccgagatt	1111
Q	y	1117	ccagtgtacaagatggaagagcactgccggggcgccacagtcacatgccccgggtgct	1176
D	b	1119	ccagtgtacaagatggaagagcactgccggggcgccacagtcacatgccccgggtgct	1178
Q	y	1177	caagaggtgaagagccagcacaggcaactacacccctcgccctgggaactccgtgc	1236
D	b	1179	caagaggtgacagagggcagcacaggcaactacacccctcgccctgggaactccgtgc	1238
Q	y	1237	tggcctgagggcacaactcagcctggagctgggtggtaattgccccccccagatacatalga	1296
D	b	1239	tggcctgagggcacaactcagcctggagctgggtggtaattgccccccccagatacatalga	1298
Q	y	1297	gaaggaagcctctccccagcatctactcgcgtcacagcgcgagggcctcacctcac	1356
D	b	1299	gaaggaagcctctccccagcatctactcgcgtcacagcgcgagggcctcacctcac	1358
Q	y	1357	ggcctacggggtgccctgccttcagcatccagtcgagtcggcctgggacccctgg	1416
D	b	1359	ggcctacggggtgccctgccttcagcatccagtcgagtcggcctgggacccctgg	1418
Q	y	1417	caagatgtttgcaccagctagtctccggcgcgcgagcagcaagacatcagtcacagtg	1476
D	b	1419	caagatgtttgcaccagctagtctccggcgcgcgagcagcaagacatcagtcacagtg	1478
Q	y	1477	ccgtgactggagggcggtgaccacgagatgccgtgaaccccatcagagcctgggacac	1536
D	b	1479	ccgtgactggagggcggtgaccacgagatgccgtgaaccccatcagagcctgggacac	1538
Q	y	1537	ctgaccagcatttggtaggggaaagataagacttgagcaagcttgatccagaaatgc	1596
D	b	1539	ctgaccagcatttggtaggggaaagataagacttgagcaagcttgatccagaaatgc	1598
Q	y	1597	caacgtctctgccatgacaaatgtgtggtctccacaaggtggggccaggaatgagcggt	1656
D	b	1599	caacgtctctgccatgacaaatgtgtggtctccacaaggtggggccaggaatgagcggt	1658
Q	y	1657	catctactctatgtgaccacatccccgacggcttcaccatcgaatccaaagccatccga	1716
D	b	1659	catctactctatgtgaccacatccccgacggcttcaccatcgaatccaaagccatccga	1718
Q	y	1717	ggaactactagggcgagccggtgctctgagctgccaagccagcagctacaagtacga	1776
D	b	1719	ggaactactagggcgagccggtgctctgagctgccaagccagcagctacaagtacga	1778
Q	y	1777	gcattcgcgtggtaccgcctcaactctccacgtgcacagtcgcgcgcggaaacccgct	1836
D	b	1779	gcattcgcgtggtaccgcctcaactctccacgtgcacagtcgcgcgcggaaacccgct	1838
Q	y	1837	tctgctcagctgaagaacgtgcattgttgcgccacctctggccgcgcagccctggagga	1896
D	b	1839	tctgctcagctgaagaacgtgcattgttgcgccacctctggccgcgcagccctggagga	1898
Q	y	1897	ggtggcacttggggcgccgacgccacgtcagcctgaagatccccccgctgcgcgccga	1956
D	b	1899	ggtggcacttggggcgccgacgccacgtcagcctgaagatccccccgctgcgcgccga	1958
Q	y	1957	gcacgagggccactatgtgtgcgaaagtgcagaacggcgagccctgacagactgacca	2016
D	b	1959	gcacgagggccactatgtgtgcgaaagtgcagaacggcgagccctgacagactgacca	2018
Q	y	2017	caagaagaactctggtgcaggccctggaagccctcggtccagcagagaactlgaccga	2076
D	b	2019	caagaagaactctggtgcaggccctggaagccctcggtccagcagagaactlgaccga	2078
Q	y	2077	cctcctggtgaacgtgagcgactcgtcgagatgcagtgcttggtggcgagcgacgcgc	2136
D	b	2079	cctcctggtgaacgtgagcgactcgtcgagatgcagtgcttggtggcgagcgacgcgc	2138
Q	y	2137	gccacgacatcgttgtacaaagacgagaggtcgtcgaggaaaagtctggagtcgactt	2196
D	b	2139	gccacgacatcgttgtacaaagacgagaggtcgtcgaggaaaagtctggagtcgactt	2198

Qy	2197	ggcgactccaaccagaagctagcatcagcgctgcgcgagagagatgctgagacgcta	2256
Db	2199	ggcgactccaaccagaagctagcatcagcgctgcgcgagagagatgctgagacgcta	2258
Qy	2257	tcgtgcagctgtgcaacgccaaaggctgggtcaactctctccgcagcgtgacctggga	2316
Db	2259	tcgtgcagctgtgcaagaccaaaggctgggtcaactctctccgcagcgtggcctggga	2318
Qy	2317	aggtccgaggataaaggcgagcatggatcgtgatctctgtcgtaccagcgtcaatcgc	2376
Db	2319	aggtccgaggataaaggcgagcatggatcgtgatctctgtcgtaccagcgtcaatcgc	2378
Qy	2377	tgctctctcggtctctctctcatctctgttaacatggagagcgagccagccacgc	2436
Db	2379	tgctctctcggtctctctctcatctctgttaacatggagagcgagccagccacgc	2438
Qy	2437	agacataagacgggtactcgttccatcatcatggaccgccggaggtgactcttggagga	2496
Db	2439	agacataagacgggtactcgttccatcatcatggaccgccggaggtgactcttggagga	2498
Qy	2497	gcaalgcaataacctctctacgatgccagccatgggaattcccccyaaagacgtcra	2556
Db	2499	gcaalgcaataacctctctacgatgccagccatgggaattcccccyaaagacgtcra	2558
Qy	2557	cttggnnagagtgctcgctacgcgcctctcggaagtggtggaaacctcgcgtcttcgg	2616
Db	2559	cttggnnagagtgctcgctacgcgcctctcggaagtggtggaaacctcgcgtcttcgg	2618
Qy	2617	catccaaaggcagcagctgtgaacagtggcctgaaatctgaaagagggcgccac	2676
Db	2619	catccaaaggcagcagctgtgaacagtggcctgaaatctgaaagagggcgccac	2678
Qy	2677	ggcagcgagcacgcgcgtgatctcgagagctcaagatctctcatcacatcgcaacca	2736
Db	2679	ggcagcgagcacgcgcgtgatctcgagagctcaagatctctcatcacatcgcaacca	2738
Qy	2737	cttcaacgtggtcaactctctcgggcgctgcaccaagcgcagagccctctcatgtgat	2796
Db	2739	cttcaacgtggtcaactctctcgggcgctgcaccaagcgcagagccctctcatgtgat	2798
Qy	2797	cgtggagtcttgcagtcacgaactcttccacttcttgcgcgccaaagcgagagcctt	2856
Db	2799	cgtggagtcttgcagtcacgaactcttccacttcttgcgcgccaaagcgagagcctt	2858
Qy	2857	naqccctcgcgagagaactctccgagcagcgagcagcttccgcgccaaagcgagagcctt	2916
Db	2859	naqccctcgcgagagaactctccgagcagcgagcagcttccgcgccaaagcgagagcctt	2918
Qy	2917	cgcagagctgga tcggagcgccggggagcagcgcagaggtctcttctcgcgcgtcttc	2976
Db	2919	cgcagagctgga tcggagcgccggggagcagcgcagaggtctcttctcgcgcgtcttc	2978
Qy	2977	gaagaccagggcgagcagcaggggcttctccagaccagaagctgaggaacttggtct	3036
Db	2979	gaagaccagggcgagcagcaggggcttctccagaccagaagctgaggaacttggtct	3038
Qy	3037	gagccgcgtgacctggaagatcttctctgctacagcttccaggtggccagagaggaatgga	3096
Db	3039	gagccgcgtgacctggaagatcttctctgctacagcttccaggtggccagagaggaatgga	3098
Qy	3097	gttctctgcttccgaaagtgcattccagagaactggctgctcggaaacattctctctctc	3156
Db	3099	gttctctgcttccgaaagtgcattccagagaactggctgctcggaaacattctctctctc	3158
Qy	3157	ggaaagcgacgttgaaatcttctgacttttgcttctcccgagacattctaraaagacc	3216
Db	3159	ggaaagcgacgttgaaatcttctgacttttgcttctcccgagacattctaraaagacc	3218
Qy	3217	tgaatacgtccgcaaggcgagtgcccgctgccctggaatggatggcccttgaaagcat	3276
Db	3219	cgaatacgtccgcaaggcgagtgcccgctgccctggaatggatggcccttgaaagcat	3278

Qy	3277	cttcagacaaggctatcacaccacagagtgacagctggtggtccctcttggtggtgctctctctcagga	3333
Db	3279	cttcagacaaggctatcacaccacagagtgacagctggtggtccctcttggtggtgctctctcagga	3338
Qy	3337	gatctctctcttgagggcctcccctacccctggggtgcagatcaaatgaggaagttctgcca	3396
Db	3339	gatctctctcttgagggcctcccctacccctggggtgcagatcaaatgaggaagttctgcca	3398
Qy	3397	gcggcttgagagacggcacaaaggatgaggggcccccggagctggccactcccgccatacagccg	3456
Db	3399	gcggcttgagagacggcacaaaggatgaggggcccccggagctggccactcccgccatacagcca	3458
Qy	3457	catcatctgaactgctgcttcggaagaccccaagcgaagacctgcattctcggagctcggc	3516
Db	3459	catcatctgaactgctgcttcggaagaccccaagcgaagacctgcattctcggagctcggc	3518
Qy	3517	ggagatcctctggggggaactgctctccagggcaggggcctgcgaagagggaagggaggtctgcat	3576
Db	3519	ggagatcctctggggggaactgctctccagggcaggggcctgcgaagagggaagggaggtctgcat	3578
Qy	3577	ggccccgcgagctctcagagcttcgaagaagagggcagcttctcgaaggtgctccaccalggc	3636
Db	3579	ggccccgcgagctctcagagcttcgaagaagagggcagcttctcgaaggtgctccaccalggc	3638
Qy	3637	cctacacatcgccacggctgacgctgagagcagccgcgaagcctgcagcggccacagcct	3696
Db	3639	cctacacatcgccacggctgacgctgagagcagccgcgaagcctgcagcggccacagcct	3698
Qy	3697	ggccgcaggatatacaacttggtgctcttcccgggggtgcttgccgacagaggggtgagac	3756
Db	3699	ggccgcaggatatacaacttggtgctcttcccgggggtgcttgccgacagaggggtgagac	3758
Qy	3757	ccgtggttctctccaggatgaagacatttgaggaattcccccatgaccccaacgacactacaa	3816
Db	3759	ccgtggttctctccaggatgaagacatttgaggaattcccccatgaccccaacgacactacaa	3818
Qy	3817	aggctctgtggacaaccagacagacagtgaggatggtgcttgccctggccgacagaggtgagac	3876
Db	3819	aggctctgtggacaaccagacagacagtgaggatggtgcttgccctggccgacagaggtgagac	3878
Qy	3877	gatagagcagcggcatagacaagaagcggctctcag	3912
Db	3879	gatagagcagcggcatagacaagaagcggctctcag	3914
RESULT	11		
AAQ49753/C			
ID	AAQ49753	standard; DNA; 6827 BP.	
XX	AC	AAQ49753;	
XX	DT	10-MAR-1994 (first entry)	
XX	DE	pTK gene SAL-S1.	
XX	KW	pTK; protein tyrosine kinase; catalytic domain; c-kit; FLT/FLK;	
KW	KW	fetal liver kinase; megakaryocyte; amplification; primer;	
XX	XX	polymerase chain reaction; PCR; ds.	
OS	XX	Homo sapiens.	
XX	Key	Location/Qualifiers	
FT	CDS	complement (1877..2923)	
FT		/tag= a	
FT	misc_difference	3026	
FT		/tag= b	
FT		/note= "base labelled as x in the specification"	
FT	misc_difference	5000	
FT		/tag= c	
FT		/note= "base illegible in the specification"	
FT	misc_difference	5699..5700	
FT		/tag= d	
FT		/note= "bases illegible in the specification"	

PT Agonist antibodies which activate specific protein tyrosine
PT kinase(s) - also activate chimeric proteins of kinase extracellular
PT domain and Ig constant domain, useful for studying, and therapeutic
PT modulation of, cell growth and differentiation
XX
PS Disclosure; Page 39-46; 125pp; English.
XX
CC DNA probes based on protein tyrosine-kinase (pTK) sequences were used
CC to screen cDNA libraries to identify novel pTK genes. The SAL-S1
CC gene (see also A030309) was isolated from several megakaryocytic cell
CC libraries. The gene can be used to produce recombinant SAL-S1 or ILS
CC fragments, to detect related genes, and to design drugs, peptides
CC or antisense nucleotides that modulate pTK activity.
XX
SQ Sequence 6827 BP; 1558 A; 1870 C; 1738 G; 1660 T; 1 other;

Query Match		23.1%;	Score 950;	DB 16;	Length 6827;
Best Local Similarity		99.9%;	Pred. No. 0;		
Matches 1000;		Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
Qy	2869	ggagaagtctcccgagcagcgagcgtctccgcgcgcattggtgagctcgcaggtcga	2928		
Db	2924	GGAGAACTCTCCCGAGCAGCGCGACGCTTCCGCGCCATGCTGCGAGCTCCGAGCTGA	2865		
Qy	2929	tcgagagcgccgggagcagcagcagggctctcttcgcgcggttctcgaagccgaagg	2988		
Nb	2864	TCCGAGCGCGCGGGGAGCAGCGAGGGGTCTCTTCGCGCGGTCTCGAAGACCGAGGG	2805		
Qy	2989	cggagcagcgcggtctctccagaccgaagcgtgagcgtggtgagccgcgtgac	3048		
Db	2804	CGGAGCGAGCGGGCTTCTCCAGACCAAGAAGCTGAGGACCTGTGGCTGAGCCGCTGAC	2745		
Qy	3049	catgaagatcttctcgtctacagcttccaggttccagggaggtgaggttctcgtctc	3108		
Db	2744	CATGGAAGATCTTCTCTGTACAGCTTCCAGGTGCCAGAGGAGGATGAGTTCCTGCTTC	2685		
Qy	3109	ccgaantgcatcacagagacctggctcgcgaacatctcgtcgtcgaagacacgt	3168		
Db	2684	CCGAAGTGCATCACAGAGACCTGGCTGCTCGGAACATTTCTGCTGCGAAGACGACGT	2625		
Qy	3169	qqiqaagatctgtgactttggccttgcgcggagacatctacaaagacrtctactacgtc	3228		
Db	2624	GCTGAAGATCTGTGACTTTGGCCTTGGCCCGGGACATCTACAAAGACCCGACTACGTCCG	2565		
Qy	3229	caagggcagtcgccggctgcccctgaagtggatggcggccctgaaagcattctcgaaggt	3288		
Db	2564	CAAGGGCAGTGCCCGGCTGCCCTGAAAGTGATGGCCGCCCTCAAAGCATCTTCCAAAGGT	2505		
Qy	3289	gtacaccacgcagagtgagctgtgctcttggggtgcttctcgtggaagatctctctct	3348		
Db	2504	GTACACCACGAGAGTCACGTGTGCTCTTTGGGGTGCTTCTCTGGGAGATCTTCTCTCT	2445		
Qy	3349	gggggctctcccgctacccctgggtgcacatcaatgagaggttcttgcagcggtcgaaga	3408		
Db	2444	GCGGGCTTCCCGCTACCTTGGGTGCCAGATCAATGAGGAGTTCTTGCCAGCGCTGAGAGA	2385		
Qy	3409	cggcaagagatgaggcccccggagctggccactlcccgccatcagccgcacatctctgaa	3468		
Db	2384	CGGCACAAGGATGAGGGCCCGGAGCTGGCCACTTCCCGCCATACGCCGATCATGCTGAA	2325		
Qy	3469	ctgctgttccgagagaccccaagcagacccctgcatctcggagcttggtagatctctgag	3528		
Db	2324	CTGCTGTGTCGGAGACCCCAAGGCGAGACTGCAATTTCTCGAGCTGTGGAGATCTTGGG	2265		
Qy	3529	ggacctgctcraggcgagggtcctgcaagaggaagaggtcttgcactgcccctcagcag	3588		
Db	2264	GGACCTGCTCAGGCCAGGGGCTTCCAAAGAGGAAGAGAGGTCTGTCATGCGCCGCGCAG	2205		
Qy	3589	ctctcagagctcgaagagggcagctctctcagcaggtgtccaccatggccctacacatcgc	3648		
Db	2204	CTCTCAGAGCTCAGAACAGGGCAGCTTCTCCAGGTGTCCACCATGCGCCCTAGACATCGC	2145		

Qy	3649	ccaggtgacgcctgagagcagccgccaagcctgcagccacagcagcctggccgccaagta	3708
Db	2144	CCAGGCTGACGCTGAGACAGCGCCCAAGCGCTGCAGCGCCACAGCTTGGCCGCCAGGTA	2085
Qy	3709	ttacaactgggtgtctcttcccggtgcttgcaccagagggctgagaccgtgattctc	3768
Db	2084	TTACAACCTGGGTGCTCTTCCCGGGTGCTTGGCCAGAGGGGCTGAGACCCGTGTTCTTC	2025
Qy	3769	caggatgaagacatttgagaaattccccatgaccccaacgacactacaaaggctctgtgga	3828
Db	2024	CAGATGAACACATTTTGAGAAATTCCTCCATGACCCCAACGACCTACAAAGGCTCTGTGGA	1965
Qy	3829	caaccagacagcagtgggatggtgctgacctcgaggaggt	3869
Db	1964	CAACCAGACAGACAGTGGGATGCTGCTGGCTCGGAGGAGT	1924
RESULT 13			
AAH99658			
ID	AAH99658 standard; cDNA: 574 BP.		
XX	AAH99658;		
AC			
DT	16-OCT-2001 (first entry)		
DE	Human protein encoding cDNA sequence SEQ ID NO:493.		
XX	Human; cancer; ulcer; HIV infection; human immunodeficiency virus;		
KW	antiinflammatory; antirheumatic; antiarthritic; immunosuppressive;		
KW	antibacterial; endocrine; cardiant; central nervous system; viricide;		
KW	anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia;		
KW	antiaggregant; haemostatic; vulnary; antiulcer; osteopathic; eczema;		
KW	dermatological; anti allergic; antisthmatic; antidiabetic; cytostatic;		
KW	neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;		
KW	immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;		
KW	antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;		
KW	cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;		
KW	genetic disease; haematopoietic disorder; platelet disorder; asthma;		
KW	thrombocytopaenia; osteoporosis; severe combined immunodeficiency;		
KW	allergic rhinitis; diabetes; multiple sclerosis; depression;		
KW	Alzheimer's disease; parkinson's disease; neurodegenerative disorder;		
XX	neurological disorder; ss.		
OS	Homo sapiens.		
XX	W0200153455-A2.		
XX	26-JUL-2001.		
XX	22-DEC-2000; 2000WO-US35017.		
PF			
XX	23-DEC-1999; 99US-0471275.		
PR	21-JAN-2000; 2000US-0488725.		
PR	25-APR-2000; 2000US-0552317.		
XX			
XX	(HYSE-) HYSEQ INC.		
PA			
XX			
PI	Tang YT, Liu C, Drmanac RT;		
XX			
XX	WPI; 2001-457603/49.		
DR	P-PSDB; AAM25717.		
XX			
XX	Isolated human polynucleotides encoding polypeptides, useful for the		
PT	treatment and diagnosis of e.g. cancer, ulcers and HIV infection -		
XX			
PS	Claim 1; Page 561; 1217pp; English.		
XX			
CC	AAH99166 to AAH99904 encode the human proteins given in AAM25225 to		
CC	AAM25963. The proteins can have activities based on the tissues and		
CC	cells they are expressed in, such as: antiinflammatory; antirheumatic;		
CC	antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant;		
CC	central nervous system; viricide; anti-HIV; fungicide; antimutagen;		
CC	cardiovascular; antianaemic; antiaggregant; haemostatic; vulnary;		

XX WO200075319-A1.
XX 14-DEC-2000.
XX 23-MAY-2000; 2000WO-US14142.
XX 08-JUN-1999; 99US-0138133.
XX (KEGE-) REGENERON PHARM INC.
XX Papadopoulos NJ, Davis S, Yancopoulos GD;
XX WPI: 2001-071076/08.
XX Nucleic acid molecule encoding mammalian phospholipid transfer protein,
XX and its fragments, useful for diagnosis, evaluation, and treatment of
XX diseases associated with the gene expression and for producing model
XX systems -
XX Example 17; Page 63; 159pp; English.
XX This sequence represents a PCR primer used to construct DNA
XX sequences encoding the fusion proteins of the invention between
XX the Flt1 receptor and the Fc region of IgG. The specification relates
XX to modified chimeric polypeptides with improved pharmacokinetics. The
XX modified chimeric polypeptides are preferably Flt1 receptor polypeptides
XX that have been modified to improve their pharmacokinetic profile. The
XX polypeptides can be used to decrease or inhibit plasma leakage and/or
XX vascular permeability in a mammal.
XX Sequence 38 BP; 9 A; 9 C; 11 G; 9 T; 0 other;
Query Match 0.7%; Score 30; DB 22; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0039;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 713 atccagctgtgcccggaagtcgtcgtggag 742
Db 9 atccagctgtgcccggaagtcgtcgtggag 38
RESULT 23
ARA96501
ID ABA96501 standard; cDNA; 1047 BP.
XX AHA96501;
XX 12-MAR-2002 (first entry)
XX Human extracellular signal-regulated protein kinase-2 (erk-2) cDNA.
XX Human: extracellular signal-regulated protein kinase-2; erk-2;
XX recombinant production; Escherichia coli; HeLa cell; ss.
XX Homo sapiens.
XX Key Location/Qualifiers
XX CDS 1..1047
XX /tag= a
XX /product= "Human erk-2"
XX KR98022142-A.
XX 25-JUN-1998.
XX 20-SEP-1996; 96KR-0041219.
XX 20-SEP-1996; 96KR-0041219.
XX (GLDS) LG CHEM LTD.
XX

PI Kim CH, Cho JM, Chung HH, Lee JH;
XX WPI: 1999-300710/25.
DR P-PSDB; AAW52700.
XX Process for preparing extracellular signal-regulated protein kinase-2
XX from E. coli -
XX Example 2; Fig 1a-c; 9pp; Korean.
XX The invention relates to a process for the recombinant production
XX of human extracellular signal-regulated protein kinase-2 (erk-2) in
XX Escherichia coli. The present sequence represents cDNA encoding human
XX erk-2 initially isolated from HeLa cells.
XX Sequence 1047 BP; 303 A; 255 C; 225 G; 264 T; 0 other;
Query Match 0.6%; Score 26; DB 20; Length 1047;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3173 aagatctgtgacttgcccttgcccg 3198
Db 45; aagatctgtgacttgcccttgcccg 479
RESULT 24
AAQ20261
ID AAQ20261 standard; DNA; 1467 BP.
XX AAQ20261;
XX 31-MAR-1992 (first entry)
XX ERK2.
XX Microtubule-associated protein 2; central nervous system;
XX extracellular signal-regulated kinase; ERK; CNS; MAP2; ss
XX Rat rattus.
XX Key Location/Qualifiers
XX CDS 1..1248
XX /tag= a
XX /label= ERK2
XX misc_signal 172..174
XX /tag= b
XX /label= initiation_codon
XX 202..204
XX /tag= c
XX /label= initiation_codon
XX 1246..1248
XX /tag= d
XX WO9119008-A.
XX 12-DEC-1991.
XX 03-JUN-1991; 91WO-US03894.
XX 16-MAY-1991; 91US-0701544.
XX 01-JUN-1990; 90US-0532004.
XX (KEGE-) REGENERON PHARM INC.
XX (TEXA) UNIV OF TEXAS SYSTEM.
XX Boulton TG, Cobb MH, Yancopoulos GD, Nye S, Panayotatos N;
XX WPI: 1992-007489/01.
XX P-PSDB; AAR20104.
XX DNA encoding MAP2 kinase enzyme and vectors or host cells - are
XX

PT for assaying cellular factor (e.g. NGF), and drug screening

XX Disclosure: Fig 3A: 9pp: English.

XX The identification of a family of protein serine/threonine kinases
 CC which phosphorylate microtubule-associated protein 2 (MAP2) is
 CC based, in part, on the cloning and characterisation of MAP2 kinases
 CC designated extracellular signal-regulated kinase 1, 2 and 3 (ERK1,
 CC ERK2 and ERK3) which are expressed in the central nervous system,
 CC and on the identification of another ERK family member, ERK4, with
 CC antisera.

XX ERK1-3 are represented in AAQ20260-62.

XX Sequence 1467 BP: 365 A; 382 C; 355 G; 365 T; 0 other;

Query Match 0.6%; Score 26; DB 13; Length 1467;

Best Local Similarity 100.0%; Pred. No. 0.18;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3173 aagatctgtgactttggccttgcccg 3198

|||||

Db 655 aagaletgtgactttggccttgcccg 680

RESULT 25

AAV71031
 ID AAV71031 standard; cDNA; 1815 BP.

XX AC AAV71031;

XX DT 08-FEB-1999 (first entry)

XX DE Erk2-green fluorescent protein fusion product.

XX KW Rat; Erk2 gene; fusion protein; green fluorescent protein; GFP;

XX KW Intracellular signalling; chimera; ss.

XX OS Chimeric - Aequorea victoria.

XX OS Chimeric - Rattus sp.

XX FH Key Location/Qualifiers

XX FT CDS 1..1815

XX FT /*tag= a

XX PN WO9845704-A2.

XX PD 15-OCT-1998.

XX PF 07-APR-1998; 98WO-DK00145.

XX PR 07-APR-1997; 97DK-0000392.

XX PA (NOVO) NOVO-NORDISK AS.

XX PI Kasper A, Petersen Bjorn S, Scudder K, Thastrup O;

XX PI Tullin S;

XX DR WPI: 1998-594491/50.

XX DR P-PSDB: AAW85016.

XX PT Determining effect on signalling pathways in live cells from
 PT redistribution of luminophores - specifically fusions of green
 PT fluorescent protein with a signalling component, and new apparatus,
 PT particularly for identifying toxins and potential therapeutic agents

XX PS Claim 63; Pages 122-125; 326pp; English.

XX CC The present sequence encodes a rat Erk2-green fluorescent

XX CC protein fusion product. The fusion protein is used in an assay

XX CC that exemplifies the invention. The specification describes how

XX CC quantitative information about the influence of a molecule on a cellular

XX CC response is obtained by recording the variation, caused by the molecule,

CC on mechanically intact living cells, in the spatially distributed light
 CC emitted from a luminophore present in the cells. The variation in light
 CC emission is processed to provide information that correlates spatial
 CC distribution to the degree of the molecule. The method is used to
 CC identify agents that (in)directly affect intracellular signalling,
 CC especially to screen for potential therapeutic agents or toxins, and
 CC to identify new drug targets.

XX Sequence 1815 BP: 480 A; 506 C; 451 G; 378 T; 0 other;

Query Match 0.6%; Score 26; DB 19; Length 1815;

Best Local Similarity 100.0%; Pred. No. 0.18;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3173 aagatctgtgactttggccttgcccg 3198

|||||

Db 484 aagatctgtgactttggccttgcccg 509

RESULT 26

AAV71023

ID AAV71023 standard; cDNA; 1818 BP.

XX AC AAV71023;

XX DT 08-FEB-1999 (first entry)

XX DE Green fluorescent protein-Erk2 fusion product.

XX KW Rat; Erk2 gene; fusion protein; green fluorescent protein; GFP;

XX KW Intracellular signalling; chimera; ss.

XX OS Chimeric - Aequorea victoria.

XX OS Chimeric - Rattus sp.

XX FH Key Location/Qualifiers

XX FT CDS 1..1818

XX FT /*tag= a

XX PN WO9845704-A2.

XX PD 15-OCT-1998.

XX PF 07-APR-1998; 98WO-DK00145.

XX PR 07-APR-1997; 97DK-0000392.

XX PA (NOVO) NOVO-NORDISK AS.

XX PI Kasper A, Petersen Bjorn S, Scudder K, Thastrup O;

XX PI Tullin S;

XX DR WPI: 1998-594491/50.

XX DR P-PSDB: AAW85007.

XX PT Determining effect on signalling pathways in live cells from
 PT redistribution of luminophores - specifically fusions of green
 PT fluorescent protein with a signalling component, and new apparatus,
 PT particularly for identifying toxins and potential therapeutic agents

XX PS Claim 63; Pages 71-74; 326pp; English.

XX CC The present sequence encodes a green fluorescent protein (GFP)-rat

XX CC Erk2 fusion product. The fusion protein is used in an assay

XX CC that exemplifies the invention. The specification describes how

XX CC quantitative information about the influence of a molecule on a cellular

XX CC response is obtained by recording the variation, caused by the molecule,

XX CC on mechanically intact living cells, in the spatially distributed light

XX CC emitted from a luminophore present in the cells. The variation in light

XX CC emission is processed to provide information that correlates spatial

XX CC distribution to the degree of the molecule. The method is used to

XX CC identify agents that (in)directly affect intracellular signalling,

CC especially to screen for potential therapeutic agents or toxins, and
 CC to identify new drug targets.

SQ Sequence 1818 BP; 482 A; 505 C; 451 G; 380 T; 0 other;

Query Match 0.6%; Score 26; DB 19; Length 1818;
 Best Local Similarity 100.0%; Pred. No. 0.18;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3173 aagatctgtgacttggccttgccg 3198
 |||||
 DB 1225 aagatctgtgacttggccttgccg 1250

RESULT 27

AA11370
 ID AAT13330 standard; cDNA to mRNA; 4696 BP.

AC AAT13340;

XX 09-JUL-1996 (first entry)

DE Rat type I insulin-like growth factor receptor cDNA.

XX Insulin-like growth factor I receptor; IGF 1R; somatomedin C;
 KW smooth muscle; cell growth; cell proliferation; healing;
 KW nerve regeneration; angiogenesis; antisense RNA; atherosclerosis;
 KW tumour; restenosis; ds.

XX Rattus norvegicus strain Sprague-Dawley.

XX Key Location/Qualifiers

FT CDS 46..4158

FT /*tag= a

FT sig_peptide 46..135

FT /*tag= b

FT mat_peptide 136..4155

FT /*tag= c

XX W09610401-A1.

XX 11-APR-1996.

XX 27-SEP-1995; 95WO-US12563.

XX 04-OCT-1994; 94US-0317898.

XX (UYEM-) UNIV EMORY.

XX Delafontaine P;

XX WPI; 1996-209180/21.

XX P-PSDB; AAR91430.

XX Insulin-like growth factor I receptor anti:sense RNA and
 PT ATG-directed sense oligonucleotide(s) - useful for regulating
 PT growth factor receptor gene expression for e.g. wound healing and
 PT atherosclerosis

PS Claim 18; Page 36-42; 73pp; English.

XX A cDNA clone (AAT13330) codes for rat insulin-like growth factor
 CC I receptor (IGF 1R) (AAR91430). It was obtd. from a rat brain cell
 CC cDNA library by PCR amplification (see AAT13332-33). IGF 1R plays
 CC a crucial role in vascular smooth muscle cell (VSMC) proliferative
 CC responses. The gene provides the basis for antisense methods
 CC (see AAT13325 and AAT13328) to down-regulate IGF 1R gene expression and
 CC retard VSMC growth, e.g. to treat restenosis and atherosclerosis,
 CC and also for ATP-directed sense oligonucleotide (see AAT13326)
 CC methods to stimulate VSMC growth e.g. for healing wounds and burns.

XX Sequence 4696 BP; 1151 A; 1268 C; 1241 G; 1036 T; 0 other;

Query Match 0.6%; Score 26; DB 17; Length 4696;
 Best Local Similarity 100.0%; Pred. No. 0.17;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3120 tcacagagacctggctgctcggaac 3145
 |||||
 DB 3443 tcacagagacctggctgctcggaac 3468

RESULT 28

AAA91087/c

ID AAA91087 standard; DNA; 39 BP.

XX AAA91087;

AC AAA91087;

XX 05-APR-2001 (first entry)

XX PCR primer VEGFR303/SRF.AS for Flt1 receptor fusion protein DNA sequence.

DE Flt1 receptor; fusion protein; chimeric protein; pharmacokinetic;

XX plasma leakage; vascular permeability; IgG Fc region; PCR primer; ss.

XX Unidentified.

XX WO200075319-A1.

XX 14-DEC-2000.

XX 23-MAY-2000; 2000WO-US14142.

XX 08-JUN-1999; 99US-0138133.

XX (REGE-) REGENERON PHARM INC.

XX Papadopoulos NJ, Davis S, Yancopoulos GD;

XX WPI; 2001-071076/08.

XX Nucleic acid molecule encoding mammalian phospholipid transfer protein,

PT and its fragments, useful for diagnosis, evaluation, and treatment of

PT diseases associated with the gene expression and for producing model

PT systems -

XX Example 17; Page 63; 159pp; English.

XX This sequence represents a PCR primer used to construct DNA

CC sequences encoding the fusion proteins of the invention between

CC the Flt1 receptor and the Fc region of IgG. The specification relates

CC to modified chimeric polypeptides with improved pharmacokinetics. The

CC modified chimeric polypeptides are preferably Flt1 receptor polypeptides

CC that have been modified to improve their pharmacokinetic profile. The

CC polypeptides can be used to decrease or inhibit plasma leakage and/or

CC vascular permeability in a mammal.

XX Sequence 39 BP; 9 A; 11 C; 9 G; 10 T; 0 other;

SQ

Query Match 0.6%; Score 24; DB 22; Length 39;
 Best Local Similarity 100.0%; Pred. No. 1.8;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 986 accgaggtcattgcatgaaat 1009
 |||||
 DB 39 ACCGAGGTCTATTGTCATGAAAT 16

RESULT 29

AAQ30721

ID AAQ30721 standard; DNA; 159 BP.

XX

AC AAQ30721;


```

XX 22-MAR-1993 (first entry)
XX Tyrosine kinase clone RTK-6.
XX Tyrosine kinase receptor; ss.
XX Rattus rattus.
XX
XX Key Location/Qualifiers
XX CDS 1..159
XX /*tag= a
XX
XX WO9218149-A.
XX
XX 29-OCT-1992.
XX
XX 23-APR-1992; 92WO-US03376.
XX
XX 23-APR-1991; 91US-0690199.
XX
XX 26-JUL-1991; 91US-0736559.
XX
XX (REG- ) REGENERON PHARM INC.
XX
XX Aldrich TH, DiStephano P, Furth ME, Glass D, Masiakowski;
XX P, Maison-Pierre PC, Squinto SP, Stitt T, Yancopoulos GD;
XX
XX WPI: 1992-381778/46.
XX P-PSDB: AAR28603.
XX
XX Assaying neurotrophin activity using cells that express trkB - also
XX for identifying agonists and antagonists, and new recombinant cells
XX and nucleic acid producing trkB, for diagnosis and treatment of
XX neurological disease
XX
XX Disclosure; Fig 12C; 156pp; English.
XX
XX The sequence is that of tyrosine kinase clone RTK-6, isolated
XX from adult or embryonic (E13) rat brain cDNA, which shows
XX homology to the known tyrosine kinase molecules h kit, h rsflr,
XX hpcgalfapar and mcsfpr. It may be of use in the treatment of
XX neurodegenerative disease/neurotrauma including motor neuron
XX disorders such as amyotrophic lateral sclerosis, Werdnig-Hoffman
XX disease, chronic proximal spinal muscular atrophy and Guillain-Barre
XX syndrome. It may also be of use in the treatment of neurological
XX disorders associated with diabetes, Parkinson's disease,
XX Alzheimer's disease and Huntington's chorea.
XX See also AAQ30715-Q30728.
XX
XX Sequence 159 BP; 38 A; 36 C; 50 G; 35 T; 0 other;

Query Match 0.68; Score 23; DB 13; Length 159;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3167 gtggtgaagatctgtgactttgg 3189
Db 22 gtggtgaagatctgtgactttgg 44
|||||
|||||

RESULT 30
AAV70215
ID AAV70215 standard; DNA; 159 BP.
XX
XX AC AAV70215;
XX
XX 11-FEB-1999 (first entry)
XX
XX Rat orphan tyrosine kinase receptor peptide clone RTK-6 encoding DNA.
XX
XX Receptor tyrosine kinase; Ror-1; Ror-2; Ehk-1; Ehk-2; detection;
XX neurotrophin activity; trkB; proto-oncogene; tyrosine kinase receptor;

```

```

KW binding protein; BDNF; NT-3; diagnosis; ss.
XX
XX Synthetic.
XX OS Rattus sp.
XX
XX PN US5843749-A.
XX
XX PD 01-DEC-1998.
XX
XX 06-JUN-1995; 95US-0469537.
XX
XX 17-MAR-1995; 95US-0406247.
XX
XX 26-JUL-1991; 91US-0736559.
XX
XX 28-OCT-1993; 93US-0144992.
XX
XX 06-JUN-1995; 95US-0469537.
XX
XX (REG- ) REGENERON PHARM INC.
XX
XX Maisonpierre PC, Masiakowski P, Yancopoulos GD;
XX
XX WPI: 1999-044584/04.
XX P-PSDB: AAW83155.
XX
XX DNA encoding receptor tyrosine kinase proteins - and corresponding
XX proteins
XX
XX Example; Fig 12C; 194pp; English.
XX
XX The present invention describes nucleic acid molecules for ror-1,
XX ror-2, ehk-1 and ehk-2. Also described are the corresponding proteins:
XX CC Ror-1; Ror-2; Ehk-1; and Ehk-2. The proteins are orphan receptor
XX CC tyrosine kinases. The present sequence encodes a rat orphan tyrosine
XX CC kinase receptors peptide clone from the present invention.
XX
XX Sequence 159 BP; 38 A; 36 C; 51 G; 34 T; 0 other;

Query Match 0.6%; Score 23; DB 20; Length 159;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3167 gtggtgaagatctgtgactttgg 3189
Db 22 gtggtgaagatctgtgactttgg 44
|||||
|||||

RESULT 31
AAQ54036
ID AAQ54036 standard; cDNA; 1894 BP.
XX
XX AC AAQ54036;
XX
XX 12-JUL-1994 (first entry)
XX
XX DE Flk-2ws gene.
XX
XX Polymerase chain reaction; primer; amplify; PCR; fetal liver kinase-2;
XX Flk-2; nested; mouse; mFlk-2; PCLII; inhibition; binding;
XX ligand; receptor; modulation; growth; haematopoietic progenitor cell;
XX antibody; ss.
XX
XX Mus musculus.
XX
XX Key Location/Qualifiers
XX CDS 31..1476
XX /*tag= a
XX /product= Soluble Flk-2
XX
XX WO9401576-A.
XX
XX 20-JAN-1994.
XX
XX 07-JUL-1993; 93WO-US06404.

```

```

XX 09-JUL-1992: 92US-0912122.
XX (SYST-) SYSTEMIX INC.
XX Yang Z;
XX WPI: 1994-035079/04.
XX P-PSDB: AAR47579.
XX New soluble and human foetal liver kinase-2 DNA sequences - used
XX for obtaining prods. for modulating the growth of haematopoietic
XX progenitor cells
XX Claim 1: Paqe 11-14; 2lpp: English.
XX This sequence encodes murine soluble foetal liver kinase-2 (Flk-2ws).
XX This sequence was isolated using the primer sequences given in AAQ54034-
XX 35. Primer PCLF1 corresponds to mFlk-2 nucleotide positions 1-24,
XX except that at position 2, C is changed to A, and primer PCLF
XX corresponds to mFlk-2 nucleotide positions 341-3428 (sic). This
XX sequence may be used in the production of Flk-2 protein. The
XX resulting proteins may be used in culture and in vivo for inhibiting
XX binding of the Flk-2 ligand to the Flk-2 receptor. Therefore they may
XX be used for modulating the growth of haematopoietic progenitor cells.
XX The proteins may also be used for producing antibodies for identifying
XX cells carrying Flk-2, removing soluble Flk-2 from culture fluids or
XX natural fluids, purifying Flk-2 or assaying for the presence of
XX Flk-2.
XX Sequence 1894 BP; 494 A; 459 C; 500 G; 441 T; 0 other;

Query Match 0.6%; Score 23; DB 15; Length 1894;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3167 qcggtgaagatctgtgactttgg 3189
DB 976 qcggtgaagatctgtgactttgg 998

RESULT 32
AAQ29954
ID AAQ29954 standard; cDNA: 3453 BP.
AC AAQ29954;
XX 15-MAR-1993 (first entry)
XX Murine flk-2 cDNA sequence.
XX Thymidine kinase; TK; haematopoietic; stem cells; proliferation;
XX differentiation; progenitor cells; foetal liver kinase; ss.
XX Mus musculus.
XX Key Location/Qualifiers
XX CDS 31..3009
XX sig_peptide 31..111
XX mat_peptide 112..3006
XX FT /*tag= a
XX W09217486-A.
XX PN
XX 15-OCT-1992.
XX 02-APR-1992; 92WO-US02750.
XX 02-APR-1991; 91US-0679666.
XX 28-JUN-1991; 91US-0728913.
XX 15-NOV-1991; 91US-0793065.
XX 24-DEC-1991; 91US-0813593.
XX (UYPR-) UNIV PRINCETON.

```

```

XX Lemischka IR;
XX WPI: 1992-366185/44.
XX P-PSDB: AAR28038.
XX Stimulating proliferation and/or differentiation of primitive
XX mammalian haematopoietic stem cells - using ligand that binds
XX thymidine kinase and flk-1 and flk-2
XX Claim 6: Fig 1a; 94pp; English.
XX The murine foetal liver kinase (flk) -2 clone was isolated by
XX standard PCR techniques from stem-cell receptor-contg. tissue cDNA
XX libraries. Suitable tissues include foetal liver, spleen or thymus
XX cells or adult marrow or brain cells. The PCR primers used are based
XX on known sections of the flk-2 gene. The murine flk-2 clone may be
XX used in a vector to transform haematopoietic cells. The thymidine
XX kinase encoded by flk-2 is expressed in primitive but not mature
XX haematopoietic cells. Ligand binding to the TK may be prepd. which
XX can stimulate proliferation and/or differentiation of primitive
XX haematopoietic cells in vivo. The ligands can stimulate the
XX proliferation of additional primitive stem cells, differentiation into
XX more mature progenitor cells, or both.
XX See also AAQ29955-7.
XX Sequence 3453 BP; 945 A; 822 C; 876 G; 809 T; 0 other;

Query Match 0.6%; Score 23; DB 13; Length 3453;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3167 gtggtgaagatctgtgactttgg 3189
DB 2509 gtggtgaagatctgtgactttgg 2531

RESULT 33
AAQ53502
ID AAQ53502 standard; cDNA: 3453 BP.
AC AAQ53502;
XX 27-JUN-1994 (first entry)
XX Murine flk-2 cDNA.
XX Receptor protein tyrosine kinase; pTK family; foetal liver kinase;
XX mflk; primitive; totipotent; haematopoietic cell; stem cell;
XX proliferation; stromal cell; ds.
XX Mus musculus.
XX Key Location/Qualifiers
XX CDS 31..3009
XX FT /*tag= a
XX sig_peptide 31..111
XX mat_peptide 112..3006
XX FT /*tag= b
XX FT /*tag= c
XX US5270458-A.
XX PN
XX 14-DEC-1993.
XX 02-APR-1991; 91US-0679666.
XX 02-APR-1991; 91US-0679666.
XX 28-JUN-1991; 91US-0728913.
XX 15-NOV-1991; 91US-0793065.
XX 24-DEC-1991; 91US-0813593.
XX 26-JUN-1992; 92US-0906397.

```

PR 12-NOV-1992; 92US-0975049.
 PR 19-NOV-1992; 92US-0977451.
 XX
 PA (UYPR-) UNIV PRINCETON.
 XX
 PI Lemischka IR;
 XX
 XX WPI; 1993-405021/50.
 DK P-PSDB; AAR44994.
 DR
 XX

XX Isolated nucleic acid molecules of hematopoietic stem cell
 PT receptor flk-2 - encoding mammalian receptor protein tyrosine
 PT kinases expressed in primitive haematopoietic cells
 XX
 XX Claim 2; Fig 1a; 60pp; English.
 PS
 CC Nucleic acid sequences coding for murine flk-2 and specified
 CC subfragments of it are claimed. The flk-2 polypeptide is a protein
 CC tyrosine kinase expressed only in primitive haematopoietic cells.
 CC The cDNA can be used to recombinantly produce flk-2 for stimulating
 CC self-renewal of totipotent stem cells and development of all
 CC haematopoietic cells.
 XX
 SQ Sequence 1453 BP; 947 A; 821 C; 876 G; 809 T; 0 other;

Query Match 0.6%; Score 23; DB 14; Length 3453;

Best Local Similarity 100.0%; Pred. No. 3.8;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3167 gtggtgaagatctgtgactttgg 3189
 |||||
 Db 2509 gtggtgaagatctgtgactttgg 2531

RESULT 34

AAQ35249
 ID AAQ35249 standard; cDNA; 3453 BP.

AC AAQ35249;

XX 25-JUN-1993 (first entry)

XX Murine flk-2 coding sequence.

XX Murine; receptor; protein; tyrosine kinase; pTK; primitive; mammalian;
 KW hematopoietic cell; pHC; mature; mHC; fetal; liver kinase 2; flk-2;
 KW liver; spleen; thymus; adult; brain; marrow; thymocyte; subset;
 KW multipotential; T-lymphoid; lineage; ss.

XX Mus musculus.

XX Key Location/Qualifiers
 FH CDS 31..3009
 FT /*tag= a
 FT misc_RNA 31..111
 FT /*tag= b
 FT /*note= "Hydrophobic leader"

XX WO9300349-A.

XX 07-JAN-1993.

XX 26-JUN-1992; 92WO-US05401.

XX 28-JUN-1991; 91US-0728913.

PR 15-NOV-1991; 91US-0793065.

PR 24-DEC-1991; 91US-0813593.

PR 02-APR-1992; 92WO-US02750.

XX (UYPR-) UNIV PRINCETON.

XX Lemischka IR;

PI

XX

DR WPI; 1993-036323/04.
 DR P-PSDB; AAR31375.

XX

XX Nucleic acid encoding receptor protein tyrosine kinase - allows
 PT development of ligands to stimulate proliferation and/or
 PT differentiation of mammalian haematopoietic stem cells

XX

PS Claim 5; Fig 1a; 78pp; English.

XX

CC This sequence encodes a murine receptor protein tyrosine kinase which
 CC belongs to a new functional class of protein tyrosine kinases (pTKs).
 CC pTKs in this class are expressed in primitive mammalian hematopoietic
 CC (pHC) cells but not in mature hematopoietic cells (mHC). The protein
 CC encoded by this sequence is an example of a receptor pTK and is called
 CC fetal liver kinase 2 (flk-2). flk-2 is expressed in fetal liver,
 CC spleen and thymus, and adult brain and marrow. Expression of flk-2
 CC mRNA occurs in the most primitive thymocyte subset, which is believed
 CC to be uncommitted. Therefore, thymocytes expressing flk-2 may be
 CC multipotential. flk-2 is the first receptor tyrosine kinase known to
 CC be expressed in the T-lymphoid lineage.

XX SQ

Sequence 3453 BP; 947 A; 821 C; 876 G; 809 T; 0 other;

Query Match 0.6%; Score 23; DB 14; Length 3453;

Best Local Similarity 100.0%; Pred. No. 3.8;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3167 gtggtgaagatctgtgactttgg 3189
 |||||
 Db 2509 gtggtgaagatctgtgactttgg 2531

RESULT 35

AAQ40914

ID AAQ40914 standard; cDNA; 3453 BP.

XX AAQ40914;

XX 19-OCT-1993 (first entry)

XX Murine flk-2 cDNA.

XX Murine; receptor; protein; tyrosine kinase; pTK; flk-2; primitive;
 KW hematopoietic cell; mature; family; conserved; region;
 KW catalytic domain; c-kit; fetal liver kinase; flk; fetal; spleen;
 KW thymus; adult; brain; bone marrow; multipotential; CFU-Blast colony;
 KW hierarchy; transduction; T-lymphoid; lineage; ss.

XX Mus musculus.

XX Key Location/Qualifiers
 FH CDS 31..3009
 FT /*tag= a
 FT sig_peptide 31..111
 FT /*tag= b
 FT /*note= "Hydrophobic leader sequence"
 FT mat_peptide 112..3006
 FT /*tag= c

XX WO9310136-A.

XX 27-MAY-1993.

XX 16-NOV-1992; 92WO-US09893.

XX 15-NOV-1991; 91US-0793065.

XX (UYPR-) UNIV PRINCETON.

XX Lemischka IR;

PI

XX

```

DR WPI: 1993-182479/22.
XX P-PSDB: AAR37502.
PT Totipotent haematopoietic stem cell receptors, their ligands and
PT DNA sequences - for treating anaemia(s) and bone marrow damage
PT due to e.g. cancer chemotherapy or radiotherapy
XX
XX Claim 6: Fig 1a: 127pp: English.
XX
CC This sequence encodes the murine receptor protein tyrosine kinase
CC (pTK), flk-2. This nucleic acid is expressed in primitive hemato-
CC poietic cells and not in mature hematopoietic cells. Members of
CC this family of pTK's can be recognised by the conserved amino acid
CC regions in the catalytic domain. This family of pTK's also contains
CC c-kit. These new receptors are termed fetal liver kinases (flk's)
CC after the tissue in which they were discovered. flk-2 is also
CC expressed in fetal spleen, fetal thymus, adult brain and adult
CC bone marrow. flk-2 is expressed in individual multipotential CFU-
CC Blast colonies capable of generating numerous multilineage colonies
CC upon replating. It is likely therefore, that flk-2 is expressed in
CC the entire primitive portion of the hematopoietic hierarchy. This is
CC consistent with flk-2 being important in transducing putative self-
CC renewal signals from the environment. flk-2 is the first receptor
CC pTK known to be expressed in the T-lymphoid lineage.
XX
SQ Sequence 3453 BP; 947 A; 822 C; 875 G; 809 T; 0 other;

Query Match      0.6%; Score 23; DB 14; Length 3453;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3167 gtggtgaagatctgtgactttgg 3189
    |||||
DB 2509 gtggtgaagatctgtgactttgg 2531

RESULT 36
AAQ81012
ID AAQ81012 standard; cDNA; 3453 BP.
XX
AC AAQ81012:
XX
XX 16-AUG-1995 (first entry)
XX
XX Flk2 receptor protein-tyrosine-kinase cDNA.
XX
XX Mouse Flk2; receptor protein-tyrosine-kinase; primitive
XX hematopoietic cell; fetal liver kinase; ds.
XX
XX Mus musculus.
XX
XX Key Location/Qualifiers
XX CDS 31..3009
XX
XX sig_peptide /*tag= a
XX mat_peptide 31..111
XX /*tag= b
XX /*tag= c
XX
XX WO9500554-A.
XX
XX 05-JAN-1995.
XX
XX 17-JUN-1994; 94WO-US06944.
XX
XX 18-JUN-1993; 93US-0080244.
XX 21-JUN-1993; 93US-0081508.
XX 23-NOV-1993; 93US-0157490.
XX
XX (UYPR-) UNIV PRINCETON.
XX

```

```

PI Lemischka IR;
XX
XX WPI: 1995-052014/07.
DR P-PSDB: AAR67815.
XX
XX Ligand for receptor protein tyrosine kinase - useful for the
XX stimulation of primitive haematopoietic stem cells causing
XX proliferation and/or differentiation
XX
XX Disclosure: Fig 1a: 131pp: English.
XX
XX The sequence corresponds to a cDNA encoding a mouse Flk2 (fetal
XX liver kinase) receptor protein-tyrosine-kinase. Flk2 is expressed
XX in primitive hematopoietic cells but not in mature hematopoietic
XX cells. The gene product is useful in isolation of receptor ligands,
XX which have applications in diagnosis of bone marrow disorders and in
XX stimulating proliferation and/or differentiation of primitive
XX hematopoietic stem cells.
XX
XX Sequence 3453 BP; 947 A; 822 C; 875 G; 809 T; 0 other;

Query Match      0.6%; Score 23; DB 16; Length 3453;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3167 gtggtgaagatctgtgactttgg 3189
    |||||
DB 2509 gtggtgaagatctgtgactttgg 2531

RESULT 37
AAQ79068
ID AAQ79068 standard; cDNA; 3453 BP.
XX
XX AAQ79068;
XX
XX 04-JUL-1995 (first entry)
XX
XX Mouse flk-2 cDNA.
XX
XX Fetal liver kinase-2; flk-2; protein tyrosine-kinase receptor;
XX hematopoiesis; stem cell; ds.
XX
XX Mus sp.
XX
XX Key Location/Qualifiers
XX CDS 58..3039
XX
XX sig_peptide /*tag= a
XX mat_peptide 58..138
XX /*tag= b
XX /*tag= c
XX
XX US5367057-A.
XX
XX 22-NOV-1994.
XX
XX 02-APR-1991; 91US-0679666.
XX
XX 02-APR-1991; 91US-0679666.
XX 28-JUN-1991; 91US-0728913.
XX 15-NOV-1991; 91US-0793065.
XX 24-DEC-1991; 91US-0813593.
XX 26-JUN-1992; 92US-0906397.
XX 12-NOV-1992; 92US-0975049.
XX 19-NOV-1992; 92US-0977451.
XX 30-APR-1993; 93US-0055269.
XX
XX (UYPR-) UNIV PRINCETON.
XX
XX Lemischka IR;
XX

```

```

DR WPI: 1995-005894/01.
XX P-PSDB: AAR67535.
PT Murine flk-2 receptor protein tyrosine kinase - used to stimulate
PT proliferation and/or stimulation of primitive mammalian
PT haematopoietic stem cells in vitro or in vivo.
XX
XX PS Disclosure: Fig. 1A-1F; 69pp; English.
XX
XX CC cDNAs encoding receptor protein tyrosine-kinases, mouse foetal liver
XX kinase-2 (flk-2), human flk-2 and mouse flk-1 are given in AAR67535-70,
XX respectively, and the deduced amino acid sequences in AAR67535-37,
XX respectively.
XX SQ Sequence 1453 BP; 946 A; 822 C; 876 G; 809 T; 0 other:

Query Match      0.6%; Score 23; DB 16; Length 3453;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3167 gtcgtgaagatctgtgactttgg 3189
    |||||
Db 2509 gtcgtgaagatctgtgactttgg 2531

RESULT 38
AAT38733
ID AAT38733 standard; cDNA; 3453 BP.
XX
AC AAT38733;
XX
XX 11-DEC-1996 (first entry)
XX
XX Human foetal liver kinase 2 cDNA.
XX
XX Human; foetal liver kinase 2; flk-2; protein tyrosine kinase;
XX monoclonal; antibody; extracellular domain; receptor assay;
XX haematopoietic stem cell; ligand; stimulation; proliferation;
XX differentiation; treatment; anaemia; bone marrow damage;
XX cancer chemotherapy; radiation; ds.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 31..3009
XX sig_peptide /*tag= a
XX mat_peptide /*tag= b
XX /*tag= c

US548065-A.
20-AUG-1996.
02-APR-1991; 91US-0679666.
19-NOV-1992; 92US-0977451.
02-APR-1991; 91US-0679666.
28-JUN-1991; 91US-0728913.
15-NOV-1991; 91US-0793065.
24-DEC-1991; 91US-0813593.
26-JUN-1992; 92US-0906397.
12-NOV-1992; 92US-0975049.
30-APR-1993; 93US-0055269.
31-OCT-1994; 94US-0252517.
(UYPR-) UNIV PRINCETON.
Lemischka IR;
WPI: 1996-392678/39.
XX

```

```

DR P-PSDB: AAR97418.
XX
XX Anti-foetal liver kinase 2 (flk-2) antibodies - useful in assays,
XX for isolating haematopoietic stem cells expressing receptor and for
XX obtaining ligands
XX
XX PS Disclosure: Columns 27-34; 50pp; English.
XX
XX CC The present sequence encodes human foetal liver kinase 2 (flk-2), a
XX protein tyrosine kinase. Isolated antibodies, pref. monoclonal,
XX raised against the extracellular portion of flk-2 can be used to
XX assay for flk receptors on the surface of primitive haematopoietic
XX stem cells, and to isolate positive cells. The antibodies can also
XX be used as, or to obtain ligands, which stimulate the proliferation
XX and/or differentiation of stem cells. The ligands can be used, e.g.
XX for treating anaemia, or bone marrow damage resulting from cancer
XX chemotherapy, or radiation.
XX SQ Sequence 3453 BP; 947 A; 822 C; 875 G; 809 T; 0 other:

Query Match      0.6%; Score 23; DB 17; Length 3453;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3167 gtcgtgaagatctgtgactttgg 3189
    |||||
Db 2509 gtcgtgaagatctgtgactttgg 2531

RESULT 39
AAT72118
ID AAT72118 standard; cDNA; 3453 BP.
XX
XX AAT72118;
XX
XX 19-AUG-1997 (first entry)
XX
XX Murine flk-2 receptor coding sequence.
XX
XX Human; fetal liver kinase 2; flk2; receptor protein tyrosine kinase;
XX pTK; liver; spleen; thymus; adult; brain; bone marrow; primitive portion;
XX haematopoietic hierarchy; extracellular domain; soluble form; ligand;
XX proliferation; differentiation; mammalian; haematopoietic stem cell;
XX macrocytic anaemia; aplastic anaemia; cancer; radiation; mouse; ss.
XX Mus musculus.
XX
XX Key Location/Qualifiers
XX CDS 31..3009
XX /*tag= a
XX sig_peptide /*product= Murine_flk-2
XX /*tag= b
XX mat_peptide 112..3006
XX /*tag= c

US5621090-A.
15-APR-1997.
02-APR-1991; 91US-0679666.
26-JUN-1992; 92US-0906397.
02-APR-1991; 91US-0679666.
28-JUN-1991; 91US-0728913.
15-NOV-1991; 91US-0793065.
24-DEC-1991; 91US-0813593.
(UYPR-) UNIV PRINCETON.
Lemischka IR;
XX

```

```

DR WPI: 1997-235228/21.
DR P-PSDB; AAW19874.
XX
PT Protein containing the extracellular domain of human flk-2 - used
PT for identification of primitive haematopoietic cell proliferation
PT and differentiation stimulatory ligands, e.g. for treating anaemia
XX
PS Disclosure; Fig 1A; 55pp; English.
XX
CC This sequence encodes the murine fetal liver kinase 2 (flk2). flk-2 is
CC a receptor protein tyrosine kinase (pTK) and is important in transducing
CC putative self-renewal signals from the environment. flk-2 is expressed
CC in fetal liver, spleen, fetal thymus, adult brain and adult bone marrow,
CC and it is thought that flk-2 is expressed in the entire primitive portion
CC of the haematopoietic hierarchy. The invention concerns a recombinant
CC nucleic acid, preferably mRNA, which encodes a protein containing only
CC the extracellular domain of human flk-2 and lacking the flk-2 intra-
CC cellular catalytic domain. The resultant protein represents a soluble
CC form of flk-2 which is used to isolate specific ligands for flk-2. These
CC ligands can be used to stimulate proliferation and/or differentiation of
CC mammalian haematopoietic stem cells, in vivo or in vitro, e.g. for
CC treatment of macrocytic or aplastic anaemia or bone marrow damage caused
CC by cancer treatment or radiation.
XX
SQ Sequence 3453 BP; 947 A; 822 C; 875 G; 809 T; 0 other;

Query Match      0.6%; Score 23; DB 18; Length 3453;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1167 qtaqtgaagatctgtgactttgg 3189
    |||||
DB 2509 qtggtgaagatctgtgactttgg 2531

RESULT 40
AAX77514
ID AAX77514 standard; cDNA; 3453 BP.
XX
AC AAX77514;
XX
DT 05-AUG-1999 (first entry)
XX
DE Murine flk-2 cDNA.
XX
KW Murine; flk-2; flk-1; cell isolation; fetal liver kinase; receptor;
KW monoclonal; polyclonal; antibody; tyrosine kinase; ds.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT CDS 31..3009
FT CDS /*tag= a
FT /*product= "flk-2"
XX
PN US5912133-A.
XX
PD 15-JUN-1999.
XX
PF 10-FEB-1998; 98US-0021324.
XX
PR 19-NOV-1992; 92US-0977451.
PR 02-APR-1991; 91US-0679666.
PR 28-JUN-1991; 91US-0728913.
PR 15-NOV-1991; 91US-0793065.
PR 24-DEC-1991; 91US-0813593.
PR 26-JUN-1992; 92US-0906397.
PR 12-NOV-1992; 92US-0975049.
PR 30-APR-1993; 93US-0055269.
PR 31-OCT-1994; 94US-0252498.
PR 15-FEB-1996; 96US-0601891.
XX
PA (UYPR-) UNIV PRINCETON.
XX
PI Lemischka IR;
XX
DR WPI: 1999-357194/30.
DR P-PSDB; AAY08616.
XX
PT Isolating hematopoietic cells expressing fetal liver kinase 1
PT receptors
XX
PS Disclosure; Fig 1a; 59pp; English.
XX
CC This invention describes a novel method of isolating cells expressing
CC fetal liver kinase 1 (flk-1) receptors on their surface and comprises
CC binding the cells to a polyclonal or monoclonal antibody specific to
CC the FLK-1 receptor and isolating the cells that have bound to the
CC antibody. The method can be used to isolate hematopoietic stem cells in
CC any mammal but preferably a rat, mouse, rabbit or human. The proteins of
CC the invention belong to the receptor protein family. This sequence
CC encodes the murine flk-2 protein which is used in the method of the
CC invention.
XX
SQ Sequence 3453 BP; 947 A; 822 C; 875 G; 809 T; 0 other;

Query Match      0.6%; Score 23; DB 20; Length 3453;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3167 gtggtgaagatctgtgactttgg 3189
    |||||
DB 2509 gtggtgaagatctgtgactttgg 2531

RESULT 41
AAT00801
ID AAT00801 standard; DNA; 3521 BP.
XX
AC AAT00801;
XX
DT 29-FEB-1996 (first entry)
XX
DE Flk2/flt3 tyrosine kinase receptor gene.
XX
KW Tyrosine kinase receptor; flk2; flt3; agonist; monoclonal antibody;
KW haematopoiesis; hypoplasia; anaemia; thrombocytopenia; stem cell; ss.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT CDS 82..3084
FT CDS /*tag= a
XX
PN W09527062-A1.
XX
PD 12-OCT-1995.
XX
PF 23-MAR-1995; 95WO-US03718.
XX
PR 04-APR-1994; 94US-0222299.
XX
PA (GETH ) GENENTECH INC.
XX
PI Bennett BD, Broz SD, Matthews W, Zeigler FC;
XX
DR WPI: 1995-358636/46.
DR P-PSDB; AAR81868.
XX
PT Agonist antibody which binds to flk2-flt3 tyrosine kinase receptor
PT - enhances proliferation of haematopoietic stem cells, in the
PT treatment of hypoplasia, anaemia, etc.
XX
XX Example 1; Page 34-37; 59pp; English.
PS

```

XX DNA (AAT00801) coding for murine stem cell tyrosine kinase receptor flk2
 CC (also called flt3) (AAR31868) was obtcd. by RT-PCR amplification of RNA
 CC isolated from mid-gestation mouse foetal livers using primers based
 CC on the murine flt3 sequence, and subcloning of the product into pRK5.1.
 CC An flk2/flt3 extracellular domain-IgG1 Fc fusion protein was
 CC constructed and used to raise agonist antibodies able to bind Lo, and
 CC activate, flk2/flt3.
 XX
 SQ Sequence 3521 BP; 943 A; 853 C; 908 G; 817 T; 0 other;

Query Match 0.6%; Score 23; DB 16; Length 3521;
 Best Local Similarity 100.0%; Pred. No. 3.8;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3167 gtggtgaagatctgtgactttgg 3189
 |||||
 DB 2560 gtggtgaagatctgtgactttgg 2582

RESULT 42
 AA006869
 1D AA006869 standard: DNA; 4054 BP.

XX AA006869;

XX 07-MAR-1991 (first entry)

XX Sequence encodes Platelet derived growth factor (PDGF) receptor protein.

XX Atherosclerosis; fibrotic diseases; ds.

XX Homo sapiens.

XX Key Location/Qualifiers
 FT CDS 205..3471
 FT /*tag= a

XX W09014425-A.

XX 29-NOV-1990.

XX 21-MAY-1990; 90WO-US02849.

XX 22-MAY-1989; 89US-0355018.

XX (ZYMO-) ZYMOGENETICS INC.

XX Kelly JD, Murray MJ;

XX WPI; 1990-375992/50.

XX P-PSDB; AAR08267.

XX DNA encoding platelet-derived growth factor - used to transform cells for culturing to detect PDG agonists and antagonists

XX Claim 1: Fig 1: 30pp; English.

XX Gene product may be expressed from a transformed cell. It has utility in detection of PDGF agonist and antagonist analogues, binding AA, AB and BB isoforms. PDGF agonists may be used to enhance wound healing, and antagonists may be used to block the effects of PDGF eg. in treatment of atherosclerosis or fibrotic diseases.

XX Sequence 4054 BP; 1127 A; 886 C; 1027 G; 1014 T; 0 other;

Query Match 0.6%; Score 23; DB 11; Length 4054;
 Best Local Similarity 100.0%; Pred. No. 3.7;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3170 gtgaagatctgtgactttggcct 3192
 |||||
 DB 2698 gtgaagatctgtgactttggcct 2720

RESULT 43
 AA005989
 1D AA005989 standard; cDNA; 6412 BP.

XX AA005989;

XX 16-JAN-1991 (first entry)

XX TR4 cDNA clone related to T11 gene encoding alpha type PDGF receptor.

XX Platelet derived growth factor; ss.

XX Homo sapiens.

XX Key Location/Qualifiers
 FH CDS 139..3408
 FT /*tag= a
 FT sig_peptide 139..207
 FT /*tag= b
 FT mat_peptide 208..3405
 FT /*tag= c
 FT /*product=T11 receptor
 FT exon 2701..2812
 FT /*tag= d
 FT /*label-exon a
 FT exon 2813..2912
 FT /*tag= e
 FT /*label-exon b
 FT exon 2913..3018
 FT /*tag= f
 FT /*label-exon c
 FT polyA_signal 6353..6358
 FT /*tag= g
 FT polyA_site 6376..6412
 FT /*tag= h

XX W09010013-A.

XX 07-SEP-1990.

XX 08-FEB-1990; 90WO-US00617.

XX 09-FEB-1989; 89US-0308282.

XX (USDC) US SEC OF COMMERCE.

XX Matsui T, Aaronson SA, Pierce JH;

XX WPI; 1990-290306/38.

XX P-PSDB; AAR06910.

XX Type alpha platelet-derived growth factor receptor gene - useful for transforming cells to express novel protein receptor and also susceptible to genetic engineering.

XX Claim 3; Fig 3; 64pp; English.

XX The TR4 clone is the largest cDNA clone related to the T11 genomic clone, isolated from a library prepd. from human thymus DNA. The T4 cDNA clone was isolated from a M426 human embryo fibroblast cDNA library. The exons shown were determined from the T11 genomic clone. The gene has been mapped to chromosome 4 at location q 11-12, which is within the same region as the c-kit proto-oncogene. The coding region can be introduced into the pSV2 gpt vector with a simian sarcoma virus LTR as a promoter and expressed in a host. The resulting protein is a novel PDGF receptor designated type alpha (the known receptor is designated type beta). The cDNA can be used also to investigate the

CC mechanisms of PDGF regulatory processes or in bioassays for detect-
CC ing related genes, particularly for identification of classes of
CC tumour cells or of genetic defects in connective tissue and/or
CC healing response.
XX
SQ Sequence 6412 BP; 1885 A; 1299 C; 1443 G; 1785 T; 0 other;

Query Match 0.6%; Score 23; DB 11; Length 6412;
Best Local Similarity 100.0%; Pred. No. 3.6; 0; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 0;

OY 3170 gtaagaatctgtgacttggcct 3192
|||||
Db 2632 gtaagaatctgtgacttggcct 2654

RESULT 44
AAT03102
ID AAT03102 standard; DNA; 22 BP.

XX AC AAT03102;
XX DT 14-FEB-1996 (first entry)
XX DE SAL-S1 gene PCR primer otk1.41.1.

XX KW Protein tyrosine-kinase; pTK; SAL-S1; agonist; cell growth;
XX KW differentiation; polymerase chain reaction; PCR; primer;
XX KW IgG; antibody; ss.
XX OS Synthetic.
XX PN W09527061-A1.
XX PD 12-OCT-1995.

XX PF 04-APR-1995; 95WO-US04228.
XX PR 04-APR-1994; 94US-0222616.
XX PA (GETH) GENENTECH INC.

XX PI Bennett BD, Goeddel D, Lee JM, Matthews W, Tsai SP;
XX PI Wood WI;
XX DR WPI; 1995-366160/47.

XX PR 04-APR-1994; 94US-0222616.
XX PA (GETH) GENENTECH INC.

XX PI Bennett BD, Goeddel D, Lee JM, Matthews W, Tsai SP;
XX PI Wood WI;
XX DR WPI; 1995-366160/47.

XX Aqonist antibodies which activate specific protein tyrosine
PT kinase(s) - also activate chimeric proteins of kinase extracellular
PT domain and Ig constant domain, useful for studying, and therapeutic
PT modulation of, cell growth and differentiation
XX Example 7; Page 101; 125pp; English.

XX PCR primers given in AAT03102-03 were used to amplify plasmid
CC PRK5.tkl1.1 (AAT03104) incorporating SAL-S1 (see AAT03090) DNA.
CC The product was used to construct a fusion of the SAL-S1
CC extracellular domain and human IgG1 Fc domain, which was expressed
CC in 293 and COS7 cells and used to raise antibodies having
CC protein tyrosine-kinase agonist activity.
XX Sequence 22 BP; 6 A; 3 C; 9 G; 4 T; 0 other;

Query Match 0.5%; Score 22; DB 16; Length 22;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2165 aggcctctgagagaaagtctg 2186
|||||
Db 1 aggcctctgagagaaagtctg 22

RESULT 45
AAT03103/C
ID AAT03103 standard; DNA; 32 BP.

XX AC AAT03103;
XX DT 14-FEB-1996 (first entry)
XX DE SAL-S1 gene PCR primer otk1.41.2.

XX KW Protein tyrosine-kinase; pTK; SAL-S1; agonist; cell growth;
XX KW differentiation; polymerase chain reaction; PCR; primer;
XX KW IgG; antibody; ss.
XX OS Synthetic.
XX PN W09527061-A1.
XX PD 12-OCT-1995.

XX PF 04-APR-1995; 95WO-US04228.
XX PR 04-APR-1994; 94US-0222616.
XX PA (GETH) GENENTECH INC.

XX PI Bennett BD, Goeddel D, Lee JM, Matthews W, Tsai SP;
XX PI Wood WI;
XX DR WPI; 1995-366160/47.

XX Agonist antibodies which activate specific protein tyrosine
PT kinase(s) - also activate chimeric proteins of kinase extracellular
PT domain and Ig constant domain, useful for studying, and therapeutic
PT modulation of, cell growth and differentiation
XX Example 7; Page 101; 125pp; English.
XX PCR primers given in AAT03102-03 were used to amplify plasmid
CC PRK5.tkl1.1 (AAT03104) incorporating SAL-S1 (see AAT03090) DNA.
CC The product was used to construct a fusion of the SAL-S1
CC extracellular domain and human IgG1 Fc domain, which was expressed
CC in 293 and COS7 cells and used to raise antibodies having
CC protein tyrosine-kinase agonist activity.
XX Sequence 32 BP; 4 A; 11 C; 9 G; 8 T; 0 other;

Query Match 0.5%; Score 22; DB 16; Length 32;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2323 cgaggataaggcagcatggag 2344
|||||
Db 32 CGAGGATAAGGCAGCATGGAG 11

Search completed: July 15, 2002, 23:09:35
Job time: 18393 sec

	Best Local Similarity	100.0%;	Pred. No. 0;	Matches	0;	Mismatches	0;	Indels	0;	Gaps	0;
	Matches 411;	Conservative	0;								
Qy	1	ccacgcgagcgccggagatgcagcggggcgccgcgcgtgtgcttgcaactgtggctctg	60								
Db	1	CCACGCGACGGCGGAGATGCAGCGGGCGCGCGCTGTGCCTGGGACTTGGCTCTG	60								
Qy	61	crtaggartcctggagcggccttggtagtggttaactccaatgatcccccccgaacttgaacat	120								
Db	61	CCTGGGACTCCTTGACGGCCCTTCGTAGTGGCTACTTCCAATGCCGCCGAGACTTTGAACAT	120								
Qy	121	cacggagagttcacacgttcacgcaccggtgcagaqctgtccattctcttcacagggaca	190								
Db	121	CACCGAGACATCACAGTTCATCGAACCGGTACAGCCTGTCCATTCTCTCAAGGACA	180								
Qy	181	qcacrrrclqagltgggctltqccagaaagtccagagggcgccagccarccqaqaaauqa	240								
Db	181	qACCCCCCTCAGTTCGGCTTCGGCAGGAGCTACAGSAGCGCAGCGACCGAGACAAAGA	240								
Qy	241	caqtcaaqacacgggggttggtagagactgcgagggcacagajucacagcccrlactlqrcaa	300								
Db	241	(AGCGAGACACGGGGTGGTTCGAGACTGCAGGGCACACAGCCAGGCCCTACTTCAA	300								
Qy	301	qvtlttgtctgnacgaggttacatgccaacgacacagcgagctacgtctctactataca	360								
Db	301	GCTGTTGCTGTGACGAGGTACATGCCAACGACACAGCCAGCTACGTCTGCTACTACAA	360								
Qy	361	qlacatcaagcacgcacatccagggcaccacagcccgccagctccactcgttgttcgtgaaga	420								
Db	361	GTACATCAAGGACCCCATCTGAGGGCACACCAGCCGCCAGCTTCTACGTGTTCGTGAGAGA	420								
Qy	421	cltlgagcagcatctcatcaaaagcttgacacgcctcttggttcaacaggaagaaagccat	480								
Db	421	CTTTTGACGAGCCATTATCAACAAGCCCTGACAGCCTCTTGCTCAACGAAGGACGCCAT	480								
Qy	481	glvggtgccttgttgttgttccalcccgggctcaattgtcaogcttgccttcqaaaagctc	540								
Db	481	GTGGGTGCCCTGTCTGTGTTCATCCC GGCGCTCAATCTCAGCTTGCCTCGCAAGCTC	540								
Qy	541	qvlqclgtggccagcgggraggaugttgattggaatgcrcggcgaggcatqrltqlqlc	600								
Db	541	GCTGCTGTGGCCACAGGGCGAGAGCTGCTGTGGATCACCGCGGGCGCATGCTCTGCTC	600								
Qy	601	cacygcarrlgtycaagalaqcrllqtacrlclraqtlqgaqaacraacttqqggaqncragga	660								
Db	601	CACGCCACTGTGACAGATGCGCTGTACTCTGACTGCGAGACCACTCTGGGAGAGCTAGGA	660								
Qy	661	cLtccttccraaccccttcccltqglqacatcacaggaacagagcttctatgacalcacact	720								
Db	661	CTTCTCTTCCAAACCCCTTCCCTGTGTGCACATCACAGGCAACGAGCTCTATGACATCCAGT	720								
Qy	721	gltcgrraagaauglcgcttggagcttqcttggtaauggagaagcttggcttgaarlqcaacct	780								
Db	721	CTTGCCCAAGGAATCGCTCGAGCTGCTGTTAGGGAGAAGCTTGGTCTCTGAATCACCCT	780								
Qy	781	glvggctaaaglttbaactcaggtgtcaaccttltgactlgggacttaccagaggaagcaagaga	840								
Db	781	GTGGGCTUAGTTTTAACTCAGGTGTACCTTTTACTTGGGACTACCCAGGGAAGCAGGCGAGA	840								
Qy	841	qcqyggttaagltggglgccccgagcagcrlcccagcagacccacacagaacltctcgaact	900								
Db	841	CGGGGTAACTGGGTGCCCGAGGACGCTCCACGAGACCCACACAGAACTCTCCAGCAT	900								
Qy	901	cctgaccalcacaacaglcagccagcagacacttgggcltqtlatlglqcaaqncaacaa	960								
Db	901	CCTGACCATCCACAACGTTCAGCCAGCAGCTGGGCTCTGTATGTCTGCAAGGCTCAACAA	960								
Qy	961	cggatccagcgaatttcggaggaacacccaggttcalttgtcataaaalccrltcatcag	1020								
Db	961	CGGCATCCAGCGATTTTCGGGAGACCCAGGTCATTTGTGATGAAATCCCTTCATCAG	1020								
Qy	1021	ctglcagltggctcaaaagaccctaactctgagggccacgycaggagacagagrltqtlqaauct	1080								

Qy 2161 cagagggctctgagagaaagtctgagtcgacttgcggaactccaaccagaagctgag 2220
|||||
Db 2161 CGAGAGGCTGCTGGAUAGAAAGTCTGAGTCCGACTTGGCGACTTCCAAACAGAGCTGAG 2220
Qy 2221 catccagcgtatccagagaaatccgagagactatctgtcagcgtatgcaucuccaa 2280
|||||
Db 2221 CATCCAGCGGTGGCGGAGGAGGATGCGGAGCGTATCTGTGACAGCGTGTGCAACGCCAA 2280
Qy 2281 gggctgcatcaactccctccgcgaagcgtggcgtgagagagctccagagataagagcagcat 2340
|||||
Db 2281 GGGCTGCTCAACTCTCCGCCAGCGTGGCGTGGAGGCTCCGAGGATTAAGGCGACCAT 2340
Qy 2341 ggaagatcgtatctctgtcgttacccgcgtcactcgtcgtctctctctctctctctct 2400
|||||
Db 2341 GGAGATGCTGATCTTCTCGGTACCGCGCTCATCGCTGTCTTCTCTGGTTCCTCTCCCT 2400
Qy 2401 cctcctctctgttaacatgagagagcggccacgcagagacatacaagacggtctaccctgtc 2460
|||||
Db 2401 CTCTCATCTTCTTAACTAGAGAGCGCGCGCCACGCAGACATCAAGACGGGCTACCTGTCT 2460
Qy 2461 catcatcatgagacccggggaggtgcctctgagagagcaalgcgaataacctgtcctacga 2520
|||||
Db 2461 CATCATATGACCCCGGGAGGTGCCTCTGGAGGAGCAATGCCAATACCTGTCTCTACGA 2520
Qy 2521 tgcagcagcagtggaatcccccgagagcagctacacctaggagagatgctcagctacag 2580
|||||
Db 2521 TGCCAGCGCAGTGGGAATTTCCCGGAGAGCGGCTGCACCTGGGGAGAGTGTCTGGGCTACGG 2580
Qy 2581 cgcctctcggggaagtgaggagcctcgcgtcttcgggcatccacaaagagcagcagctctga 2640
|||||
Db 2581 CGCTCTCGGGAAGCTGCTGGGAAGCTTCGCTTTCGGGATTCACAAAGGCAACGCTCTGA 2640
Qy 2641 caccctgagcagtgagaaatgctgaagagggcgccacagcagcagcagcagcagcagcag 2700
|||||
Db 2641 CACCTGTGCGCTGTAATAATGCTGAAGAGGGTGGCACGCGCCACGAGACCGCGCGCTCAT 2700
Qy 2701 gtcgagcagcagtgagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 2760
|||||
Db 2701 GTGAGAGCTCAAGATCTTCATTTACATCGGCAATCACCTCAACGCTGTCACCTCTCTCGG 2760
Qy 2761 ggcgtgacacacagcagggggccctcctatggtgatcgtgaggttcttcaagagtcagcag 2820
|||||
Db 2761 GGCCTGACCAAGCGCAGCGGCCCTCATGCTGATCTGAGTTCTGCAAGTACGGCAA 2820
Qy 2821 cctctcctcactctctgagcagcagcagcagcagcagcagcagcagcagcagcagcag 2880
|||||
Db 2821 CCTCTCCAACTTCTTGGCGGCAAGCGGGACGCTTTCAGCCCCCTCCGCGGAGAAAGTCTCC 2880
Qy 2881 cagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 2940
|||||
Db 2881 CGAGCAGCGCGAGCGCTTTCGCGGTCATGCTGAGCTTCCGAGGTGCGATTCGAGGGCGCC 2940
Qy 2941 ggggagcagcagcaggggtctctctctcagcagcagcagcagcagcagcagcagcagcag 3000
|||||
Db 2941 GGGGAGCAGCGCACAGGGTCTCTTGGCGCGTCTTCGAAGACCGAGGCGCGAGCGAGCGC 3000
Qy 3001 ggcctctcagacccaagaagctgagagacactggtcagagcagcagcagcagcagcagcag 3060
|||||
Db 3001 GGTCTCTCCACACCAAGAGTGAAGGACCTGTGGCTGAGCGCGCTGACCATCGAAGATCT 3060
Qy 3061 gctcgtctacagctccaggtgagcagagagatgagttcctggtctcccgaaagtgcat 3120
|||||
Db 3061 TGCTCTCTACAGCTTCCAGGTGCGCAGAGGATGAGTTCTCTGGCTTCCCGAAGTGTGAT 3120
Qy 3121 ccacagagacactggtcgtcagacatctctgctgtggaagcagcagcagcagcagcagcag 3180
|||||
Db 3121 CCACAGACAGCTGCTGCTCGGAACATTTCTGCTCGGAAAGCGAGCTGGTGAAGATCTG 3180
Qy 3181 gactcttgaccttgcccgagacatctacaaagacactgactacatccacagagcagcagcag 3240
|||||
Db 3181 TGACTTTGGCTTGGCGGGACATCTACAAAGACCTGACTACGTCCGCAAGGCGCACTGC 3240

Qy 3241 ccggctgccccctaaagtgaatgagccctgaaagcatcttcgacaagtggtacacacgcga 3300
|||||
Db 3241 CCGGCTGCCCCCTCAAGTGGATGGCCCTGAAAGCATCTTCGACAAAGTGTACACCAAGCA 3300
Qy 3301 gagtgcagtggtgctcttgggtgctctctgagagatctctctctctctctctctctctctct 3360
|||||
Db 3301 GACTGAGCTGTGCTCTCTTGGGTGCTTCTCTGAGAGATCTTCTCTCTGGGGCCCTCCCC 3360
Qy 3361 gtacctgggggtcagatcaatgagagttctctccagcagcagcagcagcagcagcagcag 3420
|||||
Db 3361 GTACCTTGGGTGCTAGATCAATGAGGAGTTCCTCCAGCGCTGAGAGCGGCAACAAGGAT 3420
Qy 3421 gagggcccgagagctgacactcccccatacagcccatcagccatcatctgaaactgctggtccg 3480
|||||
Db 3421 GAGGGCCCCGAGAGCTGCCACTCCCGCCATACCGCCGATCATGCTGAACCTGCTGTGTCGG 3480
Qy 3481 agaccccaagcgagacctctgcatctctcagagctgggtgagatcctctggggacctgctcaa 3540
|||||
Db 3481 AGACCCCAAGCGGAGACTGCAATTCGGAGTGGTGGAGATCTCTGGGGACCTGTCTCA 3540
Qy 3541 ggcagggggcctcagagagagagaggtctcagatggcccccgagcagcagcagcagcagc 3600
|||||
Db 3541 GGCAGGGGGCTTCAAGAGAGAGAGAGGTTCATGTGGCCCCCGGAGCTCTCAGAGCTC 3600
Qy 3601 agagagggcagctctctcagaggtgtccacccatggccctacacatcgccccagcagctgacgc 3660
|||||
Db 3601 AGAAGAGGGCAGCTTCTCGCAGGTGTCCACCATGGCCCTACACATCGCCCGAGCTGACGC 3660
Qy 3661 tgaggacagcccgccaaagcctcagcagcagcagcagcagcagcagcagcagcagcagc 3720
|||||
Db 3661 TGAGGACAGCCCGCAAGCCTGCAGCGCCACAGCCTGGCGCCAGGTATTTACAACTGGGT 3720
Qy 3721 gtccttcccggtgctcgcagagagggctgagacccgtggtctccaggaalgaagac 3780
|||||
Db 3721 GTCTTTTCCCGGTGCTGCGCCAGAGGGCTGAGACCCGTGGTTCCTCCAGGATGAAGAC 3780
Qy 3781 atttgagaaattcccatgaccccaacagcctacaaaggctctgtgacaaccagacaga 3840
|||||
Db 3781 ATTTGAGAAATTTCCCATGACCCCAACGACCTACAAAGGCTCTCTGGACAACCCAGACA 3840
Qy 3841 cagtggatggtgctgctcagcagaggttctgagcagatagagagcagcagcagcagcag 3900
|||||
Db 3841 CAGTGGATGCTGTGCTCGCCTCGGAGGAGTTTGAGCAGATAGAGAGCAGGATAGACAAGA 3900
Qy 3901 aagcgtctcagctgtaaaagacctggccagaaatgtgctgtgacacagggcacaccctga 3960
|||||
Db 3901 AAGCGCTTCACTGTAAAGACCTGCCAAGATGTGCTGTGACCAAGGCAACCCCTGA 3960
Qy 3961 ctcccaagggagcggcggcggcctgagcggggggcccgagggagggcaggtgttttaca 4020
|||||
Db 3961 CTCCCAAGGAGGCGCGCGCTGAGCGGGGGCCGAGGAGGCGCAGGTGTTTACAA 4020
Qy 4021 cagcagataggggagcgtctgagacccaagcagagagacacactgctccccgtctgccc 4080
|||||
Db 4021 CAGCGATATGGGAGCTGTGCGAGCCCAAGCGAGGAGGACCTGCTCCCCGTGTGCCCG 4080
Qy 4081 cgtgacttctcacacacacagctactaa 4111
|||||
Db 4081 CGTGACTTTCTTCACAGAACACACTACTAA 4111

RESULT 2

LOCUS AR106406
DEFINITION Sequence 3 from patent US 6107046.
ACCESSION AR106406
VERSION AR106406.1 GI:12820936
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 4795)
AUTHORS Alitalo,K., Aprelikova,O., Pajusola,K., Armstrong,E., Korhonen,J.,

Kaipainen,A. and Matikainen,M.
Antibodies to Flt4, a receptor tyrosine kinase and uses thereof
JOURNAL Patent: US 6107046-A 3 22-AUG-2000;
FEATURES Location/Qualifiers
1, 4795
SOURCE
/organism="unknown"

HASE COUNT 977 a 1490 c 1494 g 834 t
ORIGIN

Query Match 100.0%; Score 4111; DB 6; Length 4795;
Best Local Similarity 100.0%; Prod. No. 0;
Matches 4111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ccacgcgacgcccggagatgacagcgggcgccgcgtgtgcttgccagcactgtgcttctg 60
nb 1 CCACGCGCACCGCCGGAGATCAGCGGGCGCCGCGTGTGCCCTGGACCTGTGCTCTCTG 60

Qy 61 cclggagactccllgagcygacctgtagtggcttactlccatlgacccccccagaccllaacat 120
nb 61 CCTGGGACTTCCCTGGAGCGGCTCGTTCAGTGGCTACTCCATGACCCCGCCGACCTTTGAACAT 120

Qy 121 cagcaggaagtacacgctcatcgacacacgggtgacagccttgctcatctctcagagga 180
nb 121 CACGGAGGACTCACAGCTCATCGACACACGCTGTGCACAGCCTGTCCATCTCTCCACGGGACA 180

Qy 181 gcacccccctcgataggcttggccaggagctcagggagcgccagcgcacccggagacaaga 240
nb 181 GCACCCCTTCGAGCTGGGCTTGGCCAGGAGCTCAGGAGCGCCAGCGCACCGGAGACAAGCA 240

Qy 241 cagcaggaacacaggggtgggtgcgagactggaagggcacagagcgccagggcactactca 300
nb 241 CACCGAGGACACGGGGTGGTTCGAGACTTCCGAGACTTCCGAGGGCACAGCGCAGGCCCTACTGCAA 300

Qy 301 ggtgttgccttgctgcagcaggtatcagcaacgacacagcagcagctcgtctgtactaca 360
nb 301 GGTGTTGCTGCTGCACAGAGTACATGCCAACGCACACAGCGACGCTACGCTGCTACTACAA 360

Qy 361 gtacatcaaggcacgcacaggggacacacgcccagcctcactcgttctgtgagaga 420
nb 361 GTACATCAAGGACGCCATCCAGGGACCAACGGCCGCGCAGCTCTACGCTCTCTGTGAGAGA 420

Qy 421 cttlgaagcagccatcatcaacaagcctlgacacgctctlggtlcaacagaaagacacat 480
nb 421 CTTTGCACGAGCCATTGATCAACAGCTTGACAGCTCTTTGTGTAACAGAGAGAGCGCCAT 480

Qy 481 gbggggtcccttcttggtgtlccatccccggcctcaatgtcacqctgagcttgcgaaagtcc 540
nb 481 GTGGGTGCCCTCTCTGCTTCCATCCCGGCCCTCAATGTCACGCTCGCGCTCGCAAGCTC 540

Qy 541 ggtgctgtggccagacggcagaggtggtgtlgnatgacccggggggcgtatgtcgtgtc 600
nb 541 GGTGCTGTGGCCAGACGGGCGAGAGTGGTGTGGGATGACCGGCGGGGCGATGCTGTCTC 600

Qy 601 cagcccaactgctgcacgatlccctctgtacctgcagtlgcagacacactgaggaagaccagga 660
nb 601 CACGCCACTGCTGCAGGATGCCCTGTACCTGCAGTGCAGAGACACCTGSGGGAAGACCA 660

Qy 661 ctctccttccaaaccccttctggtgtacatcacaggcaacagagctctatgacatccagct 720
nb 661 CTTCTCTTTCCAAACCCCTTCTCCTGGTCACATCACAGCAACAGAGCTCTATGACATCCAGCT 720

Qy 721 gttggccaggaagtccgttagctgtctgttaggggaagagctggctcctgaacttaccct 780
nb 721 GTTGGCCAGGAAGTCCGTGGAGCTGCTGGTAGGGGAGAGCTGGCTCTCAACTGACCCCT 780

Qy 781 gtaggctgaggtttaactcaagttgtcaccttctgactgggaactaccaggaagaaatcaacga 840
nb 781 GTGGGCTGAGTTTAATCTCAGGTTGCACCTTTGACTTGGCATTACCCAGGGAACAGGCAGA 840

Qy 841 ggggggttaagtggtgtgcccgaacacagcttcccagaaagacccacagaatcttccagat 900
nb 841 GCGGGGTAAAGTGGGTGCCCGGAGCGAGCTCCAGGAGAGCCACAGAGAAGCTTTCAGCAT 900

Qy 901 cctgaccatccacaacgctcagccagcagcagcctgggtcgtatgtgtgcgaagcacaacaa 960
nb 901 CCTGACCATTCCACAACGCTCAGCCAGCACGACCTGGCTCGTATGTTGTCGAAGGCGCAACA 960

Qy 961 cggcatccagcgaattlccgggagagacccaggtcatlgtlcatgaaatcccttccalcag 1020
nb 961 CGGCATCCAGCGATTTCGGGAGAGCACCGAGGTCAATTGTGCATGAANAATCCCTTTCATCAG 1020

Qy 1021 cgtcagtlggctcaaaaggaacccatccttgaggccacagcagcagcagctgggagagct 1080
nb 1021 CGTGAGTGGCTCAAAAGACCCATCCTTGGAGGCCAGCGACGACGAGCTGGTGAAGCT 1080

Qy 1081 gccctgaaagctggcagcgttaccctcccgccggagttccagttggtacaaagagtlgaaaggg 1140
nb 1081 GCCCTGAAGCTGGCAGCGTATCCGCCCGCCGAGTTCCAGTGGTACAAAGGATGGAAGGCG 1140

Qy 1141 actgtccggggcgccacagtcacatgccctgtgttctaagagaggtgacaaagggccaaagac 1200
nb 1141 ACTGTCCGGGGCGCCACAGTCCACATGGCTGTGCTCAANGAGGTGACAGAGGCGCACGAC 1200

Qy 1201 aggcaccttacacctcgccctgtggaactccgctgtggtcctggagggcgcaacatlcagcct 1260
nb 1201 AGGCACCTACACCTCGCCCTGTGGAAGTCCGCTGTGCTGTGAGGCGCAACATCAGCCT 1260

Qy 1261 ggagctggtggtgaaatgtgccccccagatatcatlgaaagagggcctcctccccagcat 1320
nb 1261 GGAGCTGCTGTAATGTGCCCGCCAGATACATCAGAAGGAGGCGCTCTCTCCCGCAGCAT 1320

Qy 1321 ctactcgggtcacagcgccagggccclcaactgcacggcctacggggtggccclggcclt 1380
nb 1321 CTACTCGGCTCACAGCGCCCGCAGGCCCTCACCCTGCAGCGCCTACGGGGTGGCCCTGCTCT 1380

Qy 1381 cagcatccagtgggcactggcgccctggacacctggacccttgcaagatgtttgcccagcgtagct 1440
nb 1381 CAGCATCCAGTGGCAGCTGGCGCCCTGGACACCTTGCAAGATGTTTGGCCACGCGTAGTCT 1440

Qy 1441 ccggcgggcgacgacgaagaccctcatgcccagtgccgtgactggagggggcggtgaccac 1500
nb 1441 CCGCGCGGCGGACGACGAAGACCTCATGCCACAGCTGCCGTGACTGGAGGGCGGTGACCAC 1500

Qy 1501 gcaggatccgtgaaaccccatcgagagcctggacacctggaccctggagttlgtlgaggagaaa 1560
nb 1501 GCAGGATCCGCTGAACCCCATCGAGAGCCTGGACACCTTGGACCGAGTTTGTGGAGGAAA 1560

Qy 1561 gaaataagactgtgagcaagctggtgtatccagaaatgcacaacgtgtctgccaatgtacaagt 1620
nb 1561 GAATAAGACTGTGAGCAAGCTGGTGTATCCAGAATGCCAACGTGTCTGCCATGTACAAGTG 1620

Qy 1621 tgtggtctccaacaagtlggggccaggatgacggctcatctactlctatgtgaccacat 1680
nb 1621 TGTGCTCTCCAACAAGGTGGGCGCAGGATGAGCGCTCATCTACTTCTATGTGACACCAT 1680

Qy 1681 cccqacggcttcaccaatccaaagccatccgagagcctactagaggccagcggcgt 1740
nb 1681 CCCGACGGCTTCAACCATCGAATCCAAAGCCATCCGAGGAGCTACTAGAGGGCCAGCCGCT 1740

Qy 1741 gctcctgagctgccaagccgacagctacaagtlacagagcatctgagctgggtaccgcctcaa 1800
nb 1741 GCTCTGAGCTGCCAAGCCGACAGCTACAAAGTACGAGCATCTGCGCTGGTGGTACCCCTCAA 1800

Qy 1801 cctgtccacgctgcacgatgcgcgggaacccgctctctgcctgacatgcagaagacgtgca 1860
nb 1801 CCTGTCCACGCTGCACGATGCGACGGGAACCCCGTTCTGCTGCAGCTGCAGAACGTTGCA 1860

Qy 1861 tctgttcgccccctctctggcccgagcctggaagaggtggcactggggcgccacagc 1920
nb 1861 TCTGTTCGCCACCCCTCTGGCGCGCAGCTGGAGAGGTGGCAGCTGGGGCGCGCCACGC 1920

Qy 1921 cagcgtcagcctgagatattcccccgcgctgcgccccgagcagcagggccactatgtgcga 1980
nb 1921 CAGCCTCAGCCTGAGTATCCCGCGCTGCGCGCCGAGCAGGAGGCCACTATGTGTGCGGA 1980

AK016568
LOCUS AR016568 4195 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 1 from patent US 5776755.
ACCESSION AR016568
VERSION AR016568.1 GI:3972845
KEYWORDS
SOURCE Unknown.
ORGANISM
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 4195)
Alicalo,K., Aprelikova,O., Pajusola,K., Armstrong,E., Korhonen,J.
and Kaipainen,A.
TITLE FLT4, a receptor tyrosine kinase
JOURNAL Patent: US 5776755-A 1 07-JUL-1998;
FEATURES Location/Qualifiers
1..4195
Source /organism="unknown"
BASE COUNT 889 a 1279 c 1305 g 722 t
ORIGIN
Query Match 95.2%; Score 3912; DB 6; Length 4195;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3912; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 caacgcacgagcggcggagagatgcacgcggggcgcgcgcgtgtgcctgcgactgtgctcty 60
Db 1 CCACGCCGACGGCGCGAGATGACGGGGCGCGCGCTGTGCCTGCGACTGTGGCTCTG 60
QY 61 cctgggactcctggagcgcctggtgagtggttactctatgcacccccgcaccttgaacat 120
Db 61 CTTGGGACTCTCTGGAGCGGCTTGTGAGTGGCTACTTCCATCACCCCCCGACCTTGAACAT 120
QY 121 cacggagagatcacacgtcatcacacacgggtgacagcctgtcatctctcagaggaaca 180
Db 121 CACGGAGGAGTTCACAGCTCATGCACACCGGTGCACAGCCTGTCCATCTCTGCGAGGGACA 180
QY 181 qcacccctccantaggtctggccaggaactcagagagccagagagccagccagaggaaga 240
Db 181 GCACCCCTCTGAGTGGGCTTGGCCAGGAGCTCAGGAGGCGCGAGCCACCGAGACAAGGA 240
QY 241 caacgaagacagcggggtggtgcgaacttcagagggcacagacgcgcagacccttactgcaa 300
Db 241 CACGAGGACACGGGGGTGTCGAGACTTCCGAGGTCGAGGGCACAGACGCCCTACTGCAA 300
QY 301 ggtgtgtcgtgcracgaggtacataccacacgacacagcagctacgtcgtartacaa 360
Db 301 GGTGTTGCTCTCCACGAGGTACATGCCAACGACACAGGCAGCTACGCTCTGCTACTACAA 360
QY 361 gtacalcaaggcacgcacatcgaaggacacagcagcccccactcctactcgttctgagaa 420
Db 361 GTACATCAAGGACAGCATCGAGGGCACCGGCCACCGCCGTCAGCTCTCTGTCGAGAGA 420
QY 421 ctttgagcggcattcatcaaaagcctgacacgctcttggtcaacaggaagacgcacat 480
Db 421 CTTTGAGCAGCCATTATCAACAAGCCTGCACAGCCTTGGTCAACAGGAGGACGCCAT 480
QY 481 gtgggtgcctctgtgtgttccatcccgccctcaatgttgcgtgcgtcgcgaagctc 540
Db 481 GTGGGTGCCCTGTGTGTGTCCATCCCGGCCCTCAATGTGCAGGCTCGCGTCGCAAGGTC 540
QY 541 ggtgctgtggccagacggcagagaggtggtgtggaatgaaccggcggggcattcgtgtcc 600
Db 541 GTGTGTGTGGCCAGACGGCGAGAGGTGTTGGGATGACCGCGGGGCATGCTGTGTGTC 600
QY 601 cagccactgtctgcacgtatgccctgtacctgcagtcgagacacactctggagagacagga 660
Db 601 CAGCCACTGTCTGCAGATGCCCTGTACCTGAGTGGAGACACCACTCTGGGAGACCAAGA 660
QY 661 cttcctttccaaaccccttctggtgtgacatracaggaacagactctatgacatracgt 720
Db 661 CTTCTTTTCCAAACCCCTTCTGTGTGCATATCACAGGCAACGAGCTCTATACATCCAGCT 720

QY 721 gttgcccaggagtcgtctggagctgtctggtaggggagagctggtctctgaactgcacgct 780
Db 721 GTTGGCCAGGAAGTCCCTGGAGCTCTGCTAGGGAGAGAGTGTGCTCTTGAATGCACCGT 780
QY 781 gtgggctgagtttaactcaggtgtcacctttgactgggactaccagggagacggagga 840
Db 781 GTGGGCTGAGTTTAACTCAGGTGTACCCTTTGACTTGGGACTTACCAGGAGAGCAGGACA 840
QY 841 gcggsgtaagtgggtgcccggagcgctccccagcagaccacacacagaaactctccagat 900
Db 841 CGGGGTAAGTGGGTGCCCGAGGACGCTCCACGACAGACCCACACAGAACTCTCCAGCAT 900
QY 901 cctgacctccacaacgttcagccagcagcagcagcagcagcagcagcagcagcagcagc 960
Db 901 CTTGACCATCCACAACGTCAGCCAGCAGCAGCTGGGGCTCGTATGTGTCAAGAGGCCAACAA 960
QY 961 cggcatccagcagatctcgggagagcagcagcagcagcagcagcagcagcagcagcag 1020
Db 961 CGGCATCCAGCGATTTCGGGAGAGCAGCAGGTCATTGTGCATGAAATCCCTTCATCAG 1020
QY 1021 cgtcagtggtctcaaaaggacccatcctctggagccacggcagagcagcagcagcagcagc 1080
Db 1021 COTCGAGTGGCTCAAAAGGACCCATCTCTGGAGGCCACGGCAGGACGAGCTGGTGAAGCT 1080
QY 1081 gccgtgagctggcagcgttacccccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 1140
Db 1081 GCCCGTGAAGCTGGCAGCGTACCCCCCGCCGCGAGTTCAGTGTGTACAAAGATGGAAGGC 1140
QY 1141 actgtcccggggcgcacagtcacacatgcccctgtgtcctcaagagggtgacagagggcagcac 1200
Db 1141 ACTGTCCGGGGGCCACACTCCACATGCCCTGTGTCTCAAGGAGGTGCAGAGGCCAGCAC 1200
QY 1201 aggcacctacacccctcgcctgtggaactccgcctgtcggcctggagcgcagacatcagcct 1260
Db 1201 AGGCACCTTACACCCCTGCGCCCTGTGGAACTCCGCTCTGCGCTAGGGCGCAACATCAGCT 1260
QY 1261 gtagctgagtggtgaaatgtgccccccacagatcacatgagagaggcctctctccccagcat 1320
Db 1261 GGAGCTGTTGTTGAATGTGCCCCCCCCACATACATGAGAAGGAGGGCTCTCTCCCCAGCAT 1320
QY 1321 ctactcgcgtcacagccgcagggccctcacctgcacggcctacaggggtgcccctgcctct 1380
Db 1321 CTACTTCGGCTCACAGCCGCCAGGCCCTCACCTTGCACGCCCTAGGGGTGCCCTGCTCT 1380
QY 1381 cagcatccagtggeactggcgccctggacacccctgcaagatggttgcceagcagtaglct 1440
Db 1381 CAGCATCCAGTGGCACTGGCGGCTTGGACACCCCTGCAAGATGTTTGGCCAGCGTGTCT 1440
QY 1441 ccgcgcgcgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1500
Db 1441 CCGGCGCGGCGGACGACAGAACCTCTATGCCACAGTGGCTGACTGAGGGGGCTGACCAC 1500
QY 1501 gcagatgctcgtgaaccccaatcgagagcctggacacccctggacccaggttgttgaggggaaa 1560
Db 1501 GCAGGATCCGTGAACCCCATCGAGAGCTTGCACACCTTGGACCGAGTTTGTGGAGGAAA 1560
QY 1561 gaataagactgtgagcaagctgggtgatccagaaagcgaagtgctgtgcaatgtacaagt 1620
Db 1561 GAATAAGACTGTGAGCAAGCTGGTGTATCCAGATGCCAACCTGTGTCATGTACAAGTG 1620
QY 1621 tttgtgtctccaaacaggtggccagagtgagcggcctctacttctgtgtgaccacat 1680
Db 1621 TGTGTGTCTCCAAAGGTGGGCCAGGATGAGCGGCTCATCTACTTCTATGTGACCACTAT 1680
QY 1681 cccgcagcgttccacatcgaaatccaaagccatccgagagcgtactagagggccagccggt 1740
Db 1681 CCCCAGCGGCTTCACTCGAATCCAGGCATCCAGGAGCTACTAGAGGGCCAGCCCGGT 1740
QY 1741 gctcctgagctgccaaagccgacagctcaagtaacagagcatctgcgtcgtgttaccgctcaa 1800
Db 1741 GCTCCTGAGCTGCCAAGCCGACAGCTACAAGTACGAGCATCTGCGCTGCTGCTCCGCTCAA 1800
QY 1801 cctgtccacgtgcagcatgcgcagggaaacccgcttctgctcagactcaagaagcgtgca 1860

<hr/>					
DEFINITION	Sequence 1 from patent US 6130071.				
ACCESSION	ARI12506				
VERSION	AKI12506.1 GI:14092406				
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE:	Unclassified.				
AUTHORS	1 (bases 1 to 4416)				
TITLE	Alitalo,K. and Jonkov,V. Vascular endothelial growth factor C (VEGF-C). DELTA.Cys.sub.156 protein and gene, and uses Thereof				
JOURNAL	Patent: US 6130071-A 1 10-OCT-2000;				
FEATURES:	Location/Qualifiers				
source	1..4416				
BASE COUNT	941 a 1345 c 1355 g 774 t 1 others				
ORIGIN					
<hr/>					
Query Match	95.2%; Score 3912; DB 6; Length 4416;				
Best Local Similarity	100.0%; Pred.No. 0;				
Matches 1912; Conservative	0; Mismatches 0; Indels 0; Gaps				
Oy	1	cacgcgcagcggccggaatgacaggagcgccgcctgtgcttcgcactatgacctg	60		
Dh	1	CCAGCGCAGCGCCGGAGATGACAGCGGCCGCCTGTGCTCGACTGTGGCTTCG	60		
Oy	61	ccttggactcttgagcgccctggtgagtgtactlactlcnatgaccrcccrqadrltaaat	120		
Dh	61	CCTGCGTACTCTGGACGGCCTGGTGAGTGGCTACTTCCATGACGCCCGCCGACCTTGAACT	120		
Oy	121	cacgaggaagtcaacgctralcgcacacgglgacagcctctccatctcltgraaqaca	180		
Dh	121	CATCGAGAGTTCNACGCTCATCCACCGCGTGACAGGCTGTGCCATCTCTCGACGGGACA	180		
Oy	181	qracccccctcgaattaggtttgcaggaactcagaaggccgcagccaccqaacaaga	240		
Dh	181	GCACGCCCTCGACTGGGCTTTGCCAAGAGACTGCAGGAGCGCCACGACCGGAGAACGA	240		
Oy	241	cacgcagacacagggagtgatgcagactlrcgaagcacagagccagagcctarlcaa	300		
Dh	241	CAGCGAGACACGGGAGTGGTCCGAGACTGCAGGGCACAGACCAGGCGCTTACTGTCAA	300		
Oy	301	qqtlgtlqlrtlcacgaagtacalggccaacgucacaggaagcllacqltcltactlaraa	360		
Dh	301	GCTCTTCTGCTCGACAGGTTACATGCCAACACACAGGCAGCTACGCTCTGCTTACAA	360		
Oy	361	glacatacaggaacgcatacgaaggacacagcgccagctcctctaqtlttqlyagaga	420		
Dh	361	GTACATCAAGGCACGCATCAGGGGACCCACCGCCGCGAGCTCTACGTGTCTGTGAGA	420		
Oy	421	ctttggacgccattcatcaaacgctlgacagcctcttgttcaacaggaagagacccat	480		
Dh	421	CTTTGACAGCCATTATCAACAGCCTGACACGCTCTTSGTCAACAGGAAGACGCCAT	480		
Oy	481	qtgggtgcctctgtctggtgtccatcccgcgacctcaatgtcaagcctgcgctcgaaaqc	540		
Dh	481	GTGGGTGCCCTGTCTGCTCTCCATCCCCGGCTCAATGTCAAGCTGGCTCGCCAAAGCTC	540		
Oy	541	qglactatqgcagacggcgagggtggttgtggaglgacggcgcggaalacttqgttc	600		
Dh	541	GGTGTCTGGCCACAGCGGACGAGTGGTGTGGGATCACCGGCGGGCATGCTCTGTTC	600		
Oy	601	cacuccactctgcacgatgacctglacctnagtlgcgnanaccaccttgvggaacacaga	660		
Dh	601	CACGCCACTCTGCACGATGCCCTCTACTCTCGATGGGAGACCAACCTTGGGGAGCAGCA	660		
Oy	661	cltcttlccaaccccttcttqglucacatcacaggaacagagcttatagacatccagct	720		
Dh	661	CTTCTTTTCCAACCCCCTCTCTGTGCATATCACAGGCACAGGCTCTATGACATTCAGCT	720		
Oy	721	qllgcrcaggaagtcgctgaagatltqgttaggaagaaagctqgttcttgaactlgracct	780		

[illegible]

QY 1861 tctggttcgcacacccctcttgccgcgcagccttgaggaggtgggaacctggagagcgcgcacacg 1920
DB 1861 tctggttcgcacacccctcttgccgcgcagccttgaggaggtgggaacctggagagcgcgcacacg 1920
QY 1921 cacgctcagcctgaglatcccccgctgcgcgcgcagcagcaggggcacctatagtgtgca 1980
DB 1921 CACGCTCAGCCTCAGTATCCCGCGCTCGCGCCGAGCAGAGGGCCACTATGTGTGCCA 1980
QY 1981 agtgcgaagaccgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 2040
DB 1981 AGTCCAAGACCGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 2040
QY 2041 cctggaaacccctcggctcagcagacactgaccgacctcctgggtgaacgtgagcactc 2100
DB 2041 CCTGGAAACCCCTCGGCTCAGCGAGAACTTGACCGACCTCCTGGTGAAGCTGAGCGACTC 2100
QY 2101 gctggaaatgacatgcttggtggccggagcgcagcagcagcagcagcagcagcagcagcagc 2160
DB 2101 GCTGAAGATGCAGTGTGTGGTGGCGGAGCGCAGCGCGCCAGCATCTGTGTGTACAAAGA 2160
QY 2161 cgaagagctacttgagagaaagtctgagatcgacttgaggagactccaacagaaactgag 2220
DB 2161 CGAGAGGCTGCTGGAGGAAAGTCTGAGTTCGACTTGGCGGAGCTCCAACCAAGCTGAG 2220
QY 2221 catccagtcgctgcgcagagagatcggaagcactatctgtgcagcgtgtgcaacgcca 2280
DB 2221 CATCCAGCGCTGCGCGAGAGGATCGGGGACGCTATCTGTGCAGCGCTGTGCAAGGCCAA 2280
QY 2281 gggctggttcaactcctcgcgcagcgtggccgtgggaaggtccgagagataaaggagacat 2340
DB 2281 GGGCTGCGTCAACTCTCGGCCAGCTGGCGCGTGGGAAGGCTCCGAGCATAAAGGGCAGCAT 2340
QY 2341 gggagatcgagatccttgctggtaccgagcatcagctgcttctcttggtggtcctcctcct 2400
DB 2341 GGAGATCGTGATCCTTGTCTGGTACC GGCGTCACTCGGTGCTTCTTCTGGGTCTCTCTCT 2400
QY 2401 cctcatctcttgtaacatgaggagcgccgcacgcagacatcaagacgggctacgtgtc 2460
DB 2401 CCTCATCTTCTGTAACTGAGGAGCGCGCGCCACGCGAGCATCAAGACGGGTACCTGTC 2460
QY 2461 catcatcagaccccgaggagtgctctggagagagcagatcagatcctatcctacaga 2520
DB 2461 CATCATCATGACCCCGGAGGTGGCTCTGGAGGAGCAATGGCAATAGCTCTCTCTACGA 2520
QY 2521 tccagcagatggaattccccagagcggtgcacctggagagagctcagctcagctcagcag 2580
DB 2521 TGCCAGCCAGTGGGAATTCGCCCGCAGAGCGCTGCACTGGGAGAGTGTCTCGGCTACCG 2580
QY 2581 cgccttcgggaagtggtggaagcctcctgcttctgcaacacagggcagtagctgtga 2640
DB 2581 CGCCTTCGGGAAGGTGCTGGAGCCCTCGCTTTTCGGCATCCACAAAGGCGACAGCTGTGA 2640
QY 2641 caccgtggccatgaaatgctgaaagagggcgccagcagcagcagcagcagcagcagcagcag 2700
DB 2641 CACCGTGGCGGTGAAATGCTGAAGAGGGCGGCCACGGCAGCGCAGCAGCAGCGCGCGTGAT 2700
QY 2701 gtcgaggtcgaagatcctcatcacaacagcaaccacctcaacgtagtcaactcctcag 2760
DB 2701 GTCGGAGCTCAAGATCTCTATTACATCGGCACACCACTCAACGTGGTCAACTCTCTCGG 2760
QY 2761 ggcgtgcacaaagccgagggccctcatggtgtagctgtaggcttctgcaagtacagcaga 2820
DB 2761 GGCCTGCACCAAGCCGACGGGCCCTCATGTGTGATCGTGGAGTTCTGCAAGTACGGCAA 2820
QY 2821 cctctcaacttctgcgcgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 2880
DB 2821 CCTCTCAAGTTCTCGCGCCAAAGCGGAGCGCTTTCAGCGCCCTGGCGCGAGAAGTCTCTC 2880
QY 2881 cgaagcgcgcagcgtctcgcgcacatggtgaggtcgcagcagcagcagcagcagcagcagcag 2940
DB 2881 CGAGCAGCGCGGAGCTTCCGCCGCCATGTGTGAGCTTCGGCAGGCTCGATCGGAGCGGCC 2940

QY 2941 gggagcagcagcaggggtcctcttcgcgcggttctcgaagaccgagggcgagcgagcg 3000
DB 2941 GGGAGCAGCAGCAGGGTCTCTTCGCGGGTTCGGAAGACCGAGGCGGAGCGGAGCGC 3000
QY 3001 ggcctctccagaccagaagctgagagacctgtggctgagccgctgacatcaggaagatct 3060
DB 3001 GGCCTCTCCAGACCAAGAAGCTGAGACCTGTGGCTGAGCCCGCTGACCATGGAAGATCT 3060
QY 3061 tctctgctacaagctccagggtggccagagggatggagttccttggttcccgaaagtgc 3120
DB 3061 TCTCTGCTTACAGCTTCCAGGTGGCCAGAGGATGGAGTTCTTGGCTTCCCGAAAGTGCAT 3120
QY 3121 ccacagagacctggctgcggaacattctgctgctcggaagcgcgtggtgaaatctctg 3180
DB 3121 CCACAGAGACCTTGGCTGCTCGGAACATCTGCTGTTCGGAAGCGAGCTGGTCAAGATCTG 3180
QY 3181 tgactttggccttgcgcgggacatcatcaaaagaccctgactacgtccgcgaagggcagtcg 3240
DB 3181 TGACTTTGGCCTTGGCCGGGACATCTACAAGACCTGACTACGTCCGCAAGCGAGCTGC 3240
QY 3241 ccgagctgcccctgaagtggatggccctgaaagacatcttcgacaaggtgtacaccacga 3300
DB 3241 CCGGCTGGCCCTGAAAGTGGATGGCCCTGAAAGCATCTTCGACAAGGTGTACACCACCA 3300
QY 3301 gagtacgtgtggtcctttgggggtcttctctgggagatcttctctctggtggggtcctccc 3360
DB 3301 GAGTGACGTGTGCTCTTTGGGGTCTTCTCTGCGAGATCTTCTCTCTGGGGGCTCTCCC 3360
QY 3361 gtacctgggglycagatcaaatgagagttctgcccagcggtgagagacggcacaaagat 3420
DB 3361 GTACCTTGGGTTGCAGATCAATGAGAGTTCTGCCAGCGGCTGAGAGACGGCACAAGAT 3420
QY 3421 gaggcccgagagctggcactcccgccatagcgcagcatcagctgaaactgctgctcgg 3480
DB 3421 GAGGCCCGGAGCTGGCCACTCCCGCATACCGCCGATCATGCTGAACTGCTGCTGCTCGG 3480
QY 3481 agaccccaaggcgagacctgctctcgagctggtggagatcctcgggggacctgctcca 3540
DB 3481 ACACCCCAAGCGAGACCTGCTCTCGAGCTGCTGGAGATCTCTGGGGACCTGCTCCA 3540
QY 3541 gggcggggctgcgaagaggaagaggtctgcatggtggcccgcgagcgtctcagagctc 3600
DB 3541 GGGCAGGGGCTGCAAGAGGAAGAGAGGTCTGCATGGCCCGCGCAGCTCTCAGAGCTC 3600
QY 3601 aagaagggcagcttctcgaggtgtccaccatggccctacacatcgccagagctgagc 3660
DB 3601 AGAAGAGGCACCTTCTCGCAGGTGTCCACCATGGCCCTACACATCGCCAGGCTGAGCG 3660
QY 3661 tgagjacagccgcgaagcctgcagcgccacagcctggcgccaggtattacaactgggt 3720
DB 3661 TGAGGACAGCCCGCAAGCTTCAGCGCCACAGCTGGCCCGCAGGTATTACAACCTGGT 3720
QY 3721 gtcctttcccggggtgcctggccagagggggtgagaccgtggtcctcccgagatgaagac 3780
DB 3721 GTCTTTTCCCGGGTGCCTGGCCAGAGGGGCTGAGACCGCTGGTTCTCCAGGATGAAGAC 3780
QY 3781 atttgaqaattccccatgaccccccaacacctacaaggtctgtggaacacagacaga 3840
DB 3781 ATTTGAGGAATTTCCCATGACCCCAACGACCTTACAAAGGCTCTGTGGACAAACACACA 3840
QY 3841 cagtgggatggtgctggcctcgagaggttttgagcagatagagagcagagcatagaaga 3900
DB 3841 CAGTGGGATGCTGTGGCTCGGAGGAGTTTTCAGCAGATAGAGAGCAGGCATAGACAAGA 3900
QY 3901 agcggtctcag 3912
DB 3901 AAGCGCTTCAG 3912

RESULT 6

HSFLT4

LOCUS

DEFINITION

6
4416 bp mRNA linear PRI 30-NOV-1993
HsFLT4
H.sapiens mRNA for FLT4, class III receptor tyrosine kinase.

Qy 1141 acttccggcgccacagLccacaLgcccctggtgctcaaygagtgacagagccaqcac 1200
nb 1141 ACTGTCCGGGGCCACACATCCACATGCCCTGCTGCTCAAGGAGGTGACAGAGGCCACGCAC 1200
Qy 1201 anqacccctacacrcctLcfrccrclatggaactcgcctgcttgccctgagagcacaatacagcct 1260
Db 1201 AGGCACCTACACCCCTGCGCCCTGTGCAACTCCGCTGCTGGCTGAGGGCCCAACATCAGCCT 1260
Qy 1261 gaaacttgatgatgaaLgqcccccacatatacaLaagaagagagccctcctcrrrrcaacat 1320
Db 1261 GGAGCTGGTGGTGAATGTGGCCCTCCACATACATGAGAAGGAGGCTTCCTCCCGCAGCAT 1320
Qy 1321 ctactctggctLcacagcgccagccctcactcgaacqccctLacggggLacccctLacccct 1380
Db 1321 CTACTCGCCTCACAGCGCCAGGCCCTCACCTTGACAGGCTTACGCGGCTGCGCCCTGCTCT 1380
Qy 1381 caqraLccatLgrractggcgrrcrrLggaracccctLgaagaLctttLgrragrrqLagLct 1440
Db 1381 CAGCATCCAGTGGTACTTGGCGGCCCTGGACACCTTGCAAGATGTTTGCCCTAGCCTTAGTCT 1440
Qy 1441 cccqcgccgcaaycaqcaagaccLcaLgcccacagLcccgLgacLggaagrrqLlacccac 1500
Db 1441 CCGGCGGGGGACAGCAGAACCTCATGCCACAGTCCGCTGACTGGAGGGGGTGAACCCAC 1500
Qy 1501 qcaggaTgcgtLqaaccccatLgagagccLlgacacccLggaccagttLlqLqagagqaaa 1560
Db 1501 GCAGGATGCCGTGAACCCCATCGAGAGCTGGACACCTTGGACCCAGTTTTCTGCAUGGAAA 1560
Qy 1561 gaaTaagactgtgagcaagcttggtgtatccagaatgccaacgtgtctgccaLgtacaagt 1620
Db 1561 GAATTAAGACTGTGAGCAAGCTGGTCATCCACAGATGCCAATGCCAACGTGTGCCCATATCAAGT 1620
Qy 1621 LttLqLctLccaaagagLggaccagatLgaagrrctcaLactLctLgtLaaacacat 1680
Db 1621 TGTGTTCTCCAAACAGGTGGGCCAGATGAGCGGCTCATCTACTTCTATGTGACACCAT 1680
Qy 1681 ccccgacggctLcaacatLcgaatccaaagccalLccgagagactLartagagggccagccggt 1740
Db 1681 CCCCACAGCCTTACCACATCGAATCCAAAGCCATCCGAGGAGCTACTAGAGGCCAGCCGGT 1740
Qy 1741 gctctLgaactgccaaagccagactacaagtacagtaactgtgacttggtLaccgrrctcaa 1800
Db 1741 GCTCTTGAGCTTGCCAAAGCCGACAGTACAACTACGAGGACTTGGCGCTGGTACCGGCTCAA 1800
Qy 1801 cctLgLccagctgacgatLgqccacgaaacccgctLctgctLcgaactLcaagaactgaca 1860
Db 1801 CCTGTCCAGCTGACGATGCCACCGGAACCCGCTTCTGTCTGACTGCAAGAACGTGCA 1860
Qy 1861 tctgttcgcaacccctctggcgccagactggaagagutggcacctgggrrqcccaagc 1920
Db 1861 TCTGTTGCCCACCCCTCTGGCGCGCAGCTTGAGGAGGTGGCACCTGGGGCGCGCCACGC 1920
Qy 1921 cagctcagccttgatataLcccgcgctgcgcccagacagagggccactatgtgtgca 1980
Db 1921 CACGCTCAGCCTTGATATCCCCCGCGCTGGCGCCGACGACGAGGAGGACCTATGTGTGCGA 1980
Qy 1981 aqtgaaacccgagccagccatgacaagactgccaagactgccaagaagtacctgtcgctcaagc 2040
Db 1981 AGTGAAGACCCGGCGACCATGACAGACATGCCACAAAGATACCTTGTCCGTGCAGGC 2040
Qy 2041 cctggaagccctcggctLcagcaaaactLgaccagactcctggtgaaagctgaaqactc 2100
Db 2041 CCTGGAUCCCTCGSCTCACGCAACTTGACCGACCTCTCTGGTGAAGTGAAGTGAAGTGA 2100
Qy 2101 gctgagatgcaagtcttggtggccggaagcagcagcccagatcgtgtggtacaaaqa 2160
Db 2101 GCTGAGATGCAAGTCTGTTGGTGGCGGAGCGCACCGCCGACAGCTGCTGTGTACAAAGA 2160
Qy 2161 cgaagggctLgtagagaaaactLgaagtgaatLgacqaactccaaacaaagctgaq 2220
Db 2161 CGAGAGGCTGCTGGAGGAAAGTCTGGAGTCCACTTGGCGGACATGCAACCCAGAACTCAG 2220

Qy 2221 catcagcgctgqcgagagagatgcgggacgctatctgtcagcgctgtgcaacgcaa 2280
nb 2221 CATCCAGCGCTGCGCAGGAGGATGCGGACGCTATCTGTGCAGCGTGTGCAACGCCAA 2280
Qy 2281 gggctgcgtcaaatcctLccgccagcgtggccggtggaaggctccgaggaataaagggaagcat 2340
Db 2281 GGGTGGGTCAACTCTCCGCCAGCGTGGCGTGGAAAGGCTCCGAGGATAAGGGCAGCAT 2340
Qy 2341 ggaagtgcgatcctLgtcggLaccggcgtLcatcgctgtcttcttctgggtcctLcctcct 2400
Db 2341 GGAGATCGTATCCTTGTGGTACCGGGCTATCGCTGTCTTCTTCTGGGTCTCTCTCT 2400
Qy 2401 cctcatctctgtatacatgagggagggccggccacgcagacatacaagcggggtacctgtc 2460
Db 2401 CCTCATCTTCTGTAAATGAGGAGCGCGGCCACGCAGACATCAAGACGGCTACCTGTCT 2460
Qy 2461 catcatcatggaccccggggagglgacctctggaggagaatgcaataacctgtcctacga 2520
Db 2461 CATCATCATGACCCCGGGAGGTGCCCTCTGGAGGACAATGCGAATACCTGTCTTACGA 2520
Qy 2521 tgccagccagtggaaatLcccccgagagcggctgcacctgggagagtgctcggctacgg 2580
Db 2521 TGCCAGCCAGTGGGAATTTCCCCCGAGAGCGGCTGCACCTGGGGAGAGTGTCTGGCTACGG 2580
Qy 2581 cgcctLcgggaaggtgggtggaagcctcgcgttctcggcatccacaagggcagcagctgtga 2640
Db 2581 CGCCTCTGGGAAGTGGTGGGAAGCTCCGCTTTTCGGCATCCACAAGGGCAGCAGCTGTGA 2640
Qy 2641 caccgtggcgtgaaatgctgaaagaggcgccacggccagcgagcagcagcgcgcgtgal 2700
Db 2641 CACCGTGGCGCTGAAATGTGTAAAGAGGGCGGCACGCCAGCAGCAGCAGCGCGCTGAT 2700
Qy 2701 gtcgaactcaagatcctcattcacatcgcaacacacctcaacgtgtLcaacctLcctcgg 2760
Db 2701 GTCCGAGCTCAAGATCCTCATTCACATCGGCAACCACTCAACCGTGTGTCAACCTTCTCTGG 2760
Qy 2761 ggcgtgcaccaagcgcgaggccccctcatggtgatcgtggagttctgcaagtagtcaggcaa 2820
Db 2761 GCGGTGCACCAAGCGCAGGAGGCCCCCTCATGGTGATCGTGGAGTTCTGCAAGTACGGCAA 2820
Qy 2821 cctctcaaatctctgcgcccgaaggcgccctcagccccctgcgcggaagaagtctcc 2880
Db 2821 CCTCTCAACTTCTTGGCGGCCAAAGCGGGAGCGCTTTCAGCCCCCTGCGCGGAGAAGTCTCC 2880
Qy 2881 cgagcagcgagcgtctccgcgcctatgggtgagctgcgagagctggatcgagagcgccc 2940
Db 2881 CGACGAGCGCGAGCGCTTCCGCGCATGGTGGAGCTGCGCAGGCTGGATCGGAGCGCGCC 2940
Qy 2941 ggggagcagcagcaggggtcctcttcgcgcggttctcgaagaccgagggcgagcgagggcg 3000
Db 2941 GGGGAGCAGCGACAGGGTCTCTTTCGCGCGGTTCTCGAAGACCGAGGGCGGAGCGAGCGG 3000
Qy 3001 ggcctctccagaccaaagaactgaggacctgtggtgagccccctgacctggaagatct 3060
Db 3001 GGCTTCTCCAGACCAGAAGCTGAGGACCTGTGGCTGAGCCCCGTGACCAATGGGAAGTCT 3060
Qy 3061 tgcctctacagctccaggtgcgcaagagatgagttcctgctLcccgaagatgcat 3120
Db 3061 TGCTCTTACAGCTTCCAGGTGGCCAGAGGATGGAGTTCTTGCTTCCCCGAAAGTGCAT 3120
Qy 3121 ccacagagacctgctcgcggaacattctgctgcgcggaagcagcgtgggtgaagatctg 3180
Db 3121 CCACAGAGCCTGGCTGCTCGGAACATTCGTCTCGGAAGCGACGCTGGTGAAGATCTG 3180
Qy 3181 tgaatttgccctgcccgggacatctacaaagacccctgaactacgtccgcaagggcagtg 3240
Db 3181 TGACTTTGGCCTTGGCCGGGACATCTACAAAGACCCCTGACTTACGTCCGCAAGGCGACGTG 3240
Qy 3241 ccggtcctccctgaatggaatggccctgaagcatcttcgaagaagtgtaaccaagca 3300
Db 3241 CCGGCTGCCCTGAAGTGGATGGCCCCCTGAAAGCATCTTCGACAAGGTGTACACCAAGCA 3300
Qy 3301 gagtgaagtggtgctccttggggtgcttctctgggagatctctctctctgggggctctccc 3360

|||||
Db 1152 ATGTGCGGGGCGCCACAGTCCACATGCCCTGTGTCAAGGAGGTGACAGAGGCGGAGCAC 1211
Qy 1201 aaggarctacacccctgcccctgtggaactccgctactgaccttgagagcgcaactacagcct 1260
Db 1212 AGCGACCTACACCCCTCGCCCTGTGCAACTTCGCGTCTGCTGCGCTGAGGCGCAAAATCAGCCT 1271
Qy 1261 qjaqctgggtqntlgaaatglgcccccccaajalataluagaaqaaagcctcctctcrrcaurat 1320
Db 1272 GGAGCTGGCTGGTGAATGTGCCCGCCCGACAGATACATGAGAAAGGAGGCTGCTGCCCGCAGCAT 1331
Qy 1321 ctactcgcgttaacacgcgcgaugrctctacactgcaacgctlaagagglgccccturclet 1380
Db 1332 CTACTGCGGTACAGCGCGGACGCCCTCACCCTGCGACGGGCTTACGGGGTGCCCTGCGCTCT 1391
Qy 1381 cuuacatccagtgatgacatgggcccctggacacccctgcaagatggtttgcccacucylaglet 1440
Db 1392 CAGCATCCAGCTGGCACCTGGCGGCCCTGGACACCCCTGCAAGATGTGTCGCCAGCTAGTCT 1451
Qy 1441 ccygqgqgrragagcaadaacctcatgccacaglgccgctgactggaagggcqtacacac 1500
Db 1452 CGCGCGCGCGGACAGCAGAACCTCATGCCACAGTGGCGTGCATGAGAGGCGGCTGACCAC 1511
Qy 1501 gcaqatgcctgaaaccccatcgagagcctggacacccctggacaggtttatqagagggaaa 1560
Db 1512 GCAGGATGCCGTGAACCCCATCGAGACCTGGACACCTGGACCGAGTTGTGAGGAGAAA 1571
Qy 1561 gaaLaagactgtgagcaagcttggtgatccagaatgccaaagctgctgctgcatatcaagt 1620
Db 1572 GAATAAGACTGTGACCAAGCTGCTGATCCAGANTGCCAACCTGTGTGCCATGTACAACTG 1631
Qy 1621 tctgcttccaaagagtgggccagatlgagcggtctacttacttctatgtaaccacat 1680
Db 1632 TGTGTCTCCAAAGAGTGGCGGACAGATGAGCGGCTCATCTACTTCTATGTGACCCACAT 1691
Qy 1681 crrraacggcttcaacatgaaLccaaagccatccgagagcttactaaagggcgagccggt 1740
Db 1692 CCGCGACGCTTTCACCATCGAATCCAAGCCATCCGAGGAGCTACTAGAGGGCGCAGCGGT 1751
Qy 1741 qctcttgaqctgccaagccagacagctataaqtacagagcatctgagcttggttaacgcrtcaa 1800
Db 1752 GTTCTTGAGCTGCCAAGCCGACAGCTACAAAGTACGAGCATCTGCGCTGGTACCGGCTCAA 1811
Qy 1801 rctqtccacgtlgacagaLgcacaggggaacccgctctctgctcgactgcaagaaacgtgca 1860
Db 1812 CTGTCCACGCTGCAGATGCGCACGCGAACCGGCTTCTGCTCGACTGCCAAGACGTCCA 1871
Qy 1861 tctgttcgcccacccctctgcccgcagcctgagagagglgagcacttgaggrgrrcraagc 1920
Db 1872 TCTGTTCCGCGACCCCTCTGGCGCGCCAGCTGAGAGAGGTGGCACCTTGGGGCGCGCACGC 1931
Qy 1921 cagcgtcagcctgagtatcccccgctcgcccgagcagcagagggccactatgtatgga 1980
Db 1932 CAGGCTACGCTGAGTATCCCCCGGTCCGCGCCGACGACGAGGGGCCACTATGTGTGCGA 1991
Qy 1981 agtgcgaagccggcgagccatgacaagcactgcccacagaagtagtacctgtcggtcaggg 2040
Db 1992 AJTGCAAAGCCGGCGAGCCATGACAAGCAGCTGCCACAAGAAGTACCTGCTCGGTGCAGC 2051
Qy 2041 cctggaagcrrctcggtcaacgaqaacttgaccgacctccttgggtgaacgtgaggaclc 2100
Db 2052 CTTGGAAGCCCTTCGGCTCAGCGACAACTTTGACCGACCTTCCTGGTCAAGCTGAGGCACTC 2111
Qy 2101 gctggagaLgcagtgcttggttgqccgagcgcaacgcgcagcagcatcggtgtgtacaaaga 2160
Db 2112 GCTGGAGATGCACTTGTGTGGCGGAGCGACGCGCGGCCACCATCGTGTGTACAAAGA 2171
Qy 2161 cgaagggctgctggaggaagactgtggactcgacttggcgactcccaacraagaactgag 2220
Db 2172 CGAGAGGCTCTCGAGGAAAAGTCTGCACTGCACTTGGCGGACTGCCAACCAAGTCTAG 2231
Qy 2221 calcagagcggtgcgcgaggaagatcgagacgtatctgtcagcggtgtatcaacqcaa 2280
|||||

Db 2232 CATCCAGCGCGTCGCGAGGAGGATGCGGGACGCTATCTGTGCAGCGTGTGCAACGCCAA 2291
Qy 2281 ggggtgogtcaactcctcccgccagcgtggccgttggaaggtcccagagataaaggcgacat 2340
Db 2292 GGGTGGCTCAACTCTCCCGCAGCGTGGCGTGGAAAGGCTCCGAGGATAAAGGCAAGCAT 2351
Qy 2341 ggaatcgatgactctgtcgatccgctgcatcgctgctctctcttctgggtccctccct 2400
Db 2352 GGAGATCGTGAATCTTGTGGGTACCGGCTCATCGCTGTCTTCTTCTGGGTCTCTCTCT 2411
Qy 2401 cctcatcttctgtaacatgagagggccgcacgcagacatacaagacgggctacctgtc 2460
Db 2412 CCTCATCTTCTTAACATGAGAGGCGCGGCCACGCGACACATCAAGACGGGCTACCTGCTC 2471
Qy 2461 catcatatgaaacccccgggggggtgctcctctgagaggaatacgaaatctctgtcctacga 2520
Db 2472 CATCATCATGACCCCGGGGAGGTGCCCTCTGGAGGAGCAATGCCAATAACCTGTCTACGA 2531
Qy 2521 tggcagcagtggaattccccccagagcgctgcacctgggagagtgctcgcgtacgg 2580
Db 2532 TGCCAGCCAGTGGGAATTTCCCGCAGAGCGGCTGCACCTGGGGAGAGTGTCTGGCTACGG 2591
Qy 2581 cgccttcgggaaggtgggtggaagcctccgcttctgggcatccacaaaggcgagcagctgtga 2640
Db 2592 CGCCTTCCGGAAGGTGGTGAAGCCTCCGCTTCGGCATCCACAAGGCGACAGCTGTGA 2651
Qy 2641 caccgtgcccgtgaaatgtgaaagagggcgccacggcgacagcagcagcgcgtgat 2700
Db 2652 CACCGTGGCGGTGAAATGCTGAAAGAGGGCGCCACGGCCAGGACCCGCGCGCTGAT 2711
Qy 2701 gtcgaggtcaagatcctcatctacatcggaacacacctcaacgtgggtcaacctcctcgg 2760
Db 2712 GTCGGAGCTCAAGATCCTCATTCACATCGGCAACCAACCTCAACGTGGTCAACCTCCTCGG 2771
Qy 2761 ggcgtgaccgaagccgcagggccccctcatggtatcgaggttctctgaagtcagggcaa 2820
Db 2772 GCGGTGCACCAAGCGCGCAGGGCCCCCTCATGCTGATCTGTGGAGTTCTTCAAGTACGGCAA 2831
Qy 2821 cctctcaactctctgcgcgaagcgagcgcttcaagccccctgcgcggagagagtcctc 2880
Db 2832 CCTCTCAACTTCTTGC CGCGCAAGCGGAGCGCTTACAGCCCCCTGCGCGGAGAGTCTCC 2891
Qy 2881 cgagcagcggaagccttcccgccatggtgagctcgccaggtcggaLcggaagcgagcc 2940
Db 2892 CGAGCAGCGCGACGCTTCCGCGCATGCTGGAGTCCCGAGGCTGGATCGAGGCGGCC 2951
Qy 2941 ggggagcagcagagggctctctctcgcggttctcgaagaccgagggcgagcgagcg 3000
Db 2952 GGGGAGCAGCGCACAGGGTCTTTCGCGCGGTCTTCAAGACCCGAGGCGGAGGCGG 3011
Qy 3001 ggcctctcagaccgaagaagctgagagacctgtggctgagccgctgaccatgggaagatct 3060
Db 3012 GGCTTCTCCAGACCAAGAGCTGAGGACCTGTGGCTGAGCCCGCTGACCATGGAAGATCT 3071
Qy 3061 tgtctgtacagcttccaggtggccagaggatggagtctctggtctcccccaagtgcat 3120
Db 3072 TGTCTGTCTACAGCTTCCAGGTGGCGAGGATGGAGTTCTCTGGGTTCTCCCAAAATGTGAT 3131
Qy 3121 ccagagacactggctgctcgaaacttctgctgcgaaagcgagctggtggaagatctg 3180
Db 3132 CCACAGACACTTGGTGTCTCGAACAATTTCTGCTGCGAAGACGACGTGTGTGAAGATCTG 3191
Qy 3181 tgaacttggccttggccgggacatacaaaagacctactacgtccgcaagggcgagtg 3240
Db 3192 TGACTTTGGCCTTGCCCGGGACATCTACAAAGACCCCTGACTAGCTCCCAAGGCGAGTGC 3251
Qy 3241 ccggtgccccctgaagtggatggccccctgaagaactcttcgaacaggtgtatcacacagca 3300
Db 3252 CCGGCTGCCCTGAAAGTGGATGGCCCCCTGAAAGCATCTTCGACAAAGGTGTACACACGCA 3311
Qy 3301 gagtgacgtggtccttgggtgcttctctggagagatctctctctctctctctctctctctct 3360
Db 3312 GAGTGACGTGTGGTCTTGGGGTGTCTCTCTGGGAGATCTTCTCTCTGCGGGGCTCTCCC 3371

QY	3361	qtaccctcggggtacagatcaatgagagttctctccagcgctcagagagcggaaggaal	3420
DB	3472	GTACCCCTGGGCTCAGATCAATCAGGAGTTCTGCCAGCGCTCAGAGACGGCAAGGAT	3431
QY	3421	gagggccccggagctggcraclcccgcccalacuccgcatcatgctgaactgtaclccag	3480
DB	3432	CAGGGCCCGGAGCTGGCCACTCCCGCATACCGCCGATCATGCTGAACCTGTGGTCGG	3491
QY	3481	agaccccaagcgaacactgcatctctcgagctgggtgagatcctggggagactgctcca	3540
DB	3492	AGACCCCAAGCGAGACCTGCATTCTCGGAGCTGGTGGAGATCCTGGGGACCTGCTCCA	3551
QY	3541	ggacaggggacctcgaagaagaagagggtctgcatagggcccccgagctctcagagctc	3600
DB	3552	GGGCAAGCGGCTGCCAGAGGAAGAGGAGGCTTGCATGGCCCGCCGAGCTCTCAGAGCTC	3611
QY	3601	agaagaagcgaactctcgcagagatgctccacatgagccctacacatgcccagctcaagc	3660
DB	3612	AGAAGACGGGAGCTTCTCGCAGGTGTCCACCATGGCCCTACACATGCCCGAGGCTGACGC	3671
QY	3661	taagagcaagcccgccgaagcctgcagcgcacagcctggccgaggtatlaracttqqct	3720
DB	3672	TGAGGACAGCGCGCCAGGCTCGAGCGCCACAGCCTGGCCCGCAGGTATTTACAACTGGCT	3731
QY	3721	qlcclllccrqqgtgcttgccagaggggtctgagacccgtggtlctctccagagatgaaqar	3780
DB	3732	GTCCTTTTCGGGTGGCTGGCTGCGAGGGGCTGAGACCGCTGGTTCCCTCCCAAGATGAAGAC	3791
QY	3781	alltgaagaattccccatgaccccaagcctacaaagcctlctgagacgacccagacaga	3840
DB	3792	ATTGTAGAGAAATTCCTCCATGACCTCAAGCAGCTTCAAAAGGCTCTGTGGACAACTAGACAGA	3851
QY	3841	cagtggaalagtgtggtggtcctggaaggttctgagcagatagagagcagacataraaga	3900
DB	3852	CAGTGGCATGCTCTGGCCCTCGAGAGTGTGTGAGCAGATAGAGCAGCAGCATACACAGA	3911
QY	3901	aaagcagctllcaag	3912
DB	3912	AAGCGGCTTCAG	3923
RESULT	8		
HSU43143			
LOCUS	HSU43143	4:25 bp	mRNA linear PKI 09-JAN-1996
DEFINITION	Human receptor tyrosine Kinase Flt4 (short form) mRNA, complete cds.		
ACCESSION	U43143		
VERSION	U43143.1	GI:1150990	
KEYWORDS	human.		
SOURCE	Homo sapiens		
ORGANISM	Fukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1 (bases 1 to 4425)		
AUTHORS	Lee, J., Gray, A., Yuan, J., Luoh, S.-M., Avraham, H. and Wood, W.I.		
TITLE	Vascular Endothelial Growth Factor Related Protein (VRP): A Ligand and Specific Activator of the Tyrosine Kinase Receptor Flt4		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. (1996) In press		
REFERENCE	2 (bases 1 to 4425)		
AUTHORS	Wood, W.I.		
TITLE	Direct Submission		
JOURNAL	Submitted (12-DEC-1995) William I. Wood, Molecular Biology, Genentech, Inc., 460 Pt. San Bruno Blvd., S. San Francisco, CA 94080, USA		
FEATURES	Location/Qualifiers		
source	1..4425		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/clone="combined from clones tk1.94, tk1.65, and tk1.4"		
	/cell_line="megakaryocyte lines CMK11-5 and DAM1"		
CDS	31..3927		
	/function="receptor for vascular endothelial growth factor"		

related protein (VRP); receptor tyrosine kinase"
/note="also called SAL-S1 or tk1"
/codon_start=1
/product="Flt4"
/protein_id="AAA85215.1"
/db_xref="GI:1150991"
/translation="MORGAALCLRLMLCLGLDGLSYSMTPPTLNITEESHVIDTG
DSLSTISCRQHPLEWAPGAEATGDKDSEDGTVVRDCEGTDARPYCKVLLHVEVH
ANDGTSYCYKYIKARIEGTAASSYVVRDFEQPIINKPDTLLVNRKDAWVPCLV
STPGUNVTLRSOSSVDPDGVVMDRGMVLSTPLLDHALYIQCECTWGDQDFLSN
PFLVHITGNELYDIQLPRKLELLVGEKLVNCTVMAEFNSGVTFDWDYVCKAERG
KWPERRSOQTHTESSILTTHNSOHDGLSYCKANNIGIORFRESTEIVIPHENPFI
VENLKPILTEATAGBELVKLVKLAAYPPPEFOWYKDKALSGRSHALVLKVEVTEA
STGTYTLALMNSAAGLRNRNLSLELVVVPQITHEKEASSPIYSHRSQALCTCTAGCV
PLPLSIQIWHRPWPTCKMFAQRSLRQOQDLMPQCRDMRAVTTQDADVNPLESITWT
EFVEGKNKTVSKLVIQANVNSAMKYCVSNKVGQDERLIYFYVTTIPDGTIESKPSL
ELLEGQPVLLSCQADSYKEYEHLRWYRLNSTLHDAHGNPLLLDCKNHLHLPPLAASL
EVAPGARHATLSLSIPRAVEHEGHIYCEVQDRRSHDKHCKYVLSVOALEAPRLTQ
NLTDLLVNSOSLEMOCLVAGAHAPSIWYKDERLLEKSGVDLADSNOKLSIOHVR
EDAGRYLTSVCNAKGCYNSSASVAVEGSEDKGSMEIVILVGTGVIAVFPWVLLLIIFC
NNRPAHADIKTGYLSIIMDPGEVPLEEOCEYLSYDASOMEFFPRELRHLGRVLGYGAF
GKVBASAFGIHKGSSCDTAVKMLKEGATASEHRALMSELKILTHIHNHNLVNLIG
ACTKPGQPLMWIVPECKYGNISNLRARDAFSPCAEKSPQQRHFRAMVELAKIDRR
RPGSDRVLFAFSKTEGGARRASPDQAEADLWLSPLTMEDLCVYSFQVARGMEFLAS
PKCTHRDLAARNILLESDEVVKICDFGLARDIYKDPDYVRKMSARLPKMWAPESIFD
KYVTTQDSWFSFGVLINELFSLGASPPYFGVQINEEFQORLRDGTMRAPELATPAIKR
IMLNCWSDGPKARPAFSELVELTGLDLOQGRLOEEBEEVCMAPRSSOSEGSPSOVST
MALHTAQADAEDSPPSLHLSAARYYNWYFPGCLARGAETRGSSRMKTFEEFPMTP
TTYKGSVDNQTDSGMVLASEPFEQIESHRHROESGFR"

BASE COUNT 939 a 1348 c 1361 g 777 t
ORIGIN

Query Match	95.2%	Score	3912;	DB	9;	Length	4425;
Best Local Similarity	100.0%	Pred. No.	0;				
Matches	3912;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
QY	1	ccacgcacgcgcgagagatcagcggggcgccgcgctgtcctgcgactglggtcctg	60				
DB	12	CCACGCGCAGCGCGGAGATGACGCGGGCGCGCGCTGTGCTGCGCACTGTGGCTCTG	71				
QY	61	cttgggactcctgacgcgcctggtgagtggtactactcagcccccccgaccttgaacat	120				
DB	72	CCTGGGACTCTCTGACGGCGCTGGTGAAGTGGCTACTCCATGACCCCGCCGACCTTGAACAT	131				
QY	121	cacggaggagtcacacgtcatcgacaccggtgacagcctgtccatctcctcgaggggaca	180				
DB	132	CACGGAGGAGTCAACGCTCATCGACACCGGTGACAGCCTGTCCATCTCTCGAGGGGACA	191				
QY	181	gcacccccctcgatgggcttgccaggaagcclcaggaagcgccagccacggagagacaagga	240				
DB	192	GCACCCCTTCAGTGGGCTTTGGCCAGGAGCTCAGGAGGCGCCAGCCACCGGACACACAGGA	251				
QY	241	cagcaggacacgggggtggtgcgaactcgcagggcacagagcagggccctactgcaa	300				
DB	252	CACGAGGACACGCGGGGTGGTGCAGACTCGAGGGCACAGCGCCAGGCGCTTACTGCAA	311				
QY	301	ggtgtgctgctgcagcaggtacatgccaacgacacaggcagctacgtctgtctactacaa	360				
DB	312	GGTGTGCTGCTGTCACGAGGTACATGCCAACACACAGGAGCAGTACGTCTGTCTACTACAA	371				
QY	361	gtacatcaaggcacgcagcagggcacccagccgagcctcctacgtgttctgtgagaga	420				
DB	372	GTACATCAAGGCACGGCATCGAGGGCACCGCGCCGCGAGCTCCTACGTGTTCTGTGAGAGA	431				
QY	421	ctttagcagccattcatcaacaagcctgacacgctcttggttcaacaggaagagcccat	480				
DB	432	CTTTGAGCAGCCATTCATCAACAAGCTTCACAGCGCTTGTGGTCAACAGGAAGGACGCCAT	491				
QY	481	gtgggtgacctgtcgtgttccatccccggccctcaatgtcacgctgcgctgcacaaagctc	540				
DB	492	GTGGGTGCCCTGTCTGTGTGCTCATCCCGGCTCAATGTGTCAGCTGCGCTCGCAAGCTC	551				

db 2712 GTCCGAGCTCAAGATCCTCTATTTCATATCGGCAACACCTCAACGGTGGTCAACCTCTCTCGG 2771
Qy 2761 ggcqtcaccacgacgagggccccctcatggtgacatcgtgagttctcgaatcaccgaa 2820
Db 2772 GCGGTGACCAAGCGGCGGCCCCCTCATGCTGATCTGTGAGTTCGCAAGTACGCGAA 2831
Qy 2821 cctctctcaactctctgctgagcgaagggagacgacctctcagccccctgaggaagaatctcc 2880
Db 2832 CTTCTGCAACTTCTCTGCGCGGCAAGCGGACGCCCTTCAGCCCTCGCGGAGAGATCTCC 2891
Qy 2881 ctaagcagcgcacactctccgcgcacatgctgagctcgcagcctggatcgatcgagcgacc 2940
Db 2892 CGAGCAGCGGACGCTTCCGCGGCCATGCTGGAGCTCGCAGCGCTGATCGAGCGGCC 2951
Qy 2941 qqagatcagcgcacagggctctctcgcgcggtctcgaagacgagggagcgagcgagcg 3000
Db 2952 GCGGACGACGACACCGCTCTCTTCGCGCGGTTCTCGAAGACCGAGGCGGACGCG 3011
Qy 3001 ggtctctcagagcraaagaagctgaggaacctgtggctgagccgcctgacccatggaagatct 3060
Db 3012 GCGTTCTCAGACCAAGAGCTGAGGACCTGTGGTGAAGCGGCTCACCATTGCAAGATCT 3071
Qy 3061 tctctctcagctctcagctgagcagagggatgaggtlctctggtctccrqaatgcat 3120
Db 3072 TGTCTGCTTACACTTCCAGAGTGGCAGAGGGATGAGATTCCTGGCTTCCCGAAAGTGCAT 3131
Qy 3121 ccacagagacctggtctcgcgaacattctcgtctcgaggaagcgagtgatgaaatctg 3180
Db 3132 CCACAGAGACCTGGCTGCTCGGAACATTTCTGCTCGGAAGCGAGCTGCTGAAGATCTG 3191
Qy 3181 tgactttgacctgcccggagacatctacaagacactgactactcgcgaagcgagtcg 3240
Db 3192 TGACTTTGGCTTGGCCGGGACATCTACAAAGACCCCTGACTACGTCGCGAAGCGAGTCC 3251
Qy 3241 cggctgccccctgaaatggatggccccctgaaagcatcttcgacaaggtatcacaccacga 3300
Db 3252 CCGCTTGCCTTCAAGTGGATGCCCTCGAAAGCATCTTTCGACAAGTGTACACACGCA 3311
Qy 3301 aaataacgctggtctcttggggtgctctctctgagagatctctctctgagggaccc 3360
Db 3312 GACTGAGCTGTGGTCTTGGGGTGCTCTCTCGGGAGATCTTCTCTCTGGGGGCTTCCCC 3371
Qy 3361 qtaccttgggttgcagatcaatgagaggtcttgcagagggctgagagacgacagagat 3420
Db 3372 GTACCTTGGGTCGACATCAATCAGCAGTTCGCGACGCGCTCAGAGACGCGCACAGGAT 3431
Qy 3421 gaggggcccggaactggccactcccgccatcacgcgcgcacatcgtgaaatcgtggtcrgg 3480
Db 3432 GAGGGCCCGGAGCTGGCCACTCCGCCCATACGCCGCATCATGCTGAACCTGCTCGCG 3491
Qy 3481 agaccctcaagcgagacacctgcattctcgaagctggtggaagctctggggagacctgctcca 3540
Db 3492 AGACCCCAAGCGGAGACCTGCATCTCTCGAGCTGGTGGAGATCTCTGGGGAGCTCTCCA 3551
Qy 3541 gggcaggggctgcaagaggaagagagtgcttcaatggcccccgagcgtctcagagctc 3600
Db 3552 GGGCAGGGGCTCTCAAGAGGAGAGAGAGGCTTGCATGGCGCGCGCGAGCTCTCAGAGCTC 3611
Qy 3601 auaagagggcagctctctcagagtgctcaccatggccctacacatcgccagcgctgagcc 3660
Db 3612 AGAAGAGGGCAGGCTTCTCGAGGTGTCACCATGGGCCCTTACATCTCGCCAGCTCAGCC 3671
Qy 3661 tgggagcagcccgcccaagctcgcagcgccacagccttggcgccaggtattacaactgggt 3720
Db 3672 TGAGGACAGCCCGCCCAAGCTTCCAGCCGCACAGCTTGGCGCCAGCTATTACAACCTGGCT 3731
Qy 3721 gtcctttcccggtgctggcagagagggctgagaccccggttctctccagatgaagac 3780
Db 3732 GTCCTTTCCGGGTGCTGCGCCAGAGGGGCTGAGACCCGCTGGTTCCTCCAGGATGAAGAC 3791
Qy 3781 atttgaaggaattcccatgaaccccaacgactacaaagctctctgtagaacaacagacga 3840
Db 3792 ATTTGAGGAATTCCCATGACCCCAACGACCTTACAAGAGCTCTGTGGCAACACGACAGA 3851

Qy 3841 cagtggagtgctgctcgagggaggtttgacagatagagagcagcgatagacaaga 3900
Db 3852 CAGTGGATGCTGCTGGCTCGGAGGAGTTTGAGCAGATAGAGAGCAGCATAGACAAGA 3911
Qy 3901 aagcggtctcag 3912
Db 3912 AAGCGGCTTCAG 3923
RESULT 9
HSFLT4X
LOCUS HSFLT4X 4450 bp mRNA linear PRI 29-NOV-1993
DEFINITION H.sapiens FLT4 mRNA for transmembrane tyrosine kinase.
ACCESSION X59878.S59182
VERSION X59878.1 GI:297049
KEYWORDS transmembrane tyrosine kinase; tyrosine kinase.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 4450)
AUTHORS Galland,F., Karamysheva,A., Pebusque,M.J., Borg,J.P., Rottapel,R.,
Dubreuil,P., Rosnet,O. and Birnbaum,D.
TITLE The FLT4 gene encodes a transmembrane tyrosine kinase related to
the vascular endothelial growth factor receptor
JOURNAL Oncogene 8 (5), 1233-1240 (1993)
MEDLINE 93241723
REFERENCE 2 (bases 776 to 1200)
AUTHORS Galland,F., Karamysheva,A., Mattei,M.G., Rosnet,O., Marchetto,S.
and Birnbaum,D.
TITLE Chromosomal localization of FLT4, a novel receptor-type tyrosine
kinase gene
JOURNAL Genomics 13 (2), 475-478 (1992)
MEDLINE 92307693
REFERENCE 3 (bases 1 to 4450)
AUTHORS Galland,F.
TITLE Direct Submission
JOURNAL Submitted (28-DEC-1992) F. Galland, INSERM, Unite 119, 27 Bd Lei
Roure, Marseille 13009, FRANCE
FEATURES
source
1..4450
/organism="Homo sapiens"
/db_xref="taxon:9606"
sig_peptide
22..87
CDS
22..3918
/function="tyrosine kinase"
/note="unnamed protein product"
/citation=[1]
/codon_start=1
/protein_id="CAA49505.1"
/db_xref="GI:297050"
/db_xref="SWISS-PROT:P35916"
/translation="MQGAALCLRLMLCLGLLGLVSDYSMTPTLTNLTESHVIDTG
DLSISICRGQHPLEWAMPQAEAPATGDKDSEDTGVVVRDCEGTDARPYKVLLEHVEH
ANDTGYVYCYKYIKAREGTAASSYFVRDFEQPTDLLNVRKDMWPCVL
SIPGLNVTLRSSQSLWPDQGVVMDRRGMLVSTPLLDALYLQCCTTGGDDFLSN
PFLVHTGNYLDIOLPRKLELLVGEKLVNCTVWAEFNSGVTFWDYPGKOAERG
KWPERSQOHTHELSSILATHVSOHDLGYSCKANNGIQRFRESEVIVHENPRLS
VENLKGPILENTAGDELVKLPVLAAYPPPEFQHKDCKALSGRSHALVKVEEA
STGYTIALMNSAAGLRNLSLELVNVPPIHEKEASSPSIYSRHSRQALCTATGY
PLPLSIQHWHRPMTPCKFAQRSLSRRQQQDLMPQCRDRAVTTQDAVNPSTESLDWT
EFVGGKNTVSKLVIONANYSAMKCVVSNKVGQDERLIYFYVTTIPDGFTIESKPS
ELLEGGQVLLSCQADSYKYEHLRWYRLNLSLTHDAHGNPLLLDCKNVHLFATPLAASL
EEVAPGARHATLSLSIPRAVEHEGHYVCEVQDRRSHDKCHKYLSVOALEAPRLTO
NLTOLLVNSDSLEKQCLVAGAHAPSIWYKDERLLEEKSGVDLADSNOKLSIORVE
EDAGPYLCSVCVRPKGVNSSAVEGEDKSGMEIVLVGTGVIVFVFWVWVLLLIIFC
NMRRPAHADITKTGLYSIIMDPVEPLEEQCEYLSYDASQWEPFRERLHGLNVNLLGAF
GKVYEAFAFGTHKGSCTDVAVKMLKEGATSEQALMSSELKILIHGNHLNVNLLG
ACTYPOGPLWIVIEFGKYNLSNLRKARDFAPCAEKSPEQRFRFARMVELARLDR
RPGSSDRVLFARFESKTEGGARRASPDQAEPLWLSPLTMEDLCYSFQVARGMEFLAS
RKC1HRDLAARNILLSSEDVYKICDFGLARDIYKDPDYVRKGSARLPKMWAPESIFD
KVYITTDVMSFGVLLWEIFSLGASPIPGVQINEEFQVRDGRTRMRAPELAPAIRH

Qy 1381 cagcaLccagtgacLgagccctggacaccctgcagaatgtttgcccagcgtagctt 1440
Db 1383 CAGCATCCAGTGGCACTGGCGCCCTGGACACCCCTGCAAGATGTTTGGCCAGCGTAGTCT 1442
Qy 1441 ccggcgagcgagcgagcaagacctcatgccacagtgcctgaactgagggcggtgaaccac 1500
Db 1443 CCGCGCGCGCAGCAGCAGACAGACTCATGCCACAGTCCCGTGCATGCGAGGGCGGTGACCAC 1502
Qy 1501 ycaagatgcgclgaaccctcatcgagagcclgaacacctggaccagagtlgtlggauggaaa 1560
Db 1503 GCAGGATGCCGTGAACCCCATCGAGAGCCTGGACACCTTGGACCCGAGTTTGTGGAGGGAAA 1562
Qy 1561 gaaLaagactgtgaacaagctggtgatccagaatgccaaactgctcgtgcataatgaagt 1620
Db 1563 GAATAGACTGTGAGCAAGCTGGTGCATCCAGAAATGCCAAGCTGTGCGCATGTACAAGTG 1622
Qy 1621 tqtgcttccaacaaggltgggcagaagatgaacggtctctacttctatgtgaaccacat 1680
Db 1623 TGTGCTTCCAAAGGTGGGCCAGATGAGCGGCTCATCTACTTCTATGTGACCACCAT 1682
Qy 1681 cccagaggtctcaccatcgaaatccaaacatccagagagctactagagggccagccggt 1740
Db 1683 CCGGACGGCTTACCATCGAATCCAAAGCATCCGAGGAGCTACTAGAGGGCCACGCCGT 1742
Qy 1741 gctccttgactgccaagccagacagctacaagtacagatctgcgctggtatccgcctcaa 1800
Db 1743 GCTCCTGAGCTGCGCAAGCGCGACAGCTACAAGTACGAGCATCTGGCTGTGACCGCTCAA 1802
Qy 1801 cctgtccacgtLgcagatLgcgcagggaaaccgctctctgcactcaagaacgtgca 1860
Db 1803 CTTGTCCACGCTGCAGGATGCGCAGCGGAACCGCTTCTGCTCGACTGCAAGAACTGCA 1862
Qy 1861 tclgttcgccacccctctgtccgcagcctggagaggtggcacctggggcgccagcg 1920
Db 1863 TGTGTTTGGCAGCCCTCTGTGGCGCCAGCCTGGAGAGGTGGCACCTTGGGGCGCGCAGCG 1922
Qy 1921 caagctcaagctLgagtatcccccggtgcgcccagcacgagagccactatgtatgca 1980
Db 1923 CAGCCTTAUCCTTGATATCCCCCGGTCGCGCCCGAGACAGAGGCGCACATATGTGTGGA 1982
Qy 1981 aatLgaagaccgycgagccaLgaacaagcactgcccacagaagtagtacctgtcgtgcaagc 2040
Db 1983 ACTGCAAGACCGCGCAGCCATGACAAGCACTGCCACAAGAACTACCTGTGCGTGCAAGC 2042
Qy 2041 cctggaagccctcggtcaacgcagaactgaaccgaacctcclggtLgaacgtgaagcactc 2100
Db 2043 CTTGGAAGCCCTTCGGCTCACGCAGAACTTGACCCGACCTTCTGTTGAACGTTGAGCGACTC 2102
Qy 2101 gclLgagaLgcagtgcttgggtggcgagcgacgcgcgccagcatcgltgtgtacaaga 2160
Db 2103 GCTGGAGATGCACTGCTTGGTGGCGGAGCGCACGCGCCACGATCGTGTGTACANA 2162
Qy 2161 cgaaggtcgtLgaggaagaactctggagtcgactLggcggaactccaaaccagaagctgag 2220
Db 2163 CGAGAGGCTGCTGGAGGAAAGTCTGGAGTGCAGTTGGCGGAGTCCCAACCAAGCTGAG 2222
Qy 2221 caLccagccgtLgcgcgagagagatgcggagcgtLatctgtcacgctgtgcaacgcaaa 2280
Db 2223 CATCCAGCCGTCGCGGAGAGAGATCGGGGACCGTATCTGTGCAGCGTGTGCAGACCCAA 2282
Qy 2281 gggctLgctcaactctccgcagaggtggcgtggaaaggtcccgaggaLaaagggcagcat 2340
Db 2283 GGGCTCGGTCAACTCTTCGCCCAGCGTGGCGGTGGAGGCTCCGAGGATAAGGGCAGCAT 2342
Qy 2341 ggaatLgtLgataccttLgttcggtaccgggtcatalcgtctgtcttctgtgggtcctcct 2400
Db 2343 GGAGATCGTGATCTTGTCCGTACCGGGCTCATCGCTGTCTTCTTCTGCGTCTCTCTCT 2402
Qy 2401 cclcatctctLgtaacatgagagggccggccacgcagacatLcaagaggggctactgtc 2460
Db 2403 CCTCATCTTCTGTAMCATAGGAGCGCGGCCACGCAGACATCAAGACGGGCTACTGTCT 2462

Qy 2461 catcatatggacccccggggaggTgcctcttggaggagcaatgcaatacctgttctactcga 2520
Db 2463 CATCATATGACCCCGGGAGGTGCCTCTGAGGAGCAATGCGAATACCTGTCTCTACGA 2522
Qy 2521 tgcagccagLggaatttcccccgagagcggtgcactgggagagctcctcggtctacgg 2580
Db 2523 TGCCAGCAGTGGGAATTTCCCCCGAGAGCGGCTGCACCTGGGGAGAGTGTCTCGGCTACGG 2582
Qy 2581 cgcttctgggaaggtgggtggaaagcctccgcttctcggtcatccacaaaggcgagcagctgtga 2640
Db 2583 CGCCTTCGGGAAGTGGTGGGAAGCCTCCGCTTTCGGCATCCACAAGGGCAGCAGCTGTGA 2642
Qy 2641 caccgtggccctgaaaaatgtctgaaaggggcgccacggccaagcagcgagcacgcgcgtgat 2700
Db 2643 CACGCTGGCCGTGAAAATGCTTGAAGAGGGCGCCACGCCACAGCAGCAGCGCGCTGAT 2702
Qy 2701 gtcgagctcaagatcctcatctacatcgcaaccactcaacgtLgclcaacctLcclcg 2760
Db 2703 GTCGGAGCTCAAGATCTCTATTACATCGGCAACCACTCAACGTGTGTCAACCTTCTCGG 2762
Qy 2761 ggcgtgcaccaagcgcgaggggccccctcatggtgatcgtggagtctctgcaagtacggcaa 2820
Db 2763 GCGGTGCAACCAAGCGCAGGGGCCCTTCATGCTGATCGTGAGTCTCTCAAGTACGGCAA 2822
Qy 2821 cctctcaacttctctgcgcgaagcggtgacgcttcagccctgcgcggaagaagtctcc 2880
Db 2823 CCTCTCAACTTCTTGGCGGCCAAGCGGACGCCCTTCAGCCCCCTGCGCGGAGAAAGTCTCC 2882
Qy 2881 cgagcagcgcgagcgttccgcgcctatggtagctgcagagctggatcggaagcgcgcc 2940
Db 2883 CGAGCAGCGCGACGCTTCCGCGCCATGTTGAGCTCGCCAGGCTGGATCGAGGCGGCC 2942
Qy 2941 ggggagcagcaaggggtccctctctgcgcggtctctgaaagaccgagggcgagcgagggcg 3000
Db 2943 GGGGAGCAGCGACAGGGTCTCTTTCGCGCGTCTCTCGAAGACCAGGGCGGAGGGCAGGCG 3002
Qy 3001 ggcctctcagacccaagaagctgagggacctgtggtgagccgctgacccatLggaagatct 3060
Db 3003 GGCCTTCCACACCACCAAGAGCTGAGGACCTGTGGCTGAGCCCGCTGACCATGGAAGATCT 3062
Qy 3061 tgtctgtacagcttccaggTggccagaggatggagtctcctggtctctccgaaagtgcat 3120
Db 3063 TGTCTGCTTACAGTTCACAGTGGCGCAGAGGATGGAGTTCCTGGCTTCCCGAAAAGTGCAT 3122
Qy 3121 ccagagacctgctgctcgaaacattctgtctcgaaagcagctLggtLgaagatctg 3180
Db 3123 CCACAGAGACCTTGGCTGCTCGGAACATTTCTGCTGTGGAAGACGACGTGTGTAAGATCTG 3182
Qy 3181 tgaactttggccttgccccgggacatctacaagacccctgaactacgtccgcgaagggcagtcg 3240
Db 3183 TGACTTTGGCCTTGCCCGGGACATCTACAAAGACCCCGACTACGTCCGCAAGGGCAGTGC 3242
Qy 3241 ccgctgccccctgaagtggatgggccccctgaaagcatctctgaaaggtgtatcaccaagca 3300
Db 3243 CCGCTGGCCCCCTGAAGTGGATGGCCCCCTGAAAGGATCTTTCACAAAGGTGTACACACGCA 3302
Qy 3301 gagLgacgtLggtctcttgggtgctctctLggagatctctctctggggggtctcccc 3360
Db 3303 GAGTGACGTGTGTCCTTTGGGGTGTCTCTCTGGGAGATCTTCTCTCTGGGGGGCTTCCC 3362
Qy 3361 gtacccctgggtgagatcaaatgaggagttctctgcagcggtgagagagcgcaacaagat 3420
Db 3363 GTACCTTGGGTGCAGATCAATAGGAGTTCCTGCCAGCGCTGAGAGAGCGCACAAAGAT 3422
Qy 3421 gagggccccgagctggccactccgcacatagcgcgcatctgtctgaactgtctggtccgg 3480
Db 3423 GAGGGCCCCGAGGTGGCCACTCCGCCATACGCCACATCATGTCTGAACCTGCTGTCGG 3482
Qy 3481 agaccacaagcgagacctgcatctcgagctggtgagatcctgggaacctgctcca 3540
Db 3483 AGACCCCAAGCGAGACCTGTCATTTCTGGACCTGTTGGAGATCTTGGGGACCTGCTCCA 3542
Qy 3541 gggcaggggctgcaagaggaaggaggtctctgcatggccccgcgcagctctcagagctc 3600

Db	3543	GGCGAGGGCCCTGCAAGAGGAAGAGAGGTCTGCATGGCCCCGCCAGCTCTCAGAGCTC	3602	
Qy	3601	agaagaggcagcttctgcaggtgtccacccatggccctacacatcgcccaggctgacgc	3660	
Db	3603	AGAAGAGGCGACGTTCTCGCAGGTGTCCACCATGGCCCTACACATCGCCCGAGCTGAGCG	3662	
Qy	3661	tgagcagcgcgcgaagcctgcagccacagcctgcgcgcaggtattacaactgggt	3720	
Db	3663	TCAGGACAGCGCGCAAGCCTGCAGCGGCACACCTGGCCCGCAGGTATTACAACTGGGT	3722	
Qy	3721	gtcctttcccggtgcttgccgaggggtgagacccgtggttctccaggtgaaagac	3780	
Db	3723	GTCTTTTCCCGGTGCTTGCCGAGAGGGCTGAGACCCGTGGTTCTCCAGCATCAAGAC	3782	
Qy	3781	atttgaggaaattcccatgaccccccaagcactacaaggctctgtgacaaacccaagaga	3840	
Db	3783	ATTTCAGGAATTTCCCATGACCCCAACGACCTTACAAAGCCTCTGTGACAAACAGACAGA	3842	
Qy	3841	cagtggatggllqctggcctcgagaggtttgagcagatagagcagcagcatalaacaaga	3900	
Db	3843	CAGTGGGATGGTGTGGCCCTCGGAGGAGTTTGGACAGATAGAGACGCGCATAGACAAGA	3902	
Qy	3901	aagcggcttcag	3912	
Db	3903	AAGCGCTTCAG	3914	
RESULT 10				
LOCUS	I44515/c	6827 bp	DNA	linear
DEFINITION	Sequence 17 from patent US 5635177.			
ACCESSION	I44515			
VERSION	I44515.1			
GI	2469228			
KEYWORDS	Unknown.			
SOURCE	Unknown.			
ORGANISM	Unclassified.			
REFERENCE	1 (bases 1 to 6827)			
AUTHORS	Bennett,B.D., Goeddel,D. and Matthews,W.			
TITLE	Protein tyrosine kinase agonist antibodies			
JOURNAL	Patent: US 5635177-A 17 03-JUN-1997;			
FEATURES	Location/Qualifiers			
source	1..6827			
BASE COUNT	1558 a	1870 c	1738 g	1660 t
ORIGIN	1 others			
Query Match 23.1%; Score 950; DB 6; Length 6827;				
Best Local Similarity 99.9%; Pred. No. 0;				
Matches 1000; Conservative 0; Mismatches 1; Indels 0; Gaps 0;				
Qy	2869	gagaagatctcccgagcagcgcgagcgttcgcgcacatggttgagagctgcgcaggtgga	2928	
Db	2924	GGAGAAGTCTCCCGACGACGGGAGCGTTCGCCGCCATGTTGGAGCTGCCAGGCTGGA	2865	
Qy	2929	tcgagagcgccgggagcagcagaggtcctcttcgcaggttctcgaagaccgagg	2988	
Db	2864	TCGAGGCGCGCGGAGGAGCGACAGGGTCTCTTCGCGCGGTCTCGAAGACCGAGGG	2805	
Qy	2989	cggagcagcggggtctctccagaccaagaagctgagacacctgtggtgagcccgctgac	3048	
Db	2804	CGGAGCGAGCGGGCTTCTCCAGACCAAGAAGCTGAGGACCTGTGGCTGAGCCCGTAC	2745	
Qy	3049	catggaagatcttgtctgactacagcttccagtlgcccagagggatggagttccttggttc	3108	
Db	2744	CATGGAAGATCTTGTCTGTCTACAGCTTCCAGGTTCAGGTGGCCAGAGGGATCGAGTTCT	2685	
Qy	3109	ccgaagtgcattccacagagacctggctcgcgaacattctgctgtcggaaagcagct	3168	
Db	2684	CCGAAAGTGCATCCACAGAGACCTGGCTGCTCGGAACATTTCTGCTCGGAAGCGACGT	2625	

Qy	3169	ggtgaagatctgtgacttttgaccttgccgggacatctacaaagacctgactacgtccg	3228	
Db	2624	GGTCAAGATCTGTGACTTTTGGCCTTGGCCGGGACATCTACAAAGACCCGCACTACGTTCCG	2565	
Qy	3229	caagggcagtgcccggtgccccctgaagtgaatggccccctgaaagcatctctcgacaaggt	3288	
Db	2564	CAAGGGCAGTGCCCGGCTGCCCTGAAGTGCATGGCCCTGAAAGCATCTTTCGACAAGGT	2505	
Qy	3289	gtacaccacgacagatgacgtgtggtcctltgggggtgcttctcttgaggagatcttctctct	3348	
Db	2504	GTACACCACGACAGTGACGTGTGTCTTTTGGGGTGCCTTCTCTGGAGATCTTCTCTCT	2445	
Qy	3349	gggggctccccctaccctgggtgacagatcaatlgagaggtctctgccaagcggtcgagaga	3408	
Db	2444	GGGGGCTTCCCGGTACCTGGGTGCAGATCAATGAGGAGTTCTGCCACCGCGCTGAGACA	2385	
Qy	3409	cggcacaaagatgagggccccggagctggccactcccgccatcagcgcgcatcatctgtgaa	3468	
Db	2384	CGGCACAAGGATGAGGGCCCCGGAGCTGGCCACTCCCGCCCATACGCCGCATCATGCTCAA	2325	
Qy	3469	ctgctggtccggagagacccccaaaggcgagacctgcatctcgggaqctggllgagagatccctgg	3528	
Db	2324	CTGCTGTGTCGGGAGACCCCAAGGGCAGACCTTGCATTCTCGGAGCTGGTGGAGATCTCTGG	2265	
Qy	3529	ggacctgctccaggcgagggtcctgcaagaggaagagaggtctctgcatggccccgcgcag	3588	
Db	2264	GGACCTGCTCCAGGGCAGGGCCTTGCAAGAGGAAGAGAGGAGGTCTGCATGGCCCCCGCGAG	2205	
Qy	3589	ctctcagagctcagaagaggcgagcttctcgcaggtgtccaccttgccccctacacatcgc	3648	
Db	2204	CTCTCAGAGCTCAGAAGAGGGCAGCTTCTCGCAGGTGTCCACCATGGGCCCTACACATGCC	2145	
Qy	3649	ccaggtgacgtcagagacagcccgccaaagcctgcagcgccacacagcctggcgccaggta	3708	
Db	2144	CCAGGCTGACGCTGAGGACAGCCCGCCAAAGCTTCAGCGCCACAGCCTGGCGCGCAGGTA	2085	
Qy	3709	ttacaactgggtgtcctttcccggtgcttggccagaggggtcgtgagacccgtggtctctc	3768	
Db	2084	TTACAACCTGGGTGCTCTTTCGGGTGCTTGCCAGAGAGGGGCTGAGACCCGTGGTTCCTC	2025	
Qy	3769	caggatgaagacatttgaggaattcccccatgacccccacacacacagcctctgtgga	3828	
Db	2024	CAGGATGAAGACATTTGAGGAATTTCCCATGACCCCAACGACCTACAAAGGCTCTGTGGA	1965	
Qy	3829	caaccagacacagtgagtgatgggtgctggcctcgagagagt	3869	
Db	1964	CAACCAGACACAGTGGGATGGTGTCTGGCCTCGGAGGAGT	1924	
RESULT 11				
LOCUS	AC022095/c	127488 bp	DNA	linear
DEFINITION	Homo sapiens chromosome 5 clone CTB-3688, WORKING DRAFT SEQUENCE, 13 unordered pieces.			
ACCESSION	AC022095			
VERSION	AC022095.5			
KEYWORDS	HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
AUTHORS	1 (bases 1 to 127488)			
TITLE	Sequencing of Human Chromosome 5			
JOURNAL	Unpublished			
REFERENCE	2 (bases 1 to 127488)			
AUTHORS	DOE Joint Genome Institute.			
TITLE	Direct Submission			
JOURNAL	Submitted (26-JAN-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA			
COMMENT	On Apr 20, 2001 this sequence version replaced g1:7711676.			
	-----Genome Center			
	Center: Joint Genome Institute			


```
Center Code: JGI
Web site: http://www.jgi.doe.gov
-----
Project Information
Center Project Name: 78060
Center clone name: CIT978SKB_36B8
-----
Summary Statistics
Consensus quality: 110477 bases at least Q40
Consensus quality: 117221 bases at least Q30
Consensus quality: 120225 bases at least Q20
Estimated insert size: 131000; pulse field gel estimation
Estimated insert size: 126288; sum-of-contigs estimation
Quality coverage: 7.48 in Q20 bases; sum-of-contigs estimation
Quality coverage: 7.76 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 13 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1116: contig of 1116 bp in length
* 1117: 1216: gap of unknown length
* 1217: 2254: contig of 1038 bp in length
* 2255: 2354: gap of unknown length
* 2355: 3412: contig of 1058 bp in length
* 3412: 3512: gap of unknown length
* 3512: 5005: contig of 1493 bp in length
* 5005: 5105: gap of unknown length
* 5105: 7647: contig of 2542 bp in length
* 7647: 7748: gap of unknown length
* 7748: 10237: contig of 2490 bp in length
* 10237: 10337: gap of unknown length
* 10337: 12440: contig of 2103 bp in length
* 12440: 12540: gap of unknown length
* 12540: 15935: contig of 3395 bp in length
* 15935: 16035: gap of unknown length
* 16035: 24396: contig of 8361 bp in length
* 24396: 24497: gap of unknown length
* 24497: 39085: contig of 14589 bp in length
* 39085: 39185: gap of unknown length
* 39185: 60545: contig of 21360 bp in length
* 60545: 60645: gap of unknown length
* 60645: 79490: contig of 18845 bp in length
* 79490: 79590: gap of unknown length
* 79590: 127488: contig of 47898 bp in length.
*
* Location/Qualifiers
* source
* 1..127488
* /organism="Homo sapiens"
* /db_xref="taxon:9606"
* /chromosome="5"
* /clone_lib="CITB-36B8"
* /clone="31643 a 32392 c 31616 g 30626 t 1211 others"
BASE COUNT 31643 a 32392 c 31616 g 30626 t 1211 others
ORIGIN
FEATURES
Source
1..127488
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
/clone_lib="CITB-36B8"
/clone="31643 a 32392 c 31616 g 30626 t 1211 others"
Query Match 8.8%; Score 363; DB 2; Length 127488;
Best Local Similarity 100.0%; Pred. No. 4.e-168;
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1677 ccattcccgagcgttcacatcgatccaagccatccaggagcgtactagagggccagc 1736
|||||
Db 114615 CCATCCCGGAGCGGCTTACCATCGAATCCCAAGCCATCCGAGGAGCTACTAGAGGGCCAGC 114556
|||||
QY 1737 cggctcctgagctccagcgcagctacaagtacagcagctcgcctggtaccgcc 1796
|||||
Db 114555 CGGTGCTCTCTACGCTGCCAGCCGACAGCTACAAAGTACAGGACATCTGCCCTGTGTACCGCC 114496
|||||
QY 1797 tcaactgtccagctgcagatgcgcacgggaaccgcgtctctgctcgtactcaagaacg 1856
|||||
```

```
Db 114495 TCAACCTGTCCACGCTGCACGATGCGCAGCGGGAACCCCGCTTCTGCTCGACTCGAAGAAGC 114436
QY 1857 tgcattctgtccaccacctctgagccgcagcctgagagaggtgagcactgagggcgccgc 1916
|||||
Db 114435 TGCACTGTTCGCCACCCCTCTGGCCGCCAGCCTGGAGAGGTGGCACCTGGGGCGCGCC 114376
QY 1917 agccacgcctcagcctgagctatccccccgcgctgcgcgcccagcacagggccactatgct 1976
|||||
Db 114375 ACGCCACGCTCAGCCTGAGTATCCCGCGCTGCGCGCCGACGACGAGGCGCCACTATGTCT 114316
QY 1977 gcaagtcaagaccgcgcagccatgacaagcactgcccacagaagtagtacctgltcggtgc 2036
|||||
Db 114315 GCGAAGTGAAGACCGCGCGCAGCCATGACACCACTGCCACAGAAGTACCTGTCTCGGTGC 114256
QY 2037 agg 2039
|||
Db 114255 AGG 114253

RESULT 12
AC108083
DEFINITION Homo sapiens chromosome 5 clone CTD-2013L15, WORKING DRAFT
LOCUS AC108083
ACCESSION AC108083.1 GI:18369929
VERSION AC108083.1
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 130129)
DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 5
JOURNAL Unpublished
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (25-JAN-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
-----
Project Information
Center Project Name: 632820
Center clone name: CITB-H1_2013L15
-----
Summary Statistics
Consensus quality: 124488 bases at least Q40
Consensus quality: 128031 bases at least Q30
Consensus quality: 128842 bases at least Q20
Estimated insert size: 135000; agarose-fp estimation
Estimated insert size: 129829; sum-of-contigs estimation
Quality coverage: 7.66 in Q20 bases; agarose-fp estimation
Quality coverage: 7.97 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 4320: contig of 4320 bp in length
* 4321: 4420: gap of unknown length
* 4421: 23712: contig of 19292 bp in length
* 23713: 23812: gap of unknown length
* 23813: 48602: contig of 24790 bp in length
* 48603: 48702: gap of unknown length
* 48703: 130129: contig of 81427 bp in length.
*
* Location/Qualifiers
FEATURES
```

```
source 1. .130129
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
/clone="CTD-2013L15"
/clone_lib="CalTech human BAC library D"
BASE COUNT 35337 a 32397 c 30949 g 31146 t 300 others
ORIGIN
-----
Query Match 8.8%; Score 363; DB 2; Length 130129;
Best Local Similarity 100.0%; Pred. No. 4.4e-168;
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1677 ccattcccgacggttcaccatcgaatccaaagccatccgaggagctactagagggcagc 1736
|||||
Db 17322 CCATCCCGACGGCTTCCACATCGAATCCAAAGCCATCCGAGGAGCTACTAGAGGCCAGC 17381

Qy 1737 cggctactcttaagctgccaagccagctacaagtacagcatctgccttqatccgcc 1796
|||||
Db 17382 CGGTGCTCTTCCAGCTGCGCAAGCCGACAGCTACAAGTAGAGCATCTCGGCTGGTACC GCC 17441

Qy 1797 tcaacctgtccacgctgcacgatgcgacgggaacccgctctctgctgactgcgaagaacg 1856
|||||
Db 17442 TCACCTGTCTCACCGCTGCACCATCGCGACGGGAACCCGCTTCTGCTCGACTGCAAGAAGC 17501

Qy 1857 tgcattcttccgcaacccctctgcccgcagccttgaggaggtggccacttgggcygcgc 1916
|||||
Db 17502 TGCATCTCTTCCGACCCGCTTGGCCGCGACGCTCGAGGAGGTGGCAGCTGGGCGCGCC 17561

Qy 1917 acgcaactcagctgagtagtaccctccgcgctgcgcgcgacgacgagggccactatgtgt 1976
|||||
Db 17562 ACGGCACGCTCAGCTGAGTATCCCGCCGCTGCGCCGCGACGACGAGGGCCACTATGTGT 17621

Qy 1977 gcgaagtccaagacggcgccgacgatgacaagcactgcacaaagtagtacctgtcgtgtc 2036
|||||
Db 17622 CGGAAGTCCAAGACGGCGCGACCATGCAAGACACTGCGCAAGAAGTACCTGCGGTGC 17681

Qy 2037 agg 2039
|||
Db 17682 AGG 17684

RESULT 13
AC106813
LOCUS AC106813 173341 bp DNA linear HTG 25-JAN-2002
DEFINITION Homo sapiens chromosome 5 clone RP11-586L9, WORKING DRAFT SEQUENCE,
7 unordered pieces.
ACCESSION AC106813
VERSION AC106813.2 GI:18369924
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 173341)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 5
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 173341)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (12-JAN-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT -- Jan 25, 2002 this sequence version replaced gi:18139363.
-----
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
-----
Project Information
Center Project Name: 1519801
Center clone name: RPCI-11_586L9
```

```
-----
Summary Statistics
Consensus quality: 164442 bases at least Q40
Consensus quality: 167261 bases at least Q30
Consensus quality: 167771 bases at least Q20
Estimated insert size: 186250; agarose-fp estimation
Estimated insert size: 172741; sum-of-contigs estimation
Quality coverage: 10.29 in Q20 bases; agarose-fp estimation
Quality coverage: 11.1 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence.
* as soon as it is available and the accession number will
* be preserved.
* 1 1596: contig of 1596 bp in length
* 1597 1696: gap of unknown length
* 1697 3940: contig of 2244 bp in length
* 3941 4040: gap of unknown length
* 4041 5104: contig of 1064 bp in length
* 5105 5204: gap of unknown length
* 5205 6286: contig of 1082 bp in length
* 6287 6386: gap of unknown length
* 6387 20063: contig of 13677 bp in length
* 20064 20163: gap of unknown length
* 20164 82401: contig of 62238 bp in length
* 82402 82501: gap of unknown length
* 82502 173341: contig of 90840 bp in length.
FEATURES
Location/Qualifiers
source 1. .173341
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
/clone="RP11-586L9"
/clone_lib="RPCI human BAC library 11"
BASE COUNT 45837 a 42564 c 41389 g 42871 t 680 others
ORIGIN
```

```
Query Match 8.8%; Score 363; DB 2; Length 173341;
Best Local Similarity 100.0%; Pred. No. 4.2e-168;
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1677 ccattcccgacggttcaccatcgaatccaaagccatccgaggagctactagagggcagc 1736
|||||
Db 95297 CCATCCCGACGGCTTCCACATCGAATCCAAAGCCATCCGAGGAGCTACTAGAGGCCAGC 95356

Qy 1737 cggctactcttaagctgccaagccagctacaagtacagcatctgccttqatccgcc 1796
|||||
Db 95357 CGGTGCTCTTCCAGCTGCGCAAGCCGACAGCTACAAGTAGAGCATCTCGGCTGGTACC GCC 95416

Qy 1797 tcaacctgtccacgctgcacgatgcgacgggaacccgctctgctgacugcaagaacg 1856
|||||
Db 95417 TCAACCTGTCCACGCTGCACGATCGGCACGGGAACCCGCTTCTGCTGCTGCAAGAAGC 95476

Qy 1857 tgcattcttccgcaacccctctgcccgcagccttgaggaggtggccacttgggcygcgc 1916
|||||
Db 95477 TGCATCTCTTCCGACCCGCTTGGCCGCGACGCTGAGGAGGTGGCAGCTGGGCGCGCC 95536

Qy 1917 acgcaactcagctgagtagtaccctccgcgctgcgcgcgacgacgagggccactatgtgt 1976
|||||
Db 95537 ACGGCACGCTCAGCTGAGTATCCCGCCGCTGCGCCGCGACGACGAGGGCCACTATGTGT 95596

Qy 1977 gcgaagtccaagacggcgccgacgatgacaagcactgccacaagaagtacctgtcgtgtc 2036
|||||
Db 95597 CGGAAGTCCAAGACGGCGCGACCATGCAAGACACTGCCACAGAAGTACTCTGTGCGGTGC 95656

Qy 2037 agg 2039
|||
Db 95657 AGG 95659
```


Quality coverage: 7.97 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 4320: contig of 4320 bp in length
* 4321 4420: gap of unknown length
* 4421 23712: contig of 19292 bp in length
* 23713 23812: gap of unknown length
* 23813 48502: contig of 24790 bp in length
* 48503 48702: gap of unknown length
* 48703 130129: contig of 81427 bp in length.
*
* Location/Qualifiers
* 1..130129
* /organism="Homo sapiens"
* /db_xref="taxon:9606"
* /chromosome="5"
* /clone="CTD-2013L15"
* /clone_lib="Caltech human BAC library D"
*
BASE COUNT 35337 a 32397 c 30949 g 31146 t 300 others
ORIGIN

Query Match 4.9%; Score 202; DB 2; Length 130129;
Best Local Similarity 100.0%; Pred. No. 1.8e-88;
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3910 cagctgaaggaacctggccagaatgtggtgtgaccaggacacccctgaactcccaag 3969
|||||
DB 35967 CAGCTGTAAAGGACCTGGCCCAATGTGGCTGTGACCAGGCGACACCTGATCCCAAG 35908
|||||
QY 3970 gaggcggcgccgctgaagcggggggccgagggccaggggtgttttacaacagcagta 4029
|||||
DB 35907 GAGCGGGCGGGCGCTGAGCGGGGGGGCGGAGGAGCCAGGTGTTTACACAGCGCAGTA 35848
|||||
QY 4030 tgggaagctgtcgaagcgaagcgaaggaagcagcagctgctccctgctgcccagtaacttt 4089
|||||
DB 35847 TGGGAGCTGTGGAGCCCAAGCGAGGAGGAGCAGCAGCTGCTCCCGTCTGCCCGGTGACTTT 35788
|||||
QY 4090 cttcragacaacagctactaa 4111
|||||
DB 15787 CTTACAGACACAGCTACTAA 35766
|||||

RESULT 17
AC025336/c
LOCUS
DEFINITION Homo sapiens chromosome 5 clone RP11-451H23 map 5, WORKING DRAFT
AC025336
SEQUENCE, 32 unordered pieces.
AC025336
VERSION AC025336.2 GI:7328761
KEYWORDS HTG; HTGS-PHASE1; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 168347)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,
Boguslavsky,L., Boukhgalter,B., Brown,A., Burkett,G.,
Campopiano,A., Castelle,A., Choepe,Y., Colangelo,M., Collins,S.,
Collumore,A., Cooke,P., DeArelano,K., Dewar,K., Diaz,J.S.,
Dodge,S., Domino,M., Doyle,M., Ferreira,P., Fitzhugh,W., Gage,D.,
Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
Grand-Pierre,N., Grant,C., Hagos,B., Heaford,A., Horton,L.,

Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
Klein,J., Laroque,K., Lamazares,R., Landers,T., Lehotzky,J.,
Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N.,
McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R.,
Meidrich,J., Meneus,L., Mihoval,T., Miranda,C., Mlenga,V., Morrow,J.,
Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
O'Neill,D., Oliver,T.M., Oliver,J., Peterson,K., Pierre,N.,
Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,
Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Tessaye,S., Theodore,J., Tirrell,A., Travers,M., Triggillo,J.,
Vassiliev,H., Viel,R., Vo,A., Willson,B., Wu,X., Wyman,D., Ye,W.J.,
Young,C., Zainoun,J., Zimmer,A. and Zody,M.
Direct Submission
Submitted (08-MAR-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 25, 2000 this sequence version replaced gt:7210017.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu

Project Information
Center project name: L6686
Center clone name: 451_H_23

Summary Statistics
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 150422 bases at least Q40
Consensus quality: 159524 bases at least Q30
Consensus quality: 163013 bases at least Q20
Insert size: 165247; sum-of-contigs
Quality coverage: 3.6 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 32 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 1389: contig of 1389 bp in length
* 1390 1489: gap of 100 bp
* 1490 3130: contig of 1641 bp in length
* 3131 3230: gap of 100 bp
* 3231 4942: contig of 1712 bp in length
* 4943 5042: gap of 100 bp
* 5043 6981: contig of 1939 bp in length
* 6982 7081: gap of 100 bp
* 7082 8708: contig of 1627 bp in length
* 8709 8808: gap of 100 bp
* 8809 10286: contig of 1478 bp in length
* 10287 10386: gap of 100 bp
* 10387 12212: contig of 1826 bp in length
* 12213 12312: gap of 100 bp
* 12313 14658: contig of 2346 bp in length
* 14659 14758: gap of 100 bp
* 14759 17941: contig of 3183 bp in length
* 17942 18041: gap of 100 bp
* 18042 21297: contig of 3256 bp in length
* 21298 21397: gap of 100 bp
* 21398 24992: contig of 3595 bp in length
* 24993 25092: gap of 100 bp
* 25093 27768: contig of 2676 bp in length
* 27769 27868: gap of 100 bp
* 27869 31188: contig of 3320 bp in length
* 31189 31288: gap of 100 bp
* 31289 33714: contig of 2426 bp in length

* 42303 42402: gap of 100 bp
* 42403 47816: contig of 5414 bp in length
* 47817 47916: gap of 100 bp
* 47917 52586: contig of 4670 bp in length
* 52587 52686: gap of 100 bp
* 52687 56567: contig of 3881 bp in length
* 56568 56667: gap of 100 bp
* 56668 61557: contig of 4890 bp in length
* 61558 61657: gap of 100 bp
* 61658 66724: contig of 5067 bp in length
* 66725 66824: gap of 100 bp
* 66825 71568: contig of 4744 bp in length
* 71569 71668: gap of 100 bp
* 71669 76578: contig of 4910 bp in length
* 76579 76678: gap of 100 bp
* 76679 83312: contig of 6634 bp in length
* 83313 83412: gap of 100 bp
* 83413 90053: contig of 6641 bp in length
* 90054 90153: gap of 100 bp
* 90154 99426: contig of 9273 bp in length
* 99427 99526: gap of 100 bp
* 99527 108015: contig of 8489 bp in length
* 108016 108115: gap of 100 bp
* 108116 118144: contig of 10029 bp in length
* 118145 118244: gap of 100 bp
* 118245 130468: contig of 12224 bp in length
* 130469 130568: gap of 100 bp
* 130569 142239: contig of 11671 bp in length
* 142240 142339: gap of 100 bp
* 142340 157135: contig of 14796 bp in length
* 157136 157235: gap of 100 bp
* 157236 168347: contig of 11112 bp in length.

FEATURES

Source

Location/Qualifiers
1..168347
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
/map="5"
/clone="RP11-451H23"
/clone_lib="RPC1-11 Human Male BAC"

misc_feature 1..1389
/note="assembly_fragment"
1490..3130
misc_feature /note="assembly_fragment"
3231..4942
misc_feature /note="assembly_fragment"
5043..6981
misc_feature /note="assembly_fragment"
7082..8708
misc_feature /note="assembly_fragment"
8809..10286
misc_feature /note="assembly_fragment"
10387..12212
misc_feature /note="assembly_fragment"
12313..14658
misc_feature /note="assembly_fragment"
14759..17941
misc_feature /note="assembly_fragment"
18042..21297
misc_feature /note="assembly_fragment"
21398..24992
misc_feature /note="assembly_fragment"
25093..27768
misc_feature /note="assembly_fragment"
27869..31188
misc_feature /note="assembly_fragment"
31289..33714
misc_feature /note="assembly_fragment"
33815..37277
misc_feature /note="assembly_fragment"
37378..42302
misc_feature /note="assembly_fragment"
42403..47816

misc_feature /note="assembly_fragment"
47917..52586
misc_feature /note="assembly_fragment"
52687..56567
misc_feature /note="assembly_fragment"
56688..61557
misc_feature /note="assembly_fragment"
61658..66724
misc_feature /note="assembly_fragment"
66825..71568
misc_feature /note="assembly_fragment"
71669..76578
misc_feature /note="assembly_fragment"
76679..83312
misc_feature /note="assembly_fragment"
83413..90053
misc_feature /note="assembly_fragment"
90154..99426
misc_feature /note="assembly_fragment"
99527..108015
misc_feature /note="assembly_fragment"
108116..118144
misc_feature /note="assembly_fragment"
118245..130468
misc_feature /note="assembly_fragment"
130569..142239
/note="assembly_fragment"

Query Match 4.2%; Score 173; DB 2; Length 168347;
Best Local Similarity 100.0%; Pred. No. 3.8e-74;
Matches 173; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 832 gcaggcagagcgggtaagtgggtgcccgcagcagcgtcccagcagacccacacagaact 891
|||||
Db 3936 GCAGGCAGAGCGGGTAAAGTGGTCCCGAGCGCGCTCCAGCAGACCCACACAGAACT 3995
|||||
Qy 892 cttccagcatcctgaccatcccaacgctcagccagcagcagcctgggctcgtatgtgtcaa 951
|||||
Db 3996 CTCAGCATCTCTGACCATCCACAGCTCAGCAGCAGCAGCTGGGCTCTGTGTGCA 4055
|||||
Qy 952 ggcacaacagcgtcccgagcgtatttcgggagagcagcaggtcattgtgcagt 1004
|||||
Db 4056 GGCCAACAACGGCATCCAGCGCATTTCCGGCAGACGACCGAGGCTCATTTGTGCATG 4108
|||||

RESULT 20

HSA329747 HSA329747 780 bp DNA linear PRI 01-OCT-2001
LOCUS Homo sapiens genomic sequence surrounding NotI site, clone
DEFINITION NRI-SP18R.
ACCESSION AJ329747
VERSION AJ329747.1 GI:15874165
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM human.
REFERENCE 1 (bases 1 to 780)
AUTHORS Kutsenko,A.S., Gizatullin,R.Z., Al-Amin,A.N., Wang,F.,
Podowski,R.M., Matushkin,Y.G., Kvasha,S.M., Gyanchandani,A.,
Muravenko,O.V., Protopopov,A.I., Kashuba,V.I., Kisselev,L.L.,
Wasserman,W., Wahlestedt,C. and Zabarovsky,E.R.
TITLE Analysis of NotI flanking sequences: a new tool for gene discovery
and verification of the human genome
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 780)
AUTHORS Zabarovsky,E.R.
TITLE Direct Submission
JOURNAL Submitted (16-MAY-2001) Microbiology and Tumorbiology Centre,
Karolinska Institute, Theorells vag, 3, Box 280, Stockholm 171 77,
Sweden
FEATURES Location/Qualifiers
source 1..780

```
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="NRL-SPI8R"
BASE COUNT      126 a      222 c      278 g      149 t      5 others
(11)GIN

Query Match      4.0%; Score 165; DB 9; Length 780;
Best Local Similarity 100.0%; Pred. No. 7.3e-70;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 532 gcaaaagctcgtctgtgcccagcaggcagggtggtgtggatgacgcggcgccat 591
|||||
IB 64 CCAAGCTCGTCTGTGGCCAGACGGCAGGAGGTGCTGTGCATGACCGCGGGCCAT 123
|||||

QY 592 qclcgltccacaccactgctgcacatgacctgtacctgcaatgcagaccacctgggg 651
|||||
DB 124 GCTCGTCTCCACGCCACTGCTGCACGATGCCCTGTACCTGCAGTGGCAGACCACTGGGG 183
|||||

QY 652 aqaccagagacttccttccaaacctctcctggtggcacatcacagg 696
|||||
DB 184 AGACCAGGACTTCTTTCCAAACCCCTTCTCTGCTGCATCACAGG 228

RESULT 21
HSA334721
LOCUS      HSA334721      785 bp      DNA      linear      PRI 01-OCT-2001
DEFINITION Homo sapiens genomic sequence surrounding NotI site, clone
            NL6-BA13RS.
ACCESSION  AJ334721
VERSION    AJ334721.1 GI:15879139
KEYWORDS
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 785)
            Kutsenko,A.S., Gizatullin,R.Z., Al-Amin,A.N., Wang,F.,
            Podowski,R.M., Matushkin,Y.G., Kvasha,S.M., Gyanchandani,A.,
            Muravenko,O.V., Protopopov,A.I., Kashuba,V.I., Kisselev,L.L.,
            Wasserman,W., Wahlestedt,C. and Zabarovsky,E.R.
            Analysis of NotI flanking sequences: a new tool for gene discovery
            and verification of the human genome
            Unpublished
            2 (bases 1 to 785)
            Zabarovsky,E.R.
            Direct Submission
            TITLE
            JOURNAL
            REFERENCE
            AUTHORS
            TITLE
            JOURNAL
            SOURCE
            Karolinska Institute, Theorells vag, 3, Box 280, Stockholm 171 77,
            Sweden

FEATURES
            source
            Location/Qualifiers
            1..785
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone="NL6-BA13RS"
BASE COUNT      132 a      207 c      270 g      174 t      2 others
ORIGIN

Query Match      4.0%; Score 165; DB 9; Length 785;
Best Local Similarity 100.0%; Pred. No. 7.3e-70;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 532 gcaaaagctcgtctgtgcccagcaggcagggtggtgtggatgacgcggcgccat 591
|||||
DB 64 CCAAGCTCGTCTGTGGCCAGACGGCAGGAGGTGCTGTGCATGACCGCGGGCCAT 123
|||||

QY 592 gctcgtgtccacgccactgctgcacatgacctgtacctgcaatgcagaccacctgggg 651
|||||
DB 124 GCTCGTCTCCACGCCACTGCTGCACGATGCCCTGTACCTGCAGTGGCAGACCACTGGGG 183
|||||

QY 652 aqaccagagacttccttccaaacctctcctggtggcacatcacagg 696
|||||
```

```
DB 184 AGACCAGGACTTCTTTCCAAACCCCTTCTCTGCTGCATCACAGG 228

RESULT 22
HSA336018
LOCUS      HSA336018      802 bp      DNA      linear      PRI 01-OCT-2001
DEFINITION Homo sapiens genomic sequence surrounding NotI site, clone
            NL6-DJ118RS.
ACCESSION  AJ336018
VERSION    AJ336018.1 GI:15880436
KEYWORDS
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 802)
            Kutsenko,A.S., Gizatullin,R.Z., Al-Amin,A.N., Wang,F.,
            Podowski,R.M., Matushkin,Y.G., Kvasha,S.M., Gyanchandani,A.,
            Muravenko,O.V., Protopopov,A.I., Kashuba,V.I., Kisselev,L.L.,
            Wasserman,W., Wahlestedt,C. and Zabarovsky,E.R.
            Analysis of NotI flanking sequences: a new tool for gene discovery
            and verification of the human genome
            Unpublished
            2 (bases 1 to 802)
            Zabarovsky,E.R.
            Direct Submission
            TITLE
            JOURNAL
            REFERENCE
            AUTHORS
            TITLE
            JOURNAL
            SOURCE
            Karolinska Institute, Theorells vag, 3, Box 280, Stockholm 171 77,
            Sweden

FEATURES
            source
            Location/Qualifiers
            1..802
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone="NL6-DJ118RS"
BASE COUNT      155 a      186 c      260 g      200 t      1 others
ORIGIN

Query Match      4.0%; Score 165; DB 9; Length 802;
Best Local Similarity 100.0%; Pred. No. 7.3e-70;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 532 gcaaaagctcgtctgtgcccagcaggcagggtggtgtggatgacgcggcgccat 591
|||||
DB 64 GCAAGCTCGTCTGTGGCCAGACGGCAGGAGGTGCTGTGCATGACCGCGGGCCAT 123
|||||

QY 592 gctcgtgtccacgccactgctgcacatgacctgtacctgcaatgcagaccacctgggg 651
|||||
DB 124 GCTCGTGTCCACGCCACTGCTGCACGATGCCCTGTACCTGCAGTGGCAGACCACTGGGG 183
|||||

QY 652 agaccagagacttccttccaaacctctcctggtggcacatcacagg 696
|||||
DB 184 AGACCAGGACTTCTTTCCAAACCCCTTCTCTGCTGCATCACAGG 228

RESULT 23
AC106813/c
LOCUS      AC106813/c      17341 bp      DNA      linear      HTG 25-JAN-2002
DEFINITION Homo sapiens chromosome 5 clone RP11-586L9, WORKING DRAFT SEQUENCE,
            7 unordered pieces.
ACCESSION  AC106813
VERSION    AC106813.2 GI:18369924
KEYWORDS   HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 17341)
            DOE Joint Genome Institute.
            TITLE
            JOURNAL
            REFERENCE
            AUTHORS
            TITLE
            JOURNAL
            SOURCE
            DOE Joint Genome Institute.
            2 (bases 1 to 17341)
```

TITLE	Direct Submission
JOURNAL	Submitted (12-JAN-2002) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT	On Jan 25, 2002 this sequence version replaced g1:18139363.

AUTHORS Alitalo,K., Aprelikova,O., Pajusola,O., Armstrong,E., Korhonen,J.,
Kaipainen,A. and Matikainen,M.
TITLE Antibodies to Flc4, a receptor tyrosine kinase and uses thereof
JOURNAL Patent: US 6107046-A 7 22-AUG-2000;
FEATURES Location/Qualifiers

source
1. .70
BASE COUNT 9 a 24 c 24 g 13 t
ORIGIN

Query Match 1.4%; Score 56; DB 6; Length 70;
Best Local Similarity 100.0%; Pred. No. 8.1e-16;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 20 atgcagcggggcgcgcgtgtgcctgcgactgtgctgctggactcctctgga 75
|||||
Db 15 ATGCACGGGGCGCGCGCTGTGCCTGCGACTGTGCTCTGCTGGACTCTCTGGA 70

RESULT 27
ARI57562
LOCUS ARI57562 70 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 2 from patent US 6245530.
ACCESSION ARI57562
VERSION ARI57562.1 GI:16218511
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE
AUTHORS 1 (bases 1 to 70)
TITLE Alitalo,K. and Joukov,V.
JOURNAL Receptor ligand
PATENT: US 6245530-A 2 12-JUN-2001;
FEATURES Location/Qualifiers
source
1. .70
/organism="unknown"

BASE COUNT 9 a 24 c 24 g 13 t
ORIGIN

Query Match 1.4%; Score 56; DB 6; Length 70;
Best Local Similarity 100.0%; Pred. No. 8.1e-16;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 20 atgcagcggggcgcgcgtgtgcctgcgactgtgctgctggactcctctgga 75
|||||
Db 15 ATGCACGGGGCGCGCGCTGTGCCTGCGACTGTGCTCTGCTGGACTCTCTGGA 70

RESULT 28
HSA329585/c
LOCUS HSA329585 688 bp DNA linear PRI 01-OCT-2001
DEFINITION Homo sapiens genomic sequence surrounding NotI site, clone
NRI-SPI8C.
ACCESSION ARI57562
VERSION ARI57562.1 GI:15874003
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 688)
Kutsenko,A.S., Gizatullin,R.Z., Al-Amin,A.N., Wang,F.,
Podowski,R.M., Matushkin,Y.G., Kvasha,S.M., Gyanchandani,A.,
Muravenko,O.V., Protolopov,A.I., Kashuba,V.I., Kiselev,L.L.,
Wasserman,W., Wahlstedt,C. and Zabarovsky,E.R.
TITLE Analysis of NotI flanking sequences: a new tool for gene discovery
and verification of the human genome
Unpublished
JOURNAL 2 (bases 1 to 688)
AUTHORS Zabarovsky,E.R.
TITLE Direct Submission

JOURNAL Submitted (16-MAY-2001) Microbiology and Tumorbiology Centre,
Karolinska Institute, Theorells vag, 3, Box 280, Stockholm 171 77,
Sweden
FEATURES Location/Qualifiers

source
1. .688
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="NRI-SPI8C"
BASE COUNT 116 a 206 c 226 g 140 t
ORIGIN

Query Match 1.3%; Score 55; DB 9; Length 688;
Best Local Similarity 100.0%; Pred. No. 1.8e-15;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 418 agactttgagcagcattcatcaacagccctgacacgcctcttggtcaacaggaag 472
|||||
Db 178 AGACTTTGAGCAGCCATTTCATCAACAGCCCTGACACGCCTCTTGGTCAACAGGAAG 124

RESULT 29
AF402786
LOCUS AF402786 4254 bp mRNA linear ROD 11-OCT-2001
DEFINITION Rattus norvegicus receptor tyrosine kinase VEGFR-3kt (Vegfr3) mRNA,
complete cds, alternatively spliced.
ACCESSION AF402786
VERSION AF402786.1 GI:16033529
KEYWORDS
SOURCE Norway rat.
ORGANISM Rattus norvegicus

REFERENCE
AUTHORS 1 (bases 1 to 4254)
TITLE Krishnan,J. and Sleeman,J.P.
JOURNAL Characterization of a novel alternatively spliced form of VEGFR-3
REFERENCE Unpublished
AUTHORS 2 (bases 1 to 4254)
Krishnan,J. and Sleeman,J.P.
TITLE Direct Submission
JOURNAL Submitted (25-JUL-2001) Institut fuer Toxikologie und Genetik,
Forschungszentrum Karlsruhe, Postfach 3640, Karlsruhe 76021,
Germany
FEATURES Location/Qualifiers

source
1. .4254
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
1. .4254
/gene="Vegfr3"
1. .3279
/gene="Vegfr3"
/note="kinase domain truncated form of VEGFR-3;
alternatively spliced"
/codon_start=1
/product="receptor tyrosine kinase VEGFR-3kt"
/protein_id="AAJ13270.1"
/db_xref="GI:16033530"
/translation="MQCAALNRRLWLCGLLQGLANGYNTPTTLNITSDSVYIDTG
DSUSISCRGHPLEWTRVGAQEVLTTCGKDSQEDTVVQDCEGTPEARPYCKVLSLAOTG
ANNTGSCYCYKIYKARIEGTAASTYFVFRDEQFPINRPTLLVNRKDSMWVPCLV
SIPGLNITLRSQSSVHPDGOEVLWDDRRGMVPTLLRLDALYLQCEWTGDDDFLSN
PFLVHTGNELYDIOLYPKSLELLVGEKLVNCTYNAEFDGVTGDMVPGKQAEAL
KWPERSSQOHTLSILTIHNVSQHDLPFYCEANNGIQOQRESTEVLVHEKPFIS
VEWUKGPVLEATGDEMVKLPVLAATPPPEFYQKORRKAATGRHNHALVLEKVTGA
SAGVYTLWNSAAGLRQNLSELVNVPPHIEKESSPSIYSRHSRQTLCTCYG
PQPLSVQWHRPMTCKTFAQSLRRRQPDGMPCQRMKEVTITQDANVIESLDWT
ESVGEKNTVSKLVIODANYSAMYKCVFNKVGQDERLIYFYVTTIPDGFSESESE
DPLEQSVRLSCRADNVTYELRWYRLNLTLDACGNPLLLDCKKNVHLFATPLEANL
EEAEPGARHTLSNIPRAPEDEGDYCEVQDRRSQDKHCKHLYSQALEAPRLTQ
NLTDLLVNRHTSLEMRCPAGAHVPSIWTYKDERLLEKESGIDLDLANSLSQRVRE
EDAGRYLCSCVNAKGCNVSSASVAVEGSEDKGSMEIILITGTGVIATVFWLLLLIFC

NMKRPAHADIKTGYSLIIMDPGEVPLEEOCEYLSYDVSWQEPRERLHLGRVLHGCAF
CKVVEASAFGINKSGSSCDTVAVKMLKEGATASEHRALMSSELKILIHGNHNVNLLG
ACTKPNGLMWIVFECKYGNLSNFRVARETDFDYAEKSPQRRRRFAMVEGAKADR
RUGSDTRALFTFLMGKSARRAPFVQAEADLWLSPLTMEDLVCYSFOVARGMEFLAS
RCIHRDLAARNILLSSEDIKICDFGLARDIYKDPDYVRKGSARLPLKWMAPESIED
KVYTTQSDVSWFSGVLLWEIFSLGASYPGVOINEEFQORLKDGTMRRAPELATPAIRH
IMQSGDQPKARPAFSDLVEILADLLQGGGWQEEBECMALHSQSSEEDGFMQAST
TALHITTEADAESSPPSMHCHSEFYIYNCVSPGRLVRGTKAPGSRMKTPEELPMPD
TTRYKASVDNOTDSGMVLASEFEQIESRHRROEGSFSRKDPQHMDISRGNHPLDQGRRR
RPTOGAGGKVFYNNEYSQPCTEGDCCFCSAGSTTFADSNY*

BASE COUNT 989 a 1236 c 1224 g 805 t

ORIGIN

Query Match 1.3%; Score 54; DB 10; Length 4254;
Best Local Similarity 100.0%; Pred. No. 4.4e-15;

Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2435 gcagacatcaagcggtacctgtccatcatcatgagccccggagtgctt 2488

Db 2416 GCAGACATCAAGCGGCTACCTGTCCATCATCATGACCCCGGAGGTGCTT 2469

RESULT 30

AF402785 4360 bp mRNA linear ROD 11-OCT-2001
LOCUS Rattus norvegicus receptor tyrosine kinase VEGFR-3 (Vegfr3) mRNA,
DEFINITION complete cds, alternatively spliced.
ACCESSION AF402785
VERSION 2
KEYWORDS AF402785.1 GI:16033526
SOURCE Norway rat.

ORGANISM

Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE

AUTHORS Krishnan,J. and Sleeman,J.P.

TITLE Characterization of a novel alternatively spliced form of VEGFR-3

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 4360)

AUTHORS Krishnan,J. and Sleeman,J.P.

TITLE Direct Submission

JOURNAL Submitted (25-JUL-2001) Institut fuer Toxikologie und Genetik,
Forschungszentrum Karlsruhe, Postfach 3640, Karlsruhe 76021,
Germany

FEATURES

source Location/Qualifiers

1. .4360

/organism="Rattus norvegicus"

/strain="Sprague-Dawley"

/db_xref="taxon:10116"

1. .4360

/gene="Vegfr3"

1. .4092

/gene="Vegfr3"

/note="VEGFR-3 long form; activated by VEGF-C and VEGF-D;

alternatively spliced"

/codon_start=1

/product="receptor tyrosine kinase VEGFR-3"

/protein_id="AAL13269.1"

/db_xref="GI:16033527"

/translation="MQGAALNRRLWLCGLGLOGLANGYSMTPTLNLTEDSYVIDTG
DSLISCRGQHPLEWTWGAQEVLTGKQSDTQVQDCGTEARPYCKVLSLAQTH
ANNTGYSYCYIKARIEGTAASTYVVRDFEQFP INKPTLLVNRKDSMMWPCLV
SIPGLNITLRSOSSYLHPDQGVLDWDRGRMRVPTLLRLDALYLCQCTTWGDDFLSN
PFLVGTITNELDYIOLYPKKSLLELWGLKVLNCTVWAEFDSGVTFDWDYPCQAERA
KWPPRRSOTHTLSSILT INVSQHDLPYVCEANNIGIOQFRESTEVIHVEKPFIS
VWMLKGPVLEATAGDEMLPKVLAAYPPPEFYWKDRKATGRNHPHALYLVKEVTEA
SAGVTTLAUNSAAGLRQNLISLELVNPPHHEKEASSPSIYSRHSROTLLCTTGV
POPLSVQWHRRPWTCKTFAQSLRRRQPDGMQPCQDKMEKVTQDAVNPTESLDWT
ESVEKNTLRSLKVLQDANVSAMKYCVFNKVGDERLTIFYVTT IPDGFSTSESPSE
DEAPFCARHATLSLNI PRVAPDEGDYCEVODRRSQDKHCKKYLVSQALEAPRLTO
NLTDLNVNRTSLEMKRCVNSASVAVEGSDKSGMEIVILIGTGVIAVFWLLLIIFC
EDAGRYLCSVCNAKGVNSASVAVEGSDKSGMEIVILIGTGVIAVFWLLLIIFC
NMKRAHADIKTGYSLIIMDPGEVPLEEOCEYLSYDVSWQEPRERLHLGRVLHGCAF
CKVVEASAFGINKSGSSCDTVAVKMLKEGATASEHRALMSSELKILIHGNHNVNLLG

gene

CDS

ACTKPNGLMWIVFECKYGNLSNFRVARETDFDYAEKSPQRRRRFAMVEGAKADR
RUGSDTRALFTFLMGKSARRAPFVQAEADLWLSPLTMEDLVCYSFOVARGMEFLAS
RCIHRDLAARNILLSSEDIKICDFGLARDIYKDPDYVRKGSARLPLKWMAPESIED
KVYTTQSDVSWFSGVLLWEIFSLGASYPGVOINEEFQORLKDGTMRRAPELATPAIRH
IMQSGDQPKARPAFSDLVEILADLLQGGGWQEEBECMALHSQSSEEDGFMQAST
TALHITTEADAESSPPSMHCHSEFYIYNCVSPGRLVRGTKAPGSRMKTPEELPMPD
TTRYKASVDNOTDSGMVLASEFEQIESRHRROEGSFSRKDPQHMDISRGNHPLDQGRRR
RPTOGAGGKVFYNNEYSQPCTEGDCCFCSAGSTTFADSNY*

BASE COUNT 1008 a 1260 c 1259 g 833 t

ORIGIN

Query Match 1.3%; Score 54; DB 10; Length 4360;
Best Local Similarity 100.0%; Pred. No. 4.4e-15;

Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2435 gcagacatcaagcggtacctgtccatcatcatgagccccggagtgctt 2488

Db 2416 GCAGACATCAAGCGGCTACCTGTCCATCATCATGACCCCGGAGGTGCTT 2469

RESULT 31

MUSRTKA 5284 bp mRNA linear ROD 09-AUG-1993
LOCUS Mus musculus receptor tyrosine kinase (PLT4) mRNA, complete cds.
DEFINITION
ACCESSION L07296
VERSION L07296.1 GI:293780
KEYWORDS receptor protein tyrosine kinase.
SOURCE Mus musculus (strain C57BL/6J, sub_species domesticus) cDNA to
mRNA.

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 5284)
AUTHORS Finnerty,H., Kelleher,K., Morris,G.E., Bean,K., Merberg,D.M.,
Kriz,R., Morris,J.C., Sookdeo,H., Turner,K.J. and Wood,C.R.
TITLE Molecular cloning of murine PLT and PLT4
JOURNAL Oncogene 8, 2293-2298 (1993)
MEDLINE 93330572
FEATURES Location/Qualifiers

source 1. .5284

/organism="Mus musculus"

/strain="C57BL/6J"

/sub_species="domesticus"

/db_xref="taxon:10090"

1. .5284

/gene="PLT4"

45. .4136

/gene="PLT4"

/note="putative"

/codon_start=1

/product="receptor tyrosine kinase"

/protein_id="AAA40077.1"

/db_xref="GI:293781"

/translation="MQGAALNRRLWLCGLGLOGLANGYSMTPTLNLTEDSYVIDTG
DSLISCRGQHPLEWTWGAQEVLTGKQSDTQVQDCGTEARPYCKVLSLAQTH
ANNTGYSYCYIKARIEGTAASTYVVRDFEQFP INKPTLLVNRKDSMMWPCLV
SIPGLNITLRSOSSYLHPDQGVLDWDRGRMRVPTLLRLDALYLCQCTTWGDDFLSN
PFLVGTITNELDYIOLYPKKSLLELWGLKVLNCTVWAEFDSGVTFDWDYPCQAERA
KWPPRRSOTHTLSSILT INVSQHDLPYVCEANNIGIOQFRESTEVIHVEKPFIS
VWMLKGPVLEATAGDEMLPKVLAAYPPPEFYWKDRKATGRNHPHALYLVKEVTEA
SAGVTTLAUNSAAGLRQNLISLELVNPPHHEKEASSPSIYSRHSROTLLCTTGV
POPLSVQWHRRPWTCKTFAQSLRRRQPDGMQPCQDKMEKVTQDAVNPTESLDWT
ESVEKNTLRSLKVLQDANVSAMKYCVFNKVGDERLTIFYVTT IPDGFSTSESPSE
DEAPFCARHATLSLNI PRVAPDEGDYCEVODRRSQDKHCKKYLVSQALEAPRLTO
NLTDLNVNRTSLEMKRCVNSASVAVEGSDKSGMEIVILIGTGVIAVFWLLLIIFC
EDAGRYLCSVCNAKGVNSASVAVEGSDKSGMEIVILIGTGVIAVFWLLLIIFC
NMKRAHADIKTGYSLIIMDPGEVPLEEOCEYLSYDVSWQEPRERLHLGRVLHGCAF
CKVVEASAFGINKSGSSCDTVAVKMLKEGATASEHRALMSSELKILIHGNHNVNLLG
NMKRAHADIKTGYSLIIMDPGEVPLEEOCEYLSYDVSWQEPRERLHLGRVLHGCAF
CKVVEASAFGINKSGSSCDTVAVKMLKEGATASEHRALMSSELKILIHGNHNVNLLG
RUGSDTRALFTFLMGKSARRAPFVQAEADLWLSPLTMEDLVCYSFOVARGMEFLAS
RCIHRDLAARNILLSSEDIKICDFGLARDIYKDPDYVRKGSARLPLKWMAPESIED

KVYTTQSDVMSFVGLLWEIFSLGASPGVQVINEEFQORLKDGTMRAPELATPAIRH
IMQSCWSDPKARPAFSDVLGLDGGGWOEEFEERFMRALHSSQSEEDGMOAST
TALHITADADDSPSHCHUSLAARYNCYFPCRLARGCTKTPCQSSRKKTFEELPWP
TTYKASNDSDSNVYLAEEFEESHRPEGSFCKGPGQHMDIPRGHPDPQGRRR
RPTQAGQGRVYNNYGEVSPQCTGDCGCPGAGTFFADSSY*
BASE COUNT 1221 a 1533 c 1466 g 1064 t
ORIGIN

Query Match 1.38; Score 54; DB 10; Length 5284;
Best Local Similarity 100.08; Pred. No. 4.3e-15;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2435 gcagacatcaagcggctactctccatcatcgagcccgaggagtgccct 2488
|||||
DB 2460 GCAGACATCAAGCGGCTACCTGTCATCATCGAGCCCGGAGCGTGCCT 2513

RESULT 32
AC098957/c
LOCUS
DEFINITION AC098957 161580 bp DNA linear HTG 20-DEC-2001
*** 75 unordered pieces.
AC098957 AC098957.2 GI:17973745
HTG: HTGS_PHASE1.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE
AUTHORS
1 (bases 1 to 161580)
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-Osman,F.R., Allen,C.,
Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbaria,J.,
Benton,J., Bimae,K., Blankenburg,K., Bonnin,D., Bouck,J.,
Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C.,
Burch,P., Burkett,C., Rurrell,K.L., Byrd,N.C., Carron,T.F.,
Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R.,
Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C.,
Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C.,
Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O.,
Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H.,
Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C.,
Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J.,
Foster,P., Francoz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T.,
Garza,N., Gill,R., Gorrell,J.H., Guevara,M., Gunaratne,P., Hale,S.,
Hamilton,K., Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A.,
Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Holloway,C.,
Hollins,B., Homs,F., Howard,S., Huber,J., Hulyk,S., Hume,J.,
Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S.,
Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J.,
Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C.,
Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W.,
Louisged,H., Lozaro,R.J., Lu,X., Lucier,A., Lucier,K., Luna,R.,
Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A.,
Martinez,E., Massey,E., Mawhinney,E., McLeod,M.P., Meador,M.,
Mel,G., Metzker,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K.,
Morgan,M., Morris,S., Moser,M., Neal,D., Newton,J., Newton,N.,
Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nockenkw,S.,
Ogih,M., Okwuon,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B.,
Peery,J., Perez,L., Peters,L., Pickens,K., Primus,E., Pu,L.L.,
Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojubokan,I., Rolfe,M.,
Ruiz,S., Savary,G., Scherer,S., Scott,G., Shen,H., Shoohtari,N.,
Sisson,I., Sodergren,E., Sonalike,T., Sparks,A., Stanley,H.,
Stone,H., Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K.,
Tang,H., Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N.,
Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalón,D., Vinson,R.,
Wall,R., Wang,S., Ward-Moore,S., Warren,R., Washington,C.,
Watlington,S., Williams,G., Williamson,A., Wleczyk,R., Wooden,S.,
Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
Weinstock,G. and Gibbs,R.
Direct Submission
Unpublished

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

2 (bases 1 to 161580)
Worley,K.C.
Direct Submission
Submitted (07-NOV-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Dec 20, 2001 this sequence version replaced gi:16756151.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: G1JR
Center clone name: CH230-193G14
----- Summary Statistics
Assembly program: Phrap; version 0.990329First call to
findPhrapList

Consensus quality: 121539 bases at least Q40
Consensus quality: 129496 bases at least Q30
Consensus quality: 136265 bases at least Q20
Estimated insert size: 111412; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-gel estimation
Quality coverage: 1.5x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 75 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 5831: contig of 5831 bp in length
5832: gap of unknown length
5932: contig of 5453 bp in length
11384: gap of unknown length
11485: contig of 5411 bp in length
16895: gap of unknown length
16956: contig of 4789 bp in length
21785: gap of unknown length
21884: contig of 3470 bp in length
25354: gap of unknown length
25455: contig of 4006 bp in length
29560: gap of unknown length
29581: contig of 2747 bp in length
32307: gap of unknown length
32407: contig of 2936 bp in length
35343: gap of unknown length
35443: contig of 2773 bp in length
38216: gap of unknown length
38317: contig of 2867 bp in length
41184: gap of unknown length
43959: contig of 2676 bp in length
44059: gap of unknown length
47285: contig of 3226 bp in length
47385: gap of unknown length
50539: contig of 3154 bp in length
50639: gap of unknown length
54276: contig of 3637 bp in length
54376: gap of unknown length
57920: contig of 3544 bp in length
58020: gap of unknown length
60505: contig of 2485 bp in length
60605: gap of unknown length
62900: contig of 2295 bp in length
63000: gap of unknown length
64914: contig of 1914 bp in length
65014: gap of unknown length
67533: contig of 2519 bp in length
67633: gap of unknown length

* 67634 70777: contig of 3144 bp in length
* 70778 70778: gap of unknown length
* 70878 73509: contig of 2632 bp in length
* 73510 73510: gap of unknown length
* 73610 76056: contig of 2447 bp in length
* 76057 76156: gap of unknown length
* 76157 78450: contig of 2294 bp in length
* 78451 78450: gap of unknown length
* 78551 80050: contig of 1500 bp in length
* 80051 80150: gap of unknown length
* 80151 82169: contig of 2019 bp in length
* 82170 82269: gap of unknown length
* 82270 83776: contig of 1507 bp in length
* 83777 83876: gap of unknown length
* 83878 85847: contig of 1871 bp in length
* 85848 85847: gap of unknown length
* 85848 87906: contig of 1959 bp in length
* 87807 87906: gap of unknown length
* 87907 89679: contig of 1773 bp in length
* 89680 89779: gap of unknown length
* 89780 91266: contig of 1487 bp in length
* 91267 91366: gap of unknown length
* 91367 93812: contig of 2446 bp in length
* 93813 93912: gap of unknown length
* 93913 95639: contig of 1727 bp in length
* 95640 95739: gap of unknown length
* 95740 97396: contig of 1657 bp in length
* 97397 97496: gap of unknown length
* 97497 99145: contig of 1649 bp in length
* 99146 99245: gap of unknown length
* 99246 100913: contig of 1668 bp in length
* 100914 101013: gap of unknown length
* 101014 102955: contig of 1942 bp in length
* 102956 103055: gap of unknown length
* 103056 104468: contig of 1413 bp in length
* 104469 104568: gap of unknown length
* 104569 106375: contig of 1807 bp in length
* 106376 106475: gap of unknown length
* 106476 108591: contig of 2216 bp in length
* 108592 108791: gap of unknown length
* 108792 110626: contig of 1835 bp in length
* 110627 110726: gap of unknown length
* 110727 111801: contig of 1075 bp in length
* 111802 111901: gap of unknown length
* 111902 113358: contig of 1457 bp in length
* 113359 113458: gap of unknown length
* 113459 114629: contig of 1171 bp in length
* 114630 114729: gap of unknown length
* 114730 116364: contig of 1635 bp in length
* 116365 116464: gap of unknown length
* 116465 118200: contig of 1736 bp in length
* 118201 118300: gap of unknown length
* 118301 119530: contig of 1230 bp in length
* 119531 119630: gap of unknown length
* 119631 121318: contig of 1688 bp in length
* 121319 121418: gap of unknown length
* 121419 122620: contig of 1202 bp in length
* 122621 122720: gap of unknown length
* 122721 124128: contig of 1408 bp in length
* 124129 124228: gap of unknown length
* 124229 126159: contig of 1931 bp in length
* 126160 126259: gap of unknown length
* 126260 128394: contig of 2135 bp in length
* 128395 128494: gap of unknown length
* 128495 130496: contig of 2002 bp in length
* 130497 130596: gap of unknown length
* 130597 132111: contig of 1515 bp in length
* 132112 132211: gap of unknown length
* 132212 133294: contig of 1083 bp in length
* 133295 133394: gap of unknown length
* 133395 134851: contig of 1457 bp in length
* 134852 134951: gap of unknown length
* 134952 136002: contig of 1051 bp in length

* 136003 136102: gap of unknown length

Query Match 1.3% Score 54: DB 2: Length 161580:
Best Local Similarity 100.0%: Pred. No. 2.6e-15:
Matches 54: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

Oy 2435 gcagacatcaagcggctacctgcatcatcatcgaccgccggagggtgcct 2488
|||||
Db 28372 GCAGACATCAAGCGGCTACCTGTCATCATCATGACCCCGGAGGTGCT 28319
|||||

RESULT 33
AL646088 260266 bp DNA linear HTG 30-JAN-2002
LOCUS Mus musculus chromosome 11 clone RP23-58E13, *** SEQUENCING IN
DEFINITION PROGRESS ***, in unordered pieces.
ACCESSION AL646088
VERSION AL646088.11 GI:18476932
KEYWORDS HTG; HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (sites)
REFERENCE
AUTHORS Clark,S.
TITLE Direct Submission
JOURNAL Submitted (28-JAN-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Feb 1, 2002 this sequence version replaced gi:18151535.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: BM58E13
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 258539 bases at least Q40
Consensus quality: 258926 bases at least Q30
Consensus quality: 259227 bases at least Q20
Insert size: 259766: sum-of-contigs
Insert size: 225486; 6.3% error; agarose-fp
Quality coverage: 9.68x in Q20 bases; sum-of-contigs Quality
coverage: 11.43x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

FEATURES
source Location/Qualifiers
1. 260266
/organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="11"
/clone="RP23-58E13"
/clone_lib="RPC1-23"
1. 8902
/note="assembly_fragment:05530
fragment_chain:1"
9003. 87162
/note="assembly_fragment:05707
fragment_chain:1"
87263. 123670
/note="assembly_fragment:05852
fragment_chain:1"
123771. 188404
/note="assembly_fragment:00429"
188505. 214152
/note="assembly_fragment:05868"

```
misc_feature 214253..260266
/note="assembly_fragment:05872"
BASE COUNT 80139 a 55470 c 56089 g 68066 t 502 others
ORIGIN

Query Match
Best Local Similarity 1.3%; Score 54; DB 2; Length 260266;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2435 gcagacatcaagacgggtacctgtccatcatcatcgagcccgaggagttuacct 2488
|||||
Db 161514 GCAGACATCAAGACGGGTACCTGCTCCATCATCGAGCCCGGAGGTGCTT 161567

RESULT 34
AC022095 127488 bp DNA linear HTG 20-APR-2001
LOCUS Homo sapiens chromosome 5 clone CTB-36B8, WORKING DRAFT SEQUENCE,
DEFINITION 13 unordered pieces.
ACCESSION AC022095
VERSION HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 5
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 127488)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (26-JAN-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
on Apr 20, 2001 this sequence version replaced yf:7711676.
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
-----
Project Information
Center project Name: 78060
Center clone name: CIT978SKB_36B8
-----
Summary Statistics
Consensus quality: 110477 bases at least Q40
Consensus quality: 117221 bases at least Q30
Consensus quality: 120225 bases at least Q20
Estimated insert size: 131000; pulse field gel estimation
Estimated insert size: 126288; sum-of-contigs estimation
Quality coverage: 7.48 in Q20 bases; pulse field gel estimation
Quality coverage: 7.76 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a "working draft" sequence. It currently
* consists of 13 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 1116: contig of 1116 bp in length
* 1117 1216: gap of unknown length
* 1217 2254: contig of 1038 bp in length
* 2255 2354: gap of unknown length
* 2355 3412: contig of 1058 bp in length
* 3413 3512: gap of unknown length
* 3513 5005: contig of 1493 bp in length
* 5006 5105: gap of unknown length
* 5106 7647: contig of 2542 bp in length
* 7648 7748 10237: contig of 2490 bp in length
```

```
* 10238 10337: gap of unknown length
* 10338 12440: contig of 2103 bp in length
* 12441 12540: gap of unknown length
* 12541 15935: contig of 3395 bp in length
* 15936 16035: gap of unknown length
* 16036 24397: contig of 8361 bp in length
* 24397 24496: gap of unknown length
* 24497 39085: contig of 14589 bp in length
* 39086 39185: gap of unknown length
* 39186 60545: contig of 21360 bp in length
* 60546 60645: gap of unknown length
* 60646 79490: contig of 18845 bp in length
* 79491 79591 127488: contig of 47898 bp in length.
FEATURES
source
1..127488
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
/clone="CTB-36B8"
/clone_lib="CalTech human BAC library B"
BASE COUNT 31643 a 32392 c 31616 g 30626 t 1211 others
ORIGIN

Query Match
Best Local Similarity 1.3%; Score 53; DB 2; Length 127488;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 cggggcgccgcgtgtgcctgcgacttgctctgcctgggactcctggacgg 78
|||||
Db 65772 CGGGCGCGCGCTGTGCTCGACTGTGGCTCTGCCTGGGACTCCTGGACGG 65824

RESULT 35
AX056761 39 bp DNA linear PAT 17-JAN-2001
LOCUS Sequence 27 from Patent WO0075319.
DEFINITION AX056761
ACCESSION AX056761
VERSION AX056761.1 GI:12309736
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 39)
AUTHORS Papadopoulos,N.J., Davis,S. and Yancopoulos,G.D.
TITLE Modified chimeric polypeptides with improved pharmacokinetic
properties
JOURNAL Patent: WO 0075319-A 27 14-DEC-2000;
REGENERON PHARMACEUTICALS, INC. (US)
FEATURES
source
1..39
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="primer"
BASE COUNT 7 a 10 c 13 g 9 t
ORIGIN

Query Match
Best Local Similarity 0.9%; Score 39; DB 6; Length 39;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 713 atccagctgttgcacaggaatcgctgagctggtgta 751
|||||
Db 1 ATCCAGCTGTTGCCGAGGAGTCGCTGAGCTGCTGGTA 39

RESULT 36
AX056762/c
LOCUS Sequence 28 from Patent WO0075319.
DEFINITION AX056762
ACCESSION AX056762
```

```

VERSION      AX056762.1  GI:12309737
KEYWORDS     .
SOURCE       synthetic construct.
ORGANISM     synthetic construct.
              artificial sequence.
REFERENCE    1 (bases 1 to 39)
AUTHORS      Papadopoulos,N.J., Davis,S. and Yancopoulos,G.D.
TITLE        Modified chimeric polypeptides with improved pharmacokinetic
              properties
JOURNAL      Patent: WO 0075319-A 28 14-DEC-2000;
              REGENERON PHARMACEUTICALS, INC. (US)
FEATURES     Location/Qualifiers
              source
              1..39
              /organism="synthetic construct"
              /db_xref="taxon:32630"
              /note="primer"
BASE COUNT   9 a 12 c 7 g 11 t
ORIGIN
Query Match      0.8%; Score 39; DB 6; Length 39;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 971 cgaattcgagagaccagcaggttcattgtgcataaaat 1009
Db 39 CGATTTCCGGGAGACCCGAGGTCATTGTGCATGAAAT 1

RESULT 37
LOCUS      HSA330946              777 bp      DNA      linear      PRI 01-OCT-2001
DEFINITION Homo sapiens genomic sequence surrounding NotI site, clone
              NL6-BC23RS.
ACCESSION   AJ330946
VERSION     AJ330946.1  GI:15875364
KEYWORDS    .
SOURCE      human.
ORGANISM    Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1 (bases 1 to 777)
AUTHORS     Kutsenko,A.S., Gizatullin,R.Z., Al-Amin,A.N., Wang,F.,
              Podowski,R.M., Matushkin,Y.G., Kvasha,S.M., Gyanchandani,A.,
              Muravenko,O.V., Protodopov,A.I., Kashuba,V.I., Kisselev,L.L.,
              Wasserman,W., Wahlestedt,C. and Zabarovsky,E.R.
TITLE       Analysis of NotI flanking sequences: a new tool for gene discovery
              and verification of the human genome
JOURNAL     Unpublished
REFERENCE   2 (bases 1 to 777)
AUTHORS     Zabarovsky,E.R.
TITLE       Direct Submission
JOURNAL     Submitted (16-MAY-2001) Microbiology and Tumorbilogy Centre,
              Karolinska Institute, Theorells vag, 3, Box 280, Stockholm 171 77,
              Sweden
FEATURES     Location/Qualifiers
              source
              1..777
              /organism="Homo sapiens"
              /db_xref="taxon:9606"
              /clone="NL6-BC23RS"
BASE COUNT   161 a 180 c 223 g 209 t 4 others
ORIGIN
Query Match      0.8%; Score 34; DB 9; Length 777;
Best Local Similarity 100.0%; Pred. No. 4.3e-05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 702 agctctatgacatccagctgttgcaggagatc 735
Db 342 AGCTTATGACATCCAGCTGTTCGCCAGGAAGTC 375

VERSION      AX030379
KEYWORDS     .
SOURCE       Bos taurus tyrosine kinase receptor FLL4 mRNA, partial cds.
ORGANISM     Bos taurus
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
              Bovidae; Bovinae; Bos.
REFERENCE    1 (bases 1 to 420)
AUTHORS      Pepper,M.S., Mandriota,S.J., Jeltsch,M., Kumar,V. and Alitalo,K.
TITLE        vascular endothelial growth factor (VEGF)-C synergizes with basic
              fibroblast growth factor and VEGF in the induction of angiogenesis
              in vitro and alters endothelial cell extracellular proteolytic
              activity
JOURNAL      J. Cell. Physiol. 177 (3), 439-452 (1998)
MEDLINE      99023338
REFERENCE    2 (bases 1 to 420)
AUTHORS      Mandriota,S.J. and Pepper,M.S.
TITLE        Direct Submission
JOURNAL      Submitted (20-OCT-1997) Morphology, University Medical Center, 1,
              rue Michel Servet, 1211 Geneva 4, Switzerland
FEATURES     Location/Qualifiers
              source
              1..420
              /organism="Bos taurus"
              /db_xref="taxon:9913"
              /tissue_type="kidney"
              /dev_stage="adult"
              /note="RT-PCR product amplified from total RNA using
              degenerate primers; sequenced on both strands"
              cl..>420
              /codon_start=1
              /product="tyrosine kinase receptor Flt4"
              /protein_id="AAC78244.1"
              /db_xref="GI:2613139"
              /translation="RCPVAGTHVPSIVMYKDEKLEESGIDLADSNORLSIORVREE
              DAGHYLSCVNAKGCNVSSASVAVEGSEDKSMEIVILVGTGVIATVFWFWLLLLLFCN
              MRRPTHADIKTYLSIIMDPCVEPLEECCYLSYDASQ"
BASE COUNT   90 a 110 c 130 g 90 t
ORIGIN
Query Match      0.8%; Score 32; DB 4; Length 420;
Best Local Similarity 100.0%; Pred. No. 0.00046;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2457 tgctccatcatcatgaccccgaggagtgacct 2488
Db 347 TGTCATCATCATGACCCCGGAGGTGCCT 378

RESULT 39
LOCUS      AX056763              38 bp      DNA      linear      PAT 17-JAN-2001
DEFINITION Sequence 29 from Patent WO0075319.
ACCESSION   AX056763
VERSION     AX056763.1  GI:12309738
KEYWORDS    .
SOURCE      synthetic construct.
              synthetic construct.
              artificial sequence.
ORGANISM    1 (bases 1 to 38)
REFERENCE   Papadopoulos,N.J., Davis,S. and Yancopoulos,G.D.
AUTHORS     Modified chimeric polypeptides with improved pharmacokinetic
              properties
TITLE       Patent: WO 0075319-A 29 14-DEC-2000;
              REGENERON PHARMACEUTICALS, INC. (US)
JOURNAL     Location/Qualifiers
FEATURES     source
              1..38

```

```

/organism="synthetic construct"
/db_xref="taxon:32630"
/notice="primer"
9 a          11 g          9 t
BASE COUNT
ORIGIN

Query Match
Best Local Similarity 100.0%: Score 30; DB 6; Length 38;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 713 atccagctgttgcacgaagtcgtgag 742
|||||
Db 9 ATCCAGCTGTGTCACGAAGTCGTGCAG 38
|||||

RESULT 40
AC098957
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
AUTHORS
TITLE
JOURNAL

FEATURES
source
CDS

/organism="synthetic construct"
/db_xref="taxon:32630"
/notice="primer"
9 a          11 g          9 t
BASE COUNT
ORIGIN

Query Match
Best Local Similarity 100.0%: Score 28; DB 4; Length 534;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3165 acgtggtgaagalcgtgacttggcct 3192
|||||
Db 65 ACCTGCTGAAGATCTGTGACTTTGGCCT 92
|||||

RESULT 41
AC098957
LOCUS
DEFINITION
ACCESSION

```

VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS

TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AC098957.2 GI:17973745
HTG: HTGS_PHASE1
Norway rat.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

1 (bases 1 to 161580)
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Alsbrooks,S.L., Amaral-Lungue,H.C., Arc,J.R., Banks,T., Barbara,J.,
Benton,J., Bimaga,K., Blankenburg,K., Bonnin,D., Bouck,J.,
Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C.,
Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F.,
Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R.,
Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C.,
Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C.,
Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O.,
Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H.,
Duggan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C.,
Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J.,
Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T.,
Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S.,
Hamilton,K., Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A.,
Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Holloway,C.,
Hollins,B., Honsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J.,
Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S.,
Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J.,
Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C.,
Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W.,
Louissegue,H., Lozano,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R.,
Ma,J., Maheshwari,M., Mapa,P., Martin,R., Martindale,A.,
Martinez,E., Massey,E., Mawhiney,E., McLeod,M.P., Meador,M.,
Mei,G., Metzger,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K.,
Morgan,M., Morris,S., Moser,M., Neal,D., Newton,J., Newton,N.,
Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokkwo,S.,
Ogih,A., Okunolu,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B.,
Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L.,
Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojibokan,I., Rolfe,M.,
Ruiz,S., Savary,G., Scherer,S., Scott,G., Shen,H., Shooshtari,N.,
Sisson,I., Sodergren,E., Sonalka,T., Sparks,A., Stanley,H.,
Stone,H., Sutton,A., Svatek,A., Tabor,P., Tameria,A., Tamerisa,K.,
Tang,H., Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N.,
Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalón,D., Vinson,R.,
Wall,R., Wang,S., Ward-Moore,S., Warren,R., Washington,C.,
Watlington,S., Williams,G., Williamson,A., Wleczek,R., Wooden,S.,
Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
Weinstock,G. and Gibbs,R.

Direct Submission
Unpublished
2 (bases 1 to 161580)
Worley,K.C.
Direct Submission
Submitted (07-NOV-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Dec 20, 2001 this sequence version replaced gi:16756151.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GJIR
Center code: CH230-193G14
----- Summary Statistics
Assembly program: Phrap; version 0.990329First call to
findPhrapList
Consensus quality: 121539 bases at least Q40
Consensus quality: 129496 bases at least Q30
Consensus quality: 136265 bases at least Q20
Estimated insert size: 111412; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-fp estimation
Quality coverage: 1.5x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 75 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 5831: contig of 5831 bp in length
* 5832 5931: gap of unknown length
* 5932 11384: contig of 5453 bp in length
* 11385 11484: gap of unknown length
* 11485 16895: contig of 5411 bp in length
* 16896 16995: gap of unknown length
* 16996 21784: contig of 4789 bp in length
* 21785 21884: gap of unknown length
* 21885 25354: contig of 3470 bp in length
* 25355 25454: gap of unknown length
* 25455 29460: contig of 4006 bp in length
* 29461 29560: gap of unknown length
* 29561 32307: contig of 2747 bp in length
* 32308 32407: gap of unknown length
* 32409 35343: contig of 2936 bp in length
* 35344 35443: gap of unknown length
* 35444 38216: contig of 2773 bp in length
* 38217 38316: gap of unknown length
* 38317 41183: contig of 2867 bp in length
* 41184 41283: gap of unknown length
* 41284 43959: contig of 2676 bp in length
* 43960 44060: gap of unknown length
* 44061 47285: contig of 3226 bp in length
* 47286 47385: gap of unknown length
* 47386 50539: contig of 3154 bp in length
* 50540 50639: gap of unknown length
* 50640 54276: contig of 3637 bp in length
* 54277 54376: gap of unknown length
* 54377 57920: contig of 3544 bp in length
* 57921 58020: gap of unknown length
* 58021 60505: contig of 2485 bp in length
* 60506 60605: gap of unknown length
* 60606 62900: contig of 2295 bp in length
* 62901 63000: gap of unknown length
* 63001 64914: contig of 1914 bp in length
* 64915 65014: gap of unknown length
* 65015 67533: contig of 2519 bp in length
* 67534 67634: gap of unknown length
* 67635 70777: contig of 3144 bp in length
* 70778 70877: gap of unknown length
* 70878 73509: contig of 2632 bp in length
* 73510 73609: gap of unknown length
* 73610 76056: contig of 2447 bp in length
* 76057 76156: gap of unknown length
* 76157 78450: contig of 2294 bp in length
* 78451 78550: gap of unknown length
* 78551 80050: contig of 1500 bp in length
* 80051 80150: gap of unknown length
* 80151 82169: contig of 2019 bp in length
* 82170 82269: gap of unknown length
* 82270 83776: contig of 1507 bp in length
* 83777 83876: gap of unknown length
* 83877 85747: contig of 1871 bp in length
* 85748 85847: gap of unknown length
* 85848 87806: contig of 1959 bp in length
* 87807 87906: gap of unknown length
* 87907 89679: contig of 1773 bp in length
* 89680 89779: gap of unknown length
* 89780 91266: contig of 1487 bp in length
* 91267 91366: gap of unknown length
* 91367 93812: contig of 2446 bp in length
* 93813 93912: gap of unknown length

* 93913 95639: contig of 1727 bp in length
* 95640 97399: gap of unknown length
* 97399 97496: contig of 1657 bp in length
* 97497 97997: gap of unknown length
* 97998 99145: contig of 1649 bp in length
* 99146 99245: gap of unknown length
* 99246 100913: contig of 1668 bp in length
* 100914 101013: gap of unknown length
* 101014 102955: contig of 1942 bp in length
* 102956 103055: gap of unknown length
* 103056 104468: contig of 1413 bp in length
* 104469 104568: gap of unknown length
* 104569 106375: contig of 1807 bp in length
* 106376 106476: gap of unknown length
* 106477 108692: contig of 2216 bp in length
* 108693 108791: gap of unknown length
* 108792 110626: contig of 1835 bp in length
* 110627 110726: gap of unknown length
* 110727 111801: contig of 1075 bp in length
* 111802 111901: gap of unknown length
* 111902 113358: contig of 1457 bp in length
* 113359 113458: gap of unknown length
* 113459 114629: contig of 1171 bp in length
* 114630 114729: gap of unknown length
* 114730 116364: contig of 1635 bp in length
* 116365 116464: gap of unknown length
* 116465 118200: contig of 1736 bp in length
* 118201 118300: gap of unknown length
* 118301 119530: contig of 1230 bp in length
* 119531 119630: gap of unknown length
* 119631 121318: contig of 1688 bp in length
* 121319 121418: gap of unknown length
* 121419 122620: contig of 1202 bp in length
* 122621 122720: gap of unknown length
* 122721 124128: contig of 1408 bp in length
* 124129 124228: gap of unknown length
* 124229 126159: contig of 1931 bp in length
* 126160 126259: gap of unknown length
* 126260 128394: contig of 2135 bp in length
* 128395 128494: gap of unknown length
* 128495 130496: contig of 2002 bp in length
* 130497 130596: gap of unknown length
* 130597 132111: contig of 1515 bp in length
* 132112 132211: gap of unknown length
* 132212 133294: contig of 1083 bp in length
* 133295 133394: gap of unknown length
* 133395 134851: contig of 1457 bp in length
* 134852 134951: gap of unknown length
* 134952 136002: contig of 1051 bp in length
* 136003 136102: gap of unknown length

Query Match 0.78; Score 28; DB 2; Length 161580;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1649 gagcgccatctactctatgtgacca 1676
|||||
Db 61372 GAGCGCTCATCTACTTCTATGTGACCA 61399

RESULT 42
XELXFGFRA2
LOCUS XELXFGFRA2
DEFINITION Xenopus laevis fibroblast growth factor receptor mRNA, complete cds.
ACCESSION M62322
VERSION M62322.1 GI:214899
KEYWORDS fibroblast growth factor receptor; tyrosine kinase receptor.
SOURCE X.laevis, cDNA to mRNA.

XELXFGFRA2 2753 bp mRNA linear VRT 28-APR-1993
Xenopus laevis fibroblast growth factor receptor mRNA, complete
X.laevis, cDNA to mRNA.
ORGANISM Xenopus laevis
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
Xenopodinae; Xenopus.

REFERENCE 1 (bases 1 to 2753)
AUTHORS Friesel,R.E. and David,I.B.
TITLE cDNA cloning and developmental expression of fibroblast growth factor receptors from Xenopus laevis
JOURNAL Mol. Cell. Biol. 11, 2481-2488 (1991)
MEDLINE 91203867
FEATURES
source Location/Qualifiers
1..2753 /organism="Xenopus laevis"
/db_xref="taxon:8355"
1..2753 /gene="XFGFRA2"
154..2328 /gene="XFGFRA2"
/codon_start=1
/product="fibroblast growth factor receptor"
/protein_id="AAA49993.1"
/translation="MFSGMSLLIILGVLIGAAISVAPRPSTLPDEDAIPSAEDDDDD
/db_xref="gi:214900"
/translat ion="MFSGMSLLIILGVLIGAAISVAPRPSTLPDEDAIPSAEDDDDD
NSSEFEAAENSKPNRPLWSHPEKMEKKLHAPPAKTVKFRCPANGTPTPTLRWKNK
HAFOODRILGCKYKRSOTWSLIMDSVPSDKGNYTCIVENKYGAINTHYOLDVVERSP
IRPILUAGLPANTSVTYGTTAEFSCKYSDPQPHLOMLKHLEINGSRVASDGFYVEI
LKTAGVTSDDMEVLELHNRVTFEDAGYTCCLAANSIGISHHSALWTLVKVEDNKPAL
LASPIQETIIICYCAAFVSAMVVTIITFKMKHPSKKSDFNSQIAVHKLAKSTPLRRQ
VTSGDSSMNSGVILVRLSSSCTPMLSGLELPEDEPRWEVARDRLTIGKPLGE
QCQGVVMAEAIIGLUEKPNKTVAVKMLKSDASEKDLSDLI SEMEMKMLIGKHNI
INLIGACTODGFLXVI VETYSKGNLREYLAARRPAMEYCYNPTCVPDQLLSPKDLVS
CAYGVAMYLASKKCIHKLAAARNVLITEDNIMK LADFLANDIHHIDYKKTTNG
RLPVWMAPEALFDRITTHQSDVMSFGVLLWEIFLGSPYGPVPMELFKLKEGHR
MDKPTNCTNELMNMKDCWAMPORPTFNOLVEDLRLIALSNQYELDLSMPVNY
SPCFPTHSSTSSCGSDSVFSDHPLPDEPCLPKYSNGIILKKR"
154..216
sig_peptide /gene="XFGFRA2"
217..2325
mat_peptide /gene="XFGFRA2"
/product="fibroblast growth factor receptor"
BASE COUNT 740 a 672 c 635 g 706 t
ORIGIN

Query Match 0.7%: Score 27; DB 5; Length 2753;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3112 aaatgcacacagagacctggctgc 3138
|||||
Db 1722 AAAGTGCATCCACAGACCTGCCTGC 1748

RESULT 43
XLU24491
LOCUS
DEFINITION
XLU24491 3634 bp mRNA linear VRT 02-FEB-1996
cda
Xenopus laevis fibroblast growth factor receptor-1 mRNA, complete
ACCESSION U24491 M61687 M37201
VERSION U24491.1 GI:857677
KEYWORDS
SOURCE
ORGANISM
African clawed frog.
Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
Xenopodinae; Xenopus.
1 (bases 1 to 2439)
Musci.T.J., Anaya,E. and Kirschner,M.W.
Regulation of the fibroblast growth factor receptor in early
Xenopus embryos
Proc. Natl. Acad. Sci. U.S.A. 87 (21), 8365-8369 (1990)
9104598
2 (bases 2440 to 3634)
Robbie.E.P., Peterson,M., Anaya,E. and Musci,T.J.
Temporal regulation of the Xenopus FGF receptor in development: a
translation inhibitory element in the 3' untranslated region
Development 121 (6), 1775-1785 (1995)

95324403
3 (bases 1 to 3634)
Musci.T.J.
Direct Submission
Submitted (11-APR-1995) Thomas J. Musci, Dept. of OB/GYN,
University of California, San Francisco, Box 0556, San Francisco,
CA 94143, USA
On Jun 12, 1995 this sequence version replaced gi:214137.
FEATURES
source Location/Qualifiers
1..3634 /organism="Xenopus laevis"
/db_xref="taxon:8355"
1..2439 /codon_start=1
/product="fibroblast growth factor receptor-1"
/protein_id="AAA86868.1"
/db_xref="GI:857678"
/translation="MFSGMSLLIILGVLIGAAISVAPRPSTLPDEVAPKTKTEPEYSA
OPQDRITLQCLREDSQINWKNVQSLNTRITGEEIOISNAGPEDINGVYACVT
NGPSRTYTVLCSVNVSDALPSAEDDDDDNSSEKKAENSKPNRPLWSHPEKMEKK
LHAPPAKTVKFRCPANGTPTPTLRWLNKRAFQDQRI GGYKRSOTWSLIMDSVVP
SDKGNVTCIVENKYGALNHTYQLDVVERSPIRPILOAGLPANTSVTYGTTAEFSCKY
SDQPHIQWLRHIEINGSRVASDGFYVEIILKTAGVTSDDMEVLELHNRVTFEDAQ
YTCLAANSIGISHHSALWTLVKVEDNKPALLASPIQETIIICYCAAFVSAMVVTIIL
FKMKHPSKKSDFNSQIAVHKLAKSI PVRRQVTVSGDSSMNSGVILVRLSSSCTPM
LSGLSEYELPEDEPRWEVARDRLTIGKPLGECQGVVMAEAIIGLUEKPNKTVKAVK
MLKSDASEKDLSDLI SEMEMKMLIGKHNI INLIGACTODGFLXVI VETYSKGNLREY
LAARRPAMEYCYNPTCVPDQLLSPKDLVSCAVQVARMY LASKKCIHRLDAARNVL
LMEIFTLGSPYGPVPMELFKLKEGHRMDKPTNCTNELMNMKDCWAMPORPT
FNOLVEDLRLIALSNQYELDLSMPVNYSPCFPTHSSTSSCGSDSVFSDHPLPDE
PCLPKYSNGIILKKR"
2440..3634
2440..2619
misc_feature /note="translational inhibitory regulatory element
contained within the 3' UTR"
BASE COUNT 1015 a 827 c 806 g 986 t
ORIGIN

Query Match 0.7%: Score 27; DB 5; Length 3634;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3112 aaatgcacacagagacctggctgc 3138
|||||
Db 1833 AAAGTGCATCCACAGACCTGCCTGC 1859

RESULT 44
XELX1FGFR
LOCUS
DEFINITION
XELX1FGFR 3815 bp mRNA linear VRT 28-APR-1993
cda
Xenopus laevis fibroblast growth factor receptor mRNA, complete
ACCESSION M55163
VERSION M55163.1 GI:214893
KEYWORDS
Xenopus laevis fibroblast growth factor receptor.
Xenopus laevis XTC cell line, cDNA to mRNA.
Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
Xenopodinae; Xenopus.
1 (bases 1 to 3815)
Friesel,R.E. and David,I.B.
cDNA cloning and developmental expression of fibroblast growth
factor receptors from Xenopus laevis
Mol. Cell. Biol. 11, 2481-2488 (1991)
91203867
JOURNAL
MEDLINE
FEATURES
source Location/Qualifiers
1..3815 /organism="Xenopus laevis"
/db_xref="taxon:8355"
/cell_line="XTC"

gene	1. .3815	/gene="X1FGFR"	
CDS	137. .2581	/gene="X1FGFR"	
		/codon_start=1	
		/product="fibroblast growth factor receptor"	
		/protein_id="AA49990.1"	
		/db_xref="GI:214894"	
		/translation="MPSGRSLLMGVLLGAALSVARPPSTLIPDEVAIKTKTEVEPYSA RPGDTVTLQCRLEDVQSISWAKNGVOLLETNRTRITGEEIQISNAGPEDNGLYACVT IGPSGTVTVLFSINVSADOPSAEDDDDDSSSEKASSENKPNRPFWSIPEKMEKK LHAPAAKTKFPCPANCPTSPALRWLKNCKEPPDOORIGCYKVKSTWSLIMDSVVP SDKNGYCTTVENKYGTLNHYQILDVVERSPIRPLLOAGLPANTSVTVGSTAEFSCKVY SDPQPHLOWLRHIEINGSRVASGFPYVEILKTAGVNTSDKDMEVILHRVTFEDAGQ VTCLAANSITGISHSIAWLTVEVRDDKPALLASPLQLEIITYCTGAAPVSAMVVTIIL FKMKHPSKSDFNSQLAVHKLAKSIPLKROQTVTSGDSNSSSMHSCVILVRPSPRLSSST PMLSCVSEYELPEDPRWEVARDRLILCKPLGEGCFGOVWMAEIGLDKEKPNKRVTKVA LKMCLKDANEKDLSDLIJSEMEMKMGCKHKNINLLGACFTQDGLPVYIVVEYASKGNLR FYLKARPPQMEVCYNPCAPDQLLSFKDLYSCAYQVAKMEYLASKKCIHRDLAARN VLVTEDNVMKIADPGLARDLIHIDYTKTNGRLPVRKMAPEALFDRITYHQSDVWSF GVILMEFTLGGSPYGPVPMEEIFKLKLEKGRHMDKPTNCINELYMMMKDCWHAMPOR PTFNQLVEDLDRLILALSSNOEYLDLSMPVNOYSPCFPTDKRSTCSSGEDSVFSDPLP DEPCLPKYSNGLKKR"	
seq_peptide	137. 199	/gene="X1FGFR"	
mat_peptide	200. .2578	/gene="X1FGFR"	
		/product="fibroblast growth factor receptor"	
BASE COUNT	1030 a 879 c 881 g 1025 t		
ORIGIN			
Query Match 0.7%; Score 27; DB 5; Length 3815;			
Best Local Similarity 100.0%; Pred. No. 0.1;			
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	3112	aaagtgcacccacagacacctggctgc	3138
Db	1975	AAAGTCCATCCACAGACCTGGCTGC	2001
RESULT 45			
MMAPK42			
LUCUS		1256 bp	mRNA linear ROD 02-FEB-1999
DEFINITION		Mouse MAPK mRNA for mitogen-activated protein kinase (p42).	
ACCESSION		X58712	
VERSION		X58712.1	GI:53001
KEYWORDS		mitogen-activated protein kinase; protein kinase.	
SOURCE		house mouse.	
ORGANISM		Mus musculus	
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
		Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
		Her,J.H.	
REFERENCE		Direct Submission	
AUTHORS		Submitted (03-APR-1991) J.H. Her, University of Virginia, Dept of	
JOURNAL		Microbiology and, Cancer Center Box 441, School of Medicine,	
		Charlottesville VA 22908, USA	
		2 (bases 1 to 1256)	
REFERENCE		Her,J.H., Wu,J., Rall,T.B., Sturgill,T.W. and Weber,M.J.	
AUTHORS		Sequence of pp42/MAP kinase, a serine/threonine kinase regulated by	
TITLE		tyrosine phosphorylation	
JOURNAL		Nucleic Acids Res. 19 (13), 3743 (1991)	
MEDLINE		91305126	
FEATURES		Location/Qualifiers	
source		1. .1256	
		/organism="Mus musculus"	
		/strain="swiss"	
		/db_xref="taxon:10090"	
		/cell_line="3T3"	
		/tissue_type="fibroblast"	
		/clone_lib="lambda gt10"	
mRNA		1. .1256	

		/gene="MAPK"	
		/evidence-experimental	
		1. .1256	
		/gene="MAPK"	
		19. .1095	
		/gene="MAPK"	
		/codon_start=1	
		/product="mitogen-activated protein kinase (p42)"	
		/protein_id="CAA41548.1"	
		/db_xref="GI:53002"	
		/db_xref="MGD:MGI:105919"	
		/db_xref="SWISS-PROT:P27703"	
		/translation="MAAAAAGPEVMRGVDFDVGPRYTNLSTYIGECAYGMVC SAYDNL NKYVAIKKISPEHGYTCQRTRELKILLRPHENIGINDIRAPTLEOMKDVYIV QDLMETDILYKLLATQHLSDNHICYFLYQLRGLKYIHSANVLRHDLKPSNLIJLNTTCD LKTCDERLARVADPDHDHTGFTTEYVATRWYRAPEIMLWSKGYTKSIDTWSVGCILAE MLSNRPIFFPKHYLDQNLHILGILGSPSQEDLNCIILNKARNYLLSLPHKNKVPWNRKL FPNADSKALDLDLKMILTNPHKRIEVEQALAHPLYLEQYYDPDSEPTAEAPFKPFDMELD DLPKELKELIFEETARFOPGYRS"	
BASE COUNT	339 a 313 c 285 g 319 t		
ORIGIN			
Query Match 0.6%; Score 26; DB 10; Length 1256;			
Best Local Similarity 100.0%; Pred. No. 0.37;			
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	3173	aagatctgtgactttggccttgcgcg	3198
Db	502	AAGATCTGTGACTTTGGCCTTGCCCG	527
Search completed: July 15, 2002, 23:22:29			
Job time: 24202 sec			

```
|||||
Db 3404 AGACAGGCACAGGATGAGGGCCCGGAGCTGCCACTCCCGCATACGCGCATCATG 3463
Qy 421 ctgaactgctggtccggagaccccaaggcgagacctgcattctcggagctg 471
Db 3464 CTGAACCTGCTGTCGGAGAGACCCCAAGCGAGACCTGCATCTCTCGGAGCTG 3514

RESULT 4
HSFLT4 4116 bp mRNA linear PRI 30-NOV-1993
LOCUS H.sapiens mRNA for FLT4, class III receptor tyrosine kinase.
DEFINITION X68203
ACCESSION X68203.1 GI:31433
VERSION FLT4; tyrosine kinase receptor.
KEYWORDS human.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Aprelikova, O.
Direct Submission
Submitted (01-SEP-1992) O. Aprelikova, University of Helsinki,
Cancer Biology Laboratory, Dept of Pathology, Haartmaninkatu 3,
00290 Helsinki, FINLAND
2 (bases 1 to 4116)
Aprelikova, O., Pajusola, K., Partanen, J., Armstrong, E., Alitalo, R.,
Bailey, S.K., McMahon, J., Wasmuth, J., Huebner, K. and Alitalo, K.
FLT4, a novel class III receptor tyrosine kinase in chromosome
5q33-qter
Cancer Res. 52 (3), 746-748 (1992)
JOURNAL Cancer Res. 52 (3), 746-748 (1992)
MEDLINE 92119639
COMMENT Related sequence: X51602.
FEATURES
    source
        1..4416
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /chromosome="5q35"
            /haplotype="erythro leukemia cells"
            /cell_line="HEL"
            <1..>4416
            /gene="FLT4"
            1..4416
            /gene="FLT4"
            <1..3916
            /gene="FLT4"
            /note="class III tyrosine kinase"
            /codon_start=2
            /product="FLT4"
            /protein_id="CAA48290.1"
            /db_xref="GI:388522"
            /db_xref="SWISS-PROT:P35916"
            /translation="HAORPEMORGAALCLRLWLCGLGLVSGYSMTPTLTITEES
HVIDTGPSLSISCRGHPLEWAMPQAEAPATGDKOSEDYGVVDFDCECTDARYCKVL
LLHEVHANDGYSYCYKYKARIEGTTAASSYFVRDFEQPFINKPDTLLVNRKDM
WPCLVSPGLNVTLSRSSVLPDGOEVDVDDRMGLVSTPLLDHALYLCQETWGD
ODFLSNPLTDLLVNSDSLMQCLVAGAHAPSIWYKDERLLEKSGVDLADSNQKLS
IQRVREDAGRYLCVSCNAKCVNSASVAVEGSDKSGMEIVILVGTGVIYVFFWL
LILFLCNRRPAHADIKTGYSIIMDPCEVPLEQCEVLSYDASOWEPFRERHLGRV
LGYAGFKYVEASAFGIHKSSCDTVAKMLKEGATASEHRAELSELKILIHIGNHLN
VNVLLGATPQGPGLMIVIEFCVGNLSNFLRAKRDAPSPCAEKSPQGRGRFAMVEL
ARLDRRPSGSDRVLFARFKTEGGARRASPDQAEADLWLSPLTMDLVCLYSQVARG
MEFLASRKCIRHDLAARNILLESDDVVKICDFGLARDIYKDPDYVRKGSARLPLKWA
PESTFDKVTYQSDWAFGLWEIFSLGASPPYGVQINEEFQCRLDGRMRAPELA
TPAIRRIMLNCWSDGPKARPAFSELVEILGLDLOGRLQBEVEECVMAPRSSQSEEGS
```

```
FSQVSTMALHIAQDAEDSPSPQLQRHSLAARYNMVSPGCLARGAETRGSSRMKTFE
EFPMTPTTYKQSDVNDQDSGMVLASEFEFQIESRHQESGFR"
BASE COUNT 941 a 1345 c 1355 g 774 t 1 others
ORIGIN
Query Match 100.0%; Score 471; DB 9; Length 4416;
Best Local Similarity 100.0%; Pred. No. 2.1e-263;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ctgaccatgaaagatcttctgctacagcttcacaggtggccagagggatggagttcctg 60
|||||
Db 3044 CTGACCATGGAAGATCTTGCTGTACAGTTCACGTTCCAGTGGCCACAGGGATGGAGTTCCTG 3103
Qy 61 gcttccgaaagtgcattccacagagacctggtgctcggaacattctgctgctggaagc 120
|||||
Db 3104 GCTTCCGAAAGTGCACTCCACAGAGACCTGGCTGCTCGGAACATCTGCTGTGCGGAAGC 3163
Qy 121 gacgtggtgaagatctgtgactttggccttgcggggacatctacaaagacctgactac 180
|||||
Db 3164 GACGTGTTGAAGATCTGTGACTTTGGCTTTGCCGGGACATCTACAAAGACCCCTGACTAC 3223
Qy 181 gtccgaaagggcagtgccccggctgccccgaagtggatggcgcctcgaagcatcttcgac 240
|||||
Db 3224 GTCCGCAAGGGCAGTGCCCGGCTGCCCTGAAGTGGATGGCCCTGAAAGCATCTTCGAC 3283
Qy 241 aagtggtacaccacgacagtgacgtggtgcttcttgggtgcttctctggagatcttc 300
|||||
Db 3284 AAGGTGTACACCACGACAGATGACGTGTGCTCTTTGGGGTCTTCTCTGGGAGATCTTC 3343
Qy 301 tctctgggggctccccctgaccttgggtggtgcagatcaatgagaggtctccagcgagctg 360
|||||
Db 3344 TCTCTGGGGGCTCCCGTACCCTGGGTGCAGATCAATGAGGAGTTCTGCCAGCGGCTG 3403
Qy 361 agagacggcacaagatgagggccccggagctggccactccgccataccgcgcatcag 420
|||||
Db 3404 AGAGACGGCAAGGATGAGGGCCCCGGAGCTGGCCACTCCCGCCATACGCCGCATCATG 3463
Qy 421 ctgaactgctggtccggagaccccaaggcgagacctgcattctcggagctg 471
|||||
Db 3464 CTGAACCTGCTGTCGGAGACCCCAAGCGAGACCTGCATCTCTCGGAGCTG 3514

RESULT 5
LOCUS I44520
DEFINITION Sequence 31 from patent US 5635177.
ACCESSION I44520
VERSION I44520.1 GI:2469233
KEYWORDS .
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 4425)
AUTHORS Bennett,B.D., Goeddel,D. and Matthews,W.
TITLE Protein tyrosine kinase agonist antibodies
JOURNAL Patent: US 5635177-A 31 03-JUN-1997;
FEATURES
    source
        1..4425
            /organism="unknown"
BASE COUNT 939 a 1348 c 1361 g 777 t
ORIGIN
Query Match 100.0%; Score 471; DB 6; Length 4425;
Best Local Similarity 100.0%; Pred. No. 2.1e-263;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ctgaccatgaaagatcttctgctacagcttcacaggtggccagagggatggagttcctg 60
|||||
Db 3055 CTGACCATGGAAGATCTTGCTGTACAGTTCACAGTTCACAGTGGCCACAGGGATGGAGTTCCTG 3114
Qy 61 gcttccgaaagtgcattccacagagacctggtgctcggaacattctgctgctggaagc 120
```



```
BASE COUNT 977 a 1490 c 1494 g 834 t
ORIGIN
/organism="unknown"
Query Match 100.0%; Score 471; DB 6; Length 4795;
Best Local Similarity 100.0%; Pred. No. 2.1e-263;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ctgaccatggaagatcttctgtctacagcttccaggtgcccaggtgagggatggagttcctg 60
Db 3044 CTGACCATGGAAGATCTTGTCTGTCTACAGCTTCCAGGTGGCCAGAGGGATGGAGTTCCCTG 3103
Qy 61 gcttcccgaagatgcatccacagagacctggtgctcggaaacattctcgtctcggaaagc 120
Db 3104 GCTTCCCGAAAGTGCATCCACAGAGACCCTGGCTGCTCGGAACATTTCTGCTGTCGGAAGC 3163
Qy 121 gacgtggtgaagatctgtgactttgaccttccaggtgcccaggtgagggatggagttcctg 180
Db 3164 GACGTGCTCAAGATCTGTGACTTTGGCCCTGCCCGGGACATCTCAAAAGACCCCTGACTAC 3223
Qy 61 gcttcccgaagatgcatccacagagacctggtgctcggaaacattctcgtctcggaaagc 120
Db 3104 GCTTCCCGAAAGTGCATCCACAGAGACCCTGGCTGCTCGGAACATTTCTGCTGTCGGAAGC 3163
Qy 121 gacgtggtgaagatctgtgactttgaccttccaggtgcccaggtgagggatggagttcctg 180
Db 3164 GACGTGCTCAAGATCTGTGACTTTGGCCCTGCCCGGGACATCTCAAAAGACCCCTGACTAC 3223
Qy 181 gtcaccaagggcagtgcccggctgcccctgaagtggatggagccctgaaagcatcttcgac 240
Db 3224 GTCCGCAAGGGCAGTCCCGGCTGCCCTGAAAGTGATGGCCCTGAAAGCATCTTCGAC 3283
Qy 241 aagtggtacacacagagtgacgtggtgctcttgggtgcttctctcgtcggagatcttc 300
Db 3284 AAGTGTACACCAAGAGTACGTGTGCTTGGGTGCTTCTTGGGTGCTTCTCTGGAGATCTTC 3343
Qy 301 tctctgggggctcccgctacccctgggtgcagatcaatgaggttcttgcacgagctg 360
Db 3344 TCTCTGGGGGCTCCCGCTACCTGGGTGCAGATCAATGAGGAGTCTGTCCAGCGGCTG 3403
Qy 361 agagacggcacaaagatgagggcccggagctggcactcccgccatcagccgcatcgtg 420
Db 3404 AGAGACGGCACAAAGATGAGGGCCCCGGAGCTGGCCACTTCCCGCCATACGCCGCATCATG 3463
Qy 421 ctgaactgctggtcggagacccccaaagcagacacctgattctcggagctg 471
Db 3464 CTGAACCTGCTGTCGGAGACCCCAAGCGAGACCTGCATTTCTCGGAGCTG 3514
Qy 471 ctgaactgctggtcggagacccccaaagcagacacctgattctcggagctg 471
Db 3464 CTGAACCTGCTGTCGGAGACCCCAAGCGAGACCTGCATTTCTCGGAGCTG 3514
RESULT 8
LOCUS AR106406 4795 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 3 from patent US 6107046.
ACCESSION AR106406
VERSION AR106406.1 GI:12820936
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 4795)
AUTHORS Alikalo,K., Aprelikova,O., pajusola,K., Armstrong,E., Korhonen,J.,
Kaipainen,A. and Matikainen,M.
TITLE Antibodies to Flt4, a receptor tyrosine kinase and uses thereof
JOURNAL Patent: US 6107046-A 3 22-AUG-2000;
FEATURES
Location/Qualifiers
source
BASE COUNT 977 a 1490 c 1494 g 834 t
ORIGIN
/organism="unknown"
Query Match 100.0%; Score 471; DB 6; Length 4795;
Best Local Similarity 100.0%; Pred. No. 2.1e-263;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ctgaccatggaagatcttctgtctacagcttccaggtgcccaggtgagggatggagttcctg 60
Db 3044 CTGACCATGGAAGATCTTGTCTGTCTACAGCTTCCAGGTGGCCAGAGGGATGGAGTTCCCTG 3103
Qy 61 gcttcccgaagatgcatccacagagacctggtgctcggaaacattctcgtctcggaaagc 120
Db 3104 GCTTCCCGAAAGTGCATCCACAGAGACCCTGGCTGCTCGGAACATTTCTGCTGTCGGAAGC 3163
Qy 121 gacgtggtgaagatctgtgactttgaccttccaggtgcccaggtgagggatggagttcctg 180
Db 3164 GACGTGCTCAAGATCTGTGACTTTGGCCCTGCCCGGGACATCTCAAAAGACCCCTGACTAC 3223
Qy 181 gtcaccaagggcagtgcccggctgcccctgaagtggatggagccctgaaagcatcttcgac 240
Db 3224 GTCCGCAAGGGCAGTCCCGGCTGCCCTGAAAGTGATGGCCCTGAAAGCATCTTCGAC 3283
Qy 241 aagtggtacacacagagtgacgtggtgctcttgggtgcttctctcgtcggagatcttc 300
Db 3284 AAGTGTACACCAAGAGTACGTGTGCTTGGGTGCTTCTTGGGTGCTTCTCTGGAGATCTTC 3343
Qy 301 tctctgggggctcccgctacccctgggtgcagatcaatgaggttcttgcacgagctg 360
Db 3344 TCTCTGGGGGCTCCCGCTACCTGGGTGCAGATCAATGAGGAGTCTGTCCAGCGGCTG 3403
Qy 361 agagacggcacaaagatgagggcccggagctggcactcccgccatcagccgcatcgtg 420
Db 3404 AGAGACGGCACAAAGATGAGGGCCCCGGAGCTGGCCACTTCCCGCCATACGCCGCATCATG 3463
Qy 421 ctgaactgctggtcggagacccccaaagcagacacctgattctcggagctg 471
Db 3464 CTGAACCTGCTGTCGGAGACCCCAAGCGAGACCTGCATTTCTCGGAGCTG 3514
REFERENCE 1 (bases 1 to 6827)
AUTHORS Bennett,B.D., Goeddel,D. and Matthews,W.
TITLE Protein tyrosine kinase agonist antibodies
JOURNAL Patent: US 5635177-A 17 03-JUN-1997;
FEATURES
Location/Qualifiers
source
BASE COUNT 1558 a 1870 c 1738 g 1660 t 1 others
ORIGIN
/organism="unknown"
Query Match 89.2%; Score 420; DB 6; Length 6827;
Best Local Similarity 99.8%; Pred. No. 1.2e-233;
Matches 470; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 ctgaccatggaagatcttctgtctacagcttccaggtgcccaggtgagggatggagttcctg 60
Db 2749 CTGACCATGGAAGATCTTGTCTGTCTACAGCTTCCAGGTGGCCAGAGGGATGGAGTTCCCTG 2690
Qy 61 gcttcccgaagatgcatccacagagacctggtgctcggaaacattctcgtctcggaaagc 120
Db 2689 GCTTCCCGAAAGTGCATCCACAGAGACCCTGGCTGCTCGGAACATTTCTGCTGTCGGAAGC 2630
Qy 121 gacgtggtgaagatctgtgactttgaccttccaggtgcccaggtgagggatggagttcctg 180
Db 2629 GACGTGCTGAAGATCTGTGACTTTGGCCCTGCCCGGGACATCTCAAAAGACCCCTGACTAC 2570
Qy 181 gtcaccaagggcagtgcccggctgcccctgaagtggatggccctgaaagcatcttcgac 240
Db 2569 GTCCCAAGGGCAGTCCCGGCTGCCCTGAAAGTGAGTGGATGGCCCTGAAAGCATCTTCGAC 2510
Qy 241 aagtggtacacacagagtgacgtggtgctcttgggtgcttctcgtcggagatcttc 300
Db 2509 AAGGTGTACACCACGACGAGTGACGTGGTGGTCTTGGGTGCTTCTCTGGAGATCTTC 2450
```

```
Db 3104 GCTTCCCGAAAGTGCATCCACAGAGACCCTGGCTGCTCGGAACATTTCTGCTGCGAAAGC 3163
Qy 121 gacgtggtgaagatctgtgactttgaccttggccctgcccgggacatctacaaagaccttcgac 180
Db 3164 GACGTGCTGAAGATCTGTGACTTTGGCTTCCCGGGACATCTCAAAAGACCCCTGACTAC 3223
Qy 181 gtcaccaagggcagtgcccggctgcccctgaagtggatggccctgaaagcatcttcgac 240
Db 3224 GTCCGCAAGGGCAGTCCCGGCTGCCCTGAAAGTGAGTGGCCCTGAAAGCATCTTCGAC 3283
Qy 241 aagtggtacacacagcagagtgacgtggtgctcttgggtgcttctctcgtcggagatcttc 300
Db 3284 AAGTGTACACCAAGAGTACGTGTGCTTGGGTGCTTCTCTGGGAGATCTTC 3343
Qy 301 tctctgggggctcccgctacccctgggtgcagatcaatgagggatgtcgtccagcgagctg 360
Db 3344 TCTCTGGGGGCTCCCGCTACCTGGGTGCAGATCAATGAGGAGTCTGTCCAGCGGCTG 3403
Qy 361 agagacggcacaaagatgagggcccggagctggcactcccgccatcagccgcatcgtg 420
Db 3404 AGAGACGGCACAAAGATGAGGGCCCCGGAGCTGGCCACTTCCCGCCATACGCCGCATCATG 3463
Qy 421 ctgaactgctggtcggagacccccaaagcagacacctgattctcggagctg 471
Db 3464 CTGAACCTGCTGTCGGAGACCCCAAGCGAGACCTGCATTTCTCGGAGCTG 3514
RESULT 9
LOCUS I44515 6827 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 17 from patent US 5635177.
ACCESSION I44515
VERSION I44515.1 GI:24692228
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 6827)
AUTHORS Bennett,B.D., Goeddel,D. and Matthews,W.
TITLE Protein tyrosine kinase agonist antibodies
JOURNAL Patent: US 5635177-A 17 03-JUN-1997;
FEATURES
Location/Qualifiers
source
BASE COUNT 1558 a 1870 c 1738 g 1660 t 1 others
ORIGIN
/organism="unknown"
Query Match 89.2%; Score 420; DB 6; Length 6827;
Best Local Similarity 99.8%; Pred. No. 1.2e-233;
Matches 470; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 ctgaccatggaagatcttctgtctacagcttccaggtgcccaggtgagggatggagttcctg 60
Db 2749 CTGACCATGGAAGATCTTGTCTGTCTACAGCTTCCAGGTGGCCAGAGGGATGGAGTTCCCTG 2690
Qy 61 gcttcccgaagatgcatccacagagacctggtgctcggaaacattctcgtctcggaaagc 120
Db 2689 GCTTCCCGAAAGTGCATCCACAGAGACCCTGGCTGCTCGGAACATTTCTGCTGTCGGAAGC 2630
Qy 121 gacgtggtgaagatctgtgactttgaccttggccctgcccaggtgagggatggagttcctg 180
Db 2629 GACGTGCTGAAGATCTGTGACTTTGGCCCTGCCCGGGACATCTCAAAAGACCCCTGACTAC 2570
Qy 181 gtcaccaagggcagtgcccggctgcccctgaagtggatggccctgaaagcatcttcgac 240
Db 2569 GTCCCAAGGGCAGTCCCGGCTGCCCTGAAAGTGAGTGGATGGCCCTGAAAGCATCTTCGAC 2510
Qy 241 aagtggtacacacagcagagtgacgtggtgctcttgggtgcttctcgtcggagatcttc 300
Db 2509 AAGGTGTACACCACGACGAGTGACGTGGTGGTCTTGGGTGCTTCTCTGGAGATCTTC 2450
```

```
Oy 301 tctctggggcctccccgtaccctgggtgcagatcaatgaagagttctgcagcgctg 360
|||||
Db 2449 TCTCTGGGGCCTCCCCGTACCCTGGGTGCAGATCAATGAGAGTCTTGCAGCGGCTG 2390
|||||

Oy 361 agagacggcacagatgagggcccgagctggcactcccgccatacgccgcatcatg 420
|||||
Db 2389 AGAGACGGCACAGATGAGGGCCCGGAGCTGGCCACTCCGCCCATACGCCGCCATCATG 2330
|||||

Oy 421 ctgaactgctggtcggagagaccccaaggcagagacctgcatctcgagagctg 471
|||||
Db 2329 CTGAACCTGCTGTCGGAGACCCCAAGCGGAGACCTGCATTCCTCGAGCTG 2279
|||||

RESULT 10
HSFLT4X HSFLT4X 4450 bp mRNA linear PRI 29-NOV-1993
LOCUS
DEFINITION H.sapiens FLT4 mRNA for transmembrane tyrosine kinase.
ACCESSION X69878 S59182
VERSION X69878.1 GI:297049
KEYWORDS transmembrane tyrosine kinase; tyrosine kinase.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 4450)
AUTHORS Galland,F., Karamysheva,A., Pebusque,M.J., Borg,J.P., Rottapel,R.,
Dubreuil,P., Rosnet,O. and Birnbaum,D.
TITLE The FLT4 gene encodes a transmembrane tyrosine kinase related to
the vascular endothelial growth factor receptor
JOURNAL Oncogene 8 (5), 1233-1240 (1993)
MEDLINE 93241723
REFERENCE 2 (bases 776 to 1200)
AUTHORS Galland,F., Karamysheva,A., Mattei,M.G., Rosnet,O., Marchetto,S.
and Birnbaum,D.
TITLE Chromosomal localization of FLT4, a novel receptor-type tyrosine
kinase gene
JOURNAL Genomics 13 (2), 475-478 (1992)
MEDLINE 92307693
REFERENCE 3 (bases 1 to 4450)
AUTHORS Galland,F.
TITLE Direct Submission
JOURNAL Submitted (28-DEC-1992) F. Galland, INSERM, Unite 119, 27 Bd Lei
Roure, Marseille 13009, FRANCE
FEATURES
source
1..4450
/organism="Homo sapiens"
/db_xref="taxon:9606"
22..87
/protein_id="CAA49505.1"
/db_xref="GI:297050"
/translation="MKGAAALCLRLWLCIGLLGLDGLVSDYSMTPTPLNITBESHVIDTG
DSLSTSCRGQPLWAMPGAQEPATGDKQSEDTGVVRDCEGTDAREYCKVLLHVEH
ANDTGYCYKYIKARIEGTAASSVYFVRDFEQPIINRPDTLLYVRKDMWVPCLV
SIPGLNVLTRSSQSLVMPDGEVYVDDRRGMLVSTPLLDHALYLQCEITWDQDFLSN
PFLVHTTNGEYLDIOLPRKSLLELVGKLVNCTVMAEFNSGYTFDWDYPGKAERG
KWVPRSQOQHTLSSILTTHNYSQHDGLGYCKANNQIQRPRESEVIVHENPFI
VEMLKPILEATAGDELVKLPVLAAYPPPEFOWYKDGKALSGRHSPLALVLEKTEA
STGNTYLAWSAAGLRNLSLELVNVPQIHEKEASSPIYSRHSRQALCTCTYAT
PLPLSIQHWHPWTPCKNFAQRLRRRQQQDLMPQCRDRAVTTQDAVNPIESLDWT
EFGKNTYSLKVIQNAYSAMYKCVVSNKVGQDERLIYPVYTPIDGTIESKPE
ELLEGPVLLSCQADSYKYEHLRYRLNLSLTHAAGNPLLLDKKNVHLFATPLAAL
EVAAPRHATLSLSIPRAVRECHYVCEYQDRRSHDKHKRYLSVQALEAPRLQ
NLDTLLVNVSDLSMQCLAGAHAPSIWYKDERLLEKSGVDLADSNOKLSIQVRVE
EDAGPYLCSVRPKGCVNSAVAVEGSDKSMELVILVCTGVIAVFFNVLLLIIC
NMRRPADIKTYGLSIIIMDPCEVPLEQCEYLSYDASQWEPFRERHLGRVLGYGF
GKYVEASAFGIHKSSCDTVAVMLKEGATASEQALMSLEIKLILIHGNLVNVLIG
ACTKPGQLMWIVVEFYGNLSNFLRAKRDFAISPCAEKSPQGRFRFAMVELARLDRR
```

```
misc_feature 22..2346
/citation=[1]
/product="extracellular domain"
misc_structure 160..366
/citation=[1]
/function="IG-like domain 1"
misc_structure 481..651
/citation=[1]
/function="IG-like domain 2"
misc_structure 763..963
/citation=[1]
/function="IG-like domain 3"
misc_structure 1072..1230
/citation=[1]
/function="IG-like domain 4"
misc_structure 1342..1635
/citation=[1]
/function="IG-like domain 5"
misc_structure 1741..1992
/citation=[1]
/function="IG-like domain 6"
misc_feature 2104..2277
/citation=[1]
/product="IG-like domain 7"
misc_feature 2347..2412
/citation=[2]
/product="transmembrane domain"
misc_feature 2413..2547
/citation=[2]
/product="juxtamembrane domain"
misc_feature 2548..2853
/citation=[2]
/product="tyrosine kinase domain 1"
misc_feature 2854..3048
/citation=[1]
/citation=[2]
/product="kinase insert"
misc_feature 3049..3558
/citation=[2]
/product="tyrosine kinase domain 2"
BASE COUNT 960 a 1350 c 1354 g 786 t
ORIGIN

Query Match 64.8%; Score 305; DB 9; Length 4450;
Best Local Similarity 99.7%; Pred. No. 1.8e-166;
Matches 355; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 ctgaccatggaagatcttctgtctgtacagcttcaggtgcccagagggatgagttctcg 60
|||||
Db 3046 CTGACCATGGAAGATCTTGTCTGTCTACAGCTTCCAGGTGGCCAGAGGGATGGAGTTCTG 3105
|||||

Oy 61 gcttcccgaaagtgcattccacagagacctgctcgtcggaaacctctcgtcgtcgaaagc 120
|||||
Db 3106 GCTTCCCCAAAGTGCATCCACAGAGACTGCTGCTCGGAACATCTGCTGTCGGAAGC 3165
|||||

Oy 121 gacgtggtgaagatctgtgactttggccttgcggggacatctacaagaccctgactac 180
|||||
Db 3166 GACGTGGTGAAGATCTGTGACTTTGGCTTCCCGGGGACATCTACAAGACCCGACTAC 3225
|||||

Oy 181 gtcgcgaaggcagtgcccgcctgcccctgaagtggatgagccctgaaagcattcttcgac 240
|||||
Db 3226 GTCGCGAAGGCGAGTGGCCCGCTGCCCTGGAAGTGGATGGCCCTGAAAGCATCTTCGAC 3285
|||||
```

```

Qy 241 aaggtgtacaccacagagtgacgtggttccttgggtgctctctgagagattctc 300
|||||
Db 3286 AAGGTGTACACCACGACAGTGACGTGGTCTTTGGGGTCTCTCTGGAGATCTTC 3345
|||||
Qy 301 tctctgggggctccctacacctgaggtgagatcaatgaggaggtctgcacgc 356
|||||
Db 3346 TCCTGCTGGGGCTCCCGCTACCTGGGTGAGATCAATGAGGAGTTCTGCCACGC 3401
|||||

RESULT 11
AC022095/c 127488 bp DNA linear HTG 20-APR-2001
LOCUS Homo sapiens chromosome 5 clone CTB-36B8, WORKING DRAFT SEQUENCE,
DEFINITION 13 unordered pieces.
ACCESSION AC022095
VERSION AC022095.5 GI:13699618
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 127488)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 5
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 127488)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (26-JAN-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Apr 20, 2001 this sequence version replaced gi:7711676.
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
-----
Project Information
Center Project Name: 78060
Center clone name: CIT978SKB_36B8
-----
Summary Statistics
Consensus quality: 110477 bases at least Q40
Consensus quality: 117221 bases at least Q30
Consensus quality: 120225 bases at least Q20
Estimated insert size: 131000; pulse field gel estimation
Estimated insert size: 126288; sum-of-ctnigs estimation
Quality coverage: 7.48 in Q20 bases; pulse field gel estimation
Quality coverage: 7.76 in Q20 bases; sum-of-ctnigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 13 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 1116: contig of 1116 bp in length
* 1117 1216: contig of unknown length
* 1217 2254: contig of 1038 bp in length
* 2255 2354: gap of unknown length
* 2355 3412: contig of 1058 bp in length
* 3413 3512: gap of unknown length
* 3513 5005: contig of 1493 bp in length
* 5006 5105: gap of unknown length
* 5106 7647: contig of 2542 bp in length
* 7648 7747: gap of unknown length
* 7748 10237: contig of 2490 bp in length
* 10238 10337: gap of unknown length
* 10338 12440: contig of 2103 bp in length
* 12441 12540: gap of unknown length
* 12541 15935: contig of 3395 bp in length
* 15936 16035: gap of unknown length

```

```

FEATURES
source 1..127488
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
/clone_lib="CTB-36B8"
/clone_lib="CalTech human BAC library B"
BASE COUNT 31643 a 32392 c 31616 g 30626 t 1211 others
ORIGIN

Query Match 24.0%; Score 113; DB 2: Length 127488;
Best Local Similarity 100.0%; Pred. No. 2.3e-54;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 196 gcccggtgccccctgaagtgagtgagccctgaaagcattctcgacaaggtgtacaccacg 255
|||||
Db 106477 GCCCGGTGCCCCCTGAAGTGGATGGCCCTCGAAAGCATCTTCGACAAAGGTGTACACCACG 106418
|||||

Qy 256 cagagtgcactgtggtctcttgggtggtctctctgagagatctctctctctg 308
|||||
Db 106417 CAGAGTGACGTGCTGCTCTTTGGGGTCTTCTCTCGGAGATCTTCTCTCTGGG 106365
|||||

RESULT 12
AC108083/c 130129 bp DNA linear HTG 25-JAN-2002
LOCUS Homo sapiens chromosome 5 clone CTD-2013L15, WORKING DRAFT
DEFINITION SEQUENCE, 4 unordered pieces.
ACCESSION AC108083
VERSION AC108083.1 GI:18369929
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 130129)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 5
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 130129)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (25-JAN-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
-----
Project Information
Center Project Name: 632820
Center clone name: CITB-H1_2013L15
-----
Summary Statistics
Consensus quality: 124488 bases at least Q40
Consensus quality: 128031 bases at least Q30
Consensus quality: 128842 bases at least Q20
Estimated insert size: 135000; agarose-fp estimation
Estimated insert size: 129829; sum-of-ctnigs estimation
Quality coverage: 7.66 in Q20 bases; agarose-fp estimation
Quality coverage: 7.97 in Q20 bases; sum-of-ctnigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. The true order of the pieces

```

* is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

* 1 4320: contig of 4320 bp in length
 * 4321 4420: gap of unknown length
 * 4421 23712: contig of 19292 bp in length
 * 23713 23812: gap of unknown length
 * 23813 48602: contig of 24790 bp in length
 * 48603 48702: gap of unknown length
 * 48703 130129: contig of 81427 bp in length.

FEATURES

source

1. 130129
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="5"
 /clone="CTD-2013L15"
 /clone_lib="Caltech human BAC library D"

35337 a 32397 c 30949 g 31146 t 300 others

BASE COUNT

ORIGIN

Query Match 24.0%; Score 113; DB 2: Length 130129;
 Best Local Similarity 100.0%; Pred. No. 2.3e-54;
 Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 196 gccgcgctgccctgaagtgcctgacccctgaagcattctcgacaagtgatcacccacg 255
 |||||
 Db 46759 GCCCGCTGCCCTCAAGTGGATGCCCTGAAGCATCTTCGACAAAGTGTACACACG 46700

Qy 256 cagaatgcgcgtgctcttgggggtgctctctctggggagatctctctctggg 308
 |||||
 Db 46699 CAGACTGACGTGTGCTCTTTGGGTGCTTCTCTCGGAGATCTTCTCTCGG 46647

RESULT 13

AC025336

LOCUS AC025336 168347 bp DNA linear HTG 25-MAR-2000
 DEFINITION Homo sapiens chromosome 5 clone RP11-451H23 map 5, WORKING DRAFT
 SEQUENCE, 32 unordered pieces.

ACCESSION

AC025336

VERSION 1 (bases 1 to 168347)

KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.

SOURCE

human.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 168347)

Birken, B., Linton, L., Nusbaum, C. and Lander, E.

Homo sapiens chromosome 5, clone RP11-451H23

Unpublished

2 (bases 1 to 168347)

Birken, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,

Anderson, S., Baldwin, J., Barna, N., Bastien, V., Bedalov, F.,

Boguslavsky, L., Boukhgalter, B., Brown, A., Burkett, G.,

Campolano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S.,

Collins, A., Cooke, P., DeAurellano, K., Dewar, K., Diaz, J.S.,

Dodge, S., Domino, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D.,

Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,

Grallan-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L.,

Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,

Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczy, J.,

Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N.,

McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R.,

Meldrim, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J.,

Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,

O'Neill, D., Oliver, T.M., Oliver, J., Peterson, K., Pierre, N.,

Pisani, C., Pollara, Y., Raymond, C., Riley, R., Rogov, P., Rothman, D.,

Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,

Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,

Tesfaye, S., Theodore, J., Tirtell, A., Travers, M., Trigilio, J.,

TITLE
JOURNAL

COMMENT

Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J.,
 Young, G., Zainoun, J., Zimmer, A. and Zody, M.
 Direct Submission
 Submitted (08-MAR-2000) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Mar 25, 2000 this sequence version replaced gl:7210017.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: http://www-seq.wi.mit.edu

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L6686

Center clone name: 451_H_23

----- Summary Statistics

Sequencing vector: M13; M77815; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 150422 bases at least Q40

Consensus quality: 159524 bases at least Q30

Consensus quality: 163013 bases at least Q20

Insert size: 165247; sum-of-contigs

Quality coverage: 3.6 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 32 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

* 1 1389: contig of 1389 bp in length

* 1390 1489: gap of 100 bp

* 1490 3130: contig of 1641 bp in length

* 3131 3230: gap of 100 bp

* 3231 4942: contig of 1712 bp in length

* 4943 5042: gap of 100 bp

* 5043 6981: contig of 1939 bp in length

* 6982 7081: gap of 100 bp

* 7082 8708: contig of 1627 bp in length

* 8709 8808: gap of 100 bp

* 8809 10286: contig of 1478 bp in length

* 10287 10386: gap of 100 bp

* 10387 12212: contig of 1826 bp in length

* 12213 12312: gap of 100 bp

* 12313 14658: contig of 2346 bp in length

* 14659 14758: gap of 100 bp

* 14759 17941: contig of 3183 bp in length

* 17942 18041: gap of 100 bp

* 18042 21297: contig of 3256 bp in length

* 21298 21397: gap of 100 bp

* 21398 24992: contig of 3595 bp in length

* 24993 25092: gap of 100 bp

* 25093 27768: contig of 2676 bp in length

* 27769 27868: gap of 100 bp

* 27869 31188: contig of 3320 bp in length

* 31189 31288: gap of 100 bp

* 31289 33714: contig of 2426 bp in length

* 33715 33814: gap of 100 bp

* 33815 37277: contig of 3463 bp in length

* 37278 37377: gap of 100 bp

* 37378 42302: contig of 4925 bp in length

* 42303 42402: gap of 100 bp

* 42403 47816: contig of 5414 bp in length

* 47817 47916: gap of 100 bp

* 47917 52586: contig of 4670 bp in length

* 52587 52686: gap of 100 bp

* 52687 56567: contig of 3881 bp in length

* 56568 56667: gap of 100 bp


```

* NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 1596: contig of 1596 bp in length
* 1597 1696: gap of unknown length
* 1697 3940: contig of 2244 bp in length
* 3941 4040: gap of unknown length
* 4041 5104: contig of 1064 bp in length
* 5105 5204: gap of unknown length
* 5205 6286: contig of 1082 bp in length
* 6287 6386: gap of unknown length
* 6387 20063: contig of 13677 bp in length
* 20064 20163: gap of unknown length
* 20164 82401: contig of 62238 bp in length
* 82402 82501: gap of unknown length
* 82502 173341: contig of 90840 bp in length.
FEATURES             Location/Qualifiers
     source           1..173341
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="5"
                     /clone="RP11-586L9"
                     /clone_lib="RPC1 human BAC library 11"
BASE COUNT      45837 a 42564 c 41389 g 42871 t 680 others
ORIGIN

Query Match      24.0%; Score 113; DB 2; Length 173341;
Best Local Similarity 100.0%; Pred. No. 2.3e-54;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 196 gcccggtgcccctgaagtgccttgcctgaagcattcttcgacaaggtgtacaccacg 255
|||||
Db 103467 GCCCGGCTGCCCTGAAGTGGATGGCCCTGAAGACATCTTCGACAAGGTGTACACCACG 103526

Qy 256 cagaatgcgtgtgctcttgggtgctcttcctcggagagattctctctctggg 308
|||||
Db 103527 CAGAGTGACGTGTGCTCTCTGGGTGCTTCTCTGGGAGATCTTCTCTCTGGG 103579

RESULT 15
AC108083
LOCUS             130129 bp DNA linear HTG 25-JAN-2002
DEFINITION       Homo sapiens chromosome 5 clone CTD-2013L15, WORKING DRAFT
ACCESSION        AC108083
VERSION          AC108083.1 GI:18369929
KEYWORDS         HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE           human.
ORGANISM         Homo sapiens
                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE        1 (bases 1 to 130129)
AUTHORS          DOE Joint Genome Institute.
TITLE            Sequencing of Human Chromosome 5
JOURNAL          Unpublished
REFERENCE        2 (bases 1 to 130129)
AUTHORS          DOE Joint Genome Institute.
TITLE            Direct Submission
JOURNAL          Submitted (25-JAN-2002) Production Sequencing Facility, DOE Joint
                 Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT          -----Genome Center
                 Center: Joint Genome Institute
                 Center Code: JGI
                 Web site: http://www.jgi.doe.gov
                 -----
Project Information
Center Project Name: 632820

```

```

Center clone name: CITB-HL_2013L15
-----
Summary Statistics
Consensus quality: 124488 bases at least Q40
Consensus quality: 128031 bases at least Q30
Consensus quality: 128842 bases at least Q20
Estimated insert size: 135000; agarose-fp estimation
Estimated insert size: 129829; sum-of-contigs estimation
Quality coverage: 7.66 in Q20 bases; agarose-fp estimation
Quality coverage: 7.97 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence.
* as soon as it is available and the accession number will
* be preserved.
* 1 4320: contig of 4320 bp in length
* 4321 4420: gap of unknown length
* 4421 23712: contig of 19292 bp in length
* 23713 23812: gap of unknown length
* 23813 48602: contig of 24790 bp in length
* 48603 48702: gap of unknown length
* 48703 130129: contig of 81427 bp in length.
FEATURES             Location/Qualifiers
     source           1..130129
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="5"
                     /clone="CTD-2013L15"
                     /clone_lib="Caltech human BAC library D"
BASE COUNT      35337 a 32397 c 30949 g 31146 t 300 others
ORIGIN

Query Match      21.9%; Score 103; DB 2; Length 130129;
Best Local Similarity 100.0%; Pred. No. 1.6e-48;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 71 agtcattccacaagacctgctcggaacattctgctcggaagcgagtggtga 130
|||||
Db 22717 AGTCATCCACAGAGACCTGCTGCTCGAACATCTGCTGCGAAGGACGCGTGTGA 22776

Qy 131 agatctgtgacttggccttgcctgggacatctacaaagacc 173
|||||
Db 22777 AGATCTGTGACTTGGCCTTGCCCGGACATCTACAAAGACCC 22819

RESULT 16
AC144509
LOCUS             160 bp DNA linear PAT 07-OCT-1997
DEFINITION       Sequence 5 from patent US 5635177.
ACCESSION        AC144509
VERSION          AC144509.1 GI:2469222
KEYWORDS         .
SOURCE           Unknown.
ORGANISM         Unclassified.
REFERENCE        1 (bases 1 to 160)
AUTHORS          Bennett,B.D., Goeddel,D. and Matthews,W.
TITLE            Protein tyrosine kinase agonist antibodies
JOURNAL          Patent: US 5635177-A 5 03-JUN-1997;
FEATURES         Location/Qualifiers
     source         1..160
                     /organism="unknown"
BASE COUNT      35 a 44 c 47 g 34 t
ORIGIN

Query Match      16.1%; Score 76; DB 6; Length 160;
Best Local Similarity 100.0%; Pred. No. 9.6e-33;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Oy 98 ggaacattctgctggaagcagcgtggtgaagatctgtgacttttgcccttgcacggg 157
|||||
Db 30 GGAACATTCTGCTGTCGGAAGCGGACGCTGGTGAAGATCTGTGACTTTGGCCTTGCCCGG 89
|||||
Oy 158 acatctacaaagacc 173
|||||
Db 90 ACATCTACAAGACCC 105
|||||
RESULT 17
MUSRTKA
LOCUS MUSRTKA 5284 bp mRNA linear ROD 09-AUG-1993
DEFINITION Mus musculus receptor tyrosine kinase (FLT4) mRNA, complete cds.
ACCESSION L07296
VERSION L07296.1 GI:293780
KEYWORDS receptor protein tyrosine kinase.
SOURCE Mus musculus (strain C57BL/6J, sub_species domesticus) cDNA to
mRNA.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 5284)
AUTHORS Finnerty,H., Kelleher,K., Morris,G.E., Bean,K., Merberg,D.M.,
Kriz,R., Morris,J.C., Sookdeo,H., Turner,K.J. and Wood,C.R.
TITLE Molecular cloning of murine FLT and FLT4
JOURNAL Oncogene 8, 2293-2298 (1993)
MEDLINE 93330572
FEATURES
source Location/Qualifiers
1..5284
/organism="Mus musculus"
/strain="C57BL/6J"
/sub_species="domesticus"
/db_xref="taxon:10090"
1..5284
/gene="FLT4"
45..4136
/gene="FLT4"
/note="putative"
/codon_start=1
/product="receptor tyrosine kinase"
/protein_id="AAA40077.1"
/db_xref="GI:293781"
/translation="MQGAALNRLWLCLGLLOGLANGYSMTPTPLNTEDSYVIDTG
DSLSTCRGQPLEWTPCAQALNLTGGKDESDTRVVHDCGTEARPYCKVLLLAQTH
ANNTGSYHCYKYIKARIEGTAATSTVYVFRDKHPFINKPDTLLVNRKDSMWVPCLV
SIPGLNITURSOSSALHPDQCEVLWDRGRVPTQLLRDALYLCQETWGDQNLN
LFWVHITNQLSDYIDQLPKSMELLVGEKLVNCTVYWAEPDGVTFDMDYPKQAEARA
VWLKGPVLEATAGDELVKLPVLAAYPPPEFQWYKDKAVTGRNPHALVKEVTEA
SAGVYTLALNSAAGLRONISLELVNVPVPHIHEKEASSPSIYSRHSROTUTCTAGVT
PEVECKNTYKSLVIQDANVSNMYKCVVNVKVGDERLIYFYVTIPDGSIESEPE
DPLEGQSVRLSCRADNYTYEHLWTRNLSTLHDAQGNPLLDCKNVHLFATPLEANL
EEAEPGRHATLSLNIIPRAVEDGDEYVQDORSDKHCKKYLVSQALEAPRLTQ
NLDLLVNSDSJNMRCPVAGAHVPSIVYKDKRLEKESGIDLADSNORLSIQRVRE
EDAGRYLCSVCNKAAGSVASAVVEGDEKGSMEIVILIGTVIAVFFVLLLLIFC
NKRPAHADIKTGLSLIIMDCEVPLEQCEVLSYDASOWEFPFRHLGRVLLGNLGF
CKVVEAFGLNKGSSCDTVAKMLKCATASEHRLAMSELKILIHGNHLNVNLLG
ACTKPNGLMWIYVECKYGNLSNELRVKEDTFNPAEKSPEQRFRFAMVSGAKADR
RPGSDRLAALFRPLMGKSARRAPLVQAEIDLWLSPLTMEDLVICYSFQVARGMFLAS
RKC1HRDLARNLILLESDEIVKICDFGLARDIYKDPDYVRKGSARLPLKWAPESIFD
KYVTTQSDVWFSQPLWEIFSGLASPPGVQINEEFCQRLKDKTMRAPELATPAIRH
IMQSCWDGPKARPAFSDLVETIGDLLOGGWQEEEREMALHSQSSEEDFGWQAST
TALHTEADADSPSPMHCCHSLAARYYNCSVPPGRLARGTKTGSSRMKTFEELPMTPT
TTYKASMDNDSGMVLASEEERFEELSRHREPGSFSCKPGQHWMDIPRGHPDPQGRRR
RPTQAGQGGKVFYNNHEYGEVSQPTGEGCCPSAGSTFFADSSY"

BASE COUNT 1221 a 1533 c 1466 g 1064 t

Query Match 6.6%; Score 31; DB 10; Length 5284;
Best Local Similarity 100.0%; Pred. No. 1.8e-06;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Caps 0;
Oy 331 cagatcaatgaggagtctctccagcggctga 361
|||||
Db 3399 CAGATCAATGAGGAGTTCTGCCAGCGGCTGA 3429
|||||
RESULT 18
AL646088 260266 bp DNA linear HTG 30-JAN-2002
LOCUS Mus musculus chromosome 11 clone RP23-58E13, *** SEQUENCING IN
DEFINITION PROGRESS ***, in unordered pieces.
ACCESSION AL646088
VERSION AL646088.11 GI:18476932
KEYWORDS HTG; HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTGP.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (sites)
AUTHORS Clark,S.
TITLE Direct Submission
JOURNAL Submitted (28-JAN-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Feb 1, 2002 this sequence version replaced gi:18151535.
COMMENT ----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: BM58E13
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 258539 bases at least Q40
Consensus quality: 258926 bases at least Q30
Consensus quality: 259227 bases at least Q20
Insert size: 259766; sum-of-contigs
Quality size: 225486; 6.3% error; agarose-fp
Quality coverage: 9.68x in Q20 bases; sum-of-contigs Quality
coverage: 11.43x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
FEATURES
source Location/Qualifiers
1..260266
/organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="11"
/clone="RP23-58E13"
/clone_lib="RPC1-23"
1..8902
/note="assembly_fragment:05530
fragment_chain:1"
9003..87162
/note="assembly_fragment:05707
fragment_chain:1"
87263..123670
/note="assembly_fragment:05852
fragment_chain:1"
123771..188404
/note="assembly_fragment:00429"
188505..214152
/note="assembly_fragment:05868"
214253..260266
/note="assembly_fragment:05872"
BASE COUNT 80139 a 55470 c 56089 g 68066 t 502 others
ORIGIN

/product="SEA protein (oncogene)"

LTR

2016..2338

/note="3' LTR"

BASE COUNT 564 a 659 c 757 g 558 t

ORIGIN 1 bp upstream of HindIII site.

Query Match 4.9%; Score 23; DB 14; Length 2538;

Best Local Similarity 100.0%; Pred. NO. 0.084;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 262 gacgtgtggtcctttggggtgct 284

|||||

Db 1417 GACGTGTGCTCTTTGGGTGCT 1439

Search completed: July 15, 2002, 23:28:07

Job time: 24540 sec

Query Match 6.6%; Score 31; DB 2; Length 260266;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 331 cagatcaatgaggaattctgccagcgctga 361
|||||
Db 168147 CAGATCAATGAGGAGTCTGCCAGCGCTGA 168177

RESULT 19
LOCUS AB017155 534 bp mRNA linear MAM 02-APR-1999
DEFINITION Oryctolagus cuniculus mRNA for VEGF receptor-2/Flk-1, partial cds.
ACCESSION AB017155
VERSION AB017155.1 GI:4586885
KEYWORDS VEGF receptor-2/Flk-1.
SOURCE Oryctolagus cuniculus (strain:Japanese white) liver cDNA to mRNA.
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
REFERENCE 1 (bases 1 to 534)
AUTHORS Umeki,K., Kon,K. and Ohtaki,S.
TITLE Rabbit mRNA for vascular endothelial growth factor (VEGF) receptor-2/Flk-1, partial cds
JOURNAL Published Only in Database (1999) In press
AUTHORS Umeki,K., Kon,K. and Ohtaki,S.
TITLE Direct Submission
JOURNAL Submitted (26-AUG-1998) Kazumi Umeki, Miyazaki Medical College, Department of Laboratory Medicine; Kihara 5200, Kiyotake, Miyazaki 889-1692, Japan (E-mail:umeki@post1.miyazaki-med.ac.jp, Tel:+81-985-85-9400. Fax:+81-985-85-4709)

FEATURES
source
1..534
/organism="Oryctolagus cuniculus"
/strain="Japanese white"
/db_xref="taxon:9986"
/tissue.type="liver"
<1..>534
/codon_start=1
/product="VEGF receptor-2/Flk-1"
/protein_id="BAA76520.1"
/db_xref="GI:4586886"
/translation="LASRKC1HRDLAARNLLSEKNVVKIGDFGLARDIYKDPYVRK
GDARLPKWAPEITFDVRYTIQSDVMSFGVLLWEIFSLGASPYGVKIDFEFCRLK
ECTRMRADYTPPENYQTMDCWHGCEPNERPTFSELVEHLGNLLQASQQGKDIYIVL
PMSETLSWEEDSGLSPT"

BASE COUNT 128 a 132 c 156 g 118 t
ORIGIN

Query Match 5.9%; Score 28; DB 4; Length 534;
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 122 acgtggtgaagactgtgacttggcct 149
|||||
Db 65 ACCTGCTGAAGATCTGTGACTTGGCCT 92

RESULT 20
LOCUS XELXFGFRA2 2753 bp mRNA linear VRT 28-APR-1993
DEFINITION Xenopus laevis fibroblast growth factor receptor mRNA, complete cds.
ACCESSION M62322
VERSION M62322.1 GI:214899
KEYWORDS fibroblast growth factor receptor; tyrosine kinase receptor.
SOURCE X.laevis, cDNA to mRNA.
ORGANISM Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 2753)
AUTHORS Friesel,R.E. and David,I.B.
TITLE cDNA cloning and developmental expression of fibroblast growth factor receptors from Xenopus laevis
JOURNAL Mol. Cell. Biol. 11, 2481-2488 (1991)
MEDLINE 91203867
FEATURES
source
1..2753
/organism="Xenopus laevis"
/db_xref="taxon:8355"
1..2753
/gene="XFGFRA2"
154..2328
/gene="XFGFRA2"
/codon_start=1
/product="fibroblast growth factor receptor"
/protein_id="AAA49993.1"
/db_xref="GI:214900"

Location/Qualifiers
1..2753
/translation="MFCMSLLLMGVLGAALSVARPPSTLPDIEDALPSAEDDEDDDD
NSSSEKAAENSKPNRPLMWSHPKMEKKLHAPAAKTVCRCPANCTTPTLRWLKNG
RAPQDORIGCYKVRQTSWLSIHDSVVPDKNYTCIVENKYGAINHYYQLDVVERSP
HRPILQAGLPANTSVTVGTTAEFSCKYVSDPQHIQWLRHIEINGSRVASDGPYVEI
LKTAGVNTSDKMEVLHNRVTFEDAGQYTCLAANSIGISHHSAMLTVLKVEDNKKPAL
LASPLQLEIIIIYCTGAAFVAMVVYIIIFKMKHPSKKSDFNQSLAVHKLAKSIPLRQ
VTVSGDSSNMNCGVILVRLSSGTPMLSGSEYELPEDPRHWEARDRLIIGKPLGE
GCTGVVMAEAIGLDKPKNVTKVAVKMLKSDASEKDLSDLISEMCMKMKICKHNI
INLLGACTQDGPLYIVYETYSKGNLREYLRARPPEMEYCYNPTCVDPDLSFKDLVS
CAYOVGMDYTLASKKCIHRDLAARNVLTEDINMKIADFLARDIUIHDIYKKTNG
RLPYKMAPEALFDRIYTHOSDVMSFGVLLWEITFGGSPYGPVPMEEFLKLLKEGHR
MDKPTNCTNELYMMKDCWHAMPSQRTFNQLVEDLRLIALSSNQEYLDLSPVNOY
SCPDPTRSRSTCSSGDSVFSHDPLDPDPCLPKYSGNGLKKR"
154..216
/gene="XFGFRA2"
217..2325
/gene="XFGFRA2"
/product="fibroblast growth factor receptor"
BASE COUNT 740 a 672 c 635 g 706 t
ORIGIN

Query Match 5.7%; Score 27; DB 5; Length 2753;
Best Local Similarity 100.0%; Pred. No. 0.00039;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 69 aaagtgcacacagacacgtggctgc 95
|||||
Db 1722 AAAGTGCATCCACAGACCTGGCTGC 1748

RESULT 21
LOCUS XLU24491 3634 bp mRNA linear VRT 02-FEB-1996
DEFINITION Xenopus laevis fibroblast growth factor receptor-1 mRNA, complete cds.
ACCESSION U24491 M61687 M37201
VERSION U24491.1 GI:857677
KEYWORDS African clawed frog.
SOURCE Xenopus laevis
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
REFERENCE 1 (bases 1 to 2439)
AUTHORS Musci,T.J., Amaya,E. and Kirschner,M.W.
TITLE Regulation of the fibroblast growth factor receptor in early Xenopus embryos
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (21), 8365-8369 (1990)
MEDLINE 91045998
KEYWORDS 2 (bases 2440 to 3634)
AUTHORS Robbie,E.P., Peterson,M., Amaya,E. and Musci,T.J.
TITLE Temporal regulation of the Xenopus FGF receptor in development: a

JOURNAL MEDLINE REFERENCE 3 (bases 1 to 3634) AUTHORS Musci,T.J. JOURNAL Direct Submission Submitted (11-APR-1995) Thomas J. Musci, Dept. of OB/GYN, University of California, San Francisco, Box 0556, San Francisco, CA 94143, USA COMMENT On Jun 12, 1995 this sequence version replaced gi:214137. FEATURES Location/Qualifiers source 1. .3634 /organism="Xenopus laevis" /db_xref="taxon:8355" CDS 1. .2439 /codon_start=1 /product="fibroblast growth factor receptor-1" /protein_id="AAA86868.1" /db_xref="GI:857678" /translation="MFSGRSLLLGWVLLGAALSVARPPSTLPDVEAPKTKTEVEPYSAPGCDRITLQCLREDVQSINWKNQVQLSETNTRITGEEIOISNAGPEDNGVYACVTNGSRITYVLCVNVSDALPSAEDDDDDSSSEKAENSKPNRPLSHPEKMEKKLHAPAAKTVKFCRPAANGTPTPLRLWLNKRRAFQQDQRIQGYKVRSTQWLSLIMDSVVP SDQGNVTCIVENKYGTINHTYQLDVVERSPHRPILOAGLPANTSVTGTAAEFSDAQO YTCLAANSIGISHSNAWLTIVKVEDNKPALLASPLQLEIIIIYCTGAAPVSAMVVTIIII FKMKHPSKKSDNSQLAVHKLAKSIPVRQVTVSGDSSMSGCVILVRRLSSGTPM LSGLSEVELPEDPRWEVARDRLILGKPLGEGCFQVVMFAEIGLDEKPNKVTQKAVK MLKSDASEKDLISSEMENMKIGKHKNIINLLGACTQDGPLYVIVETSKGNLREY LRRARRPAMEYTCVCPDQLLSFKDLVSCAYOVARGMDYLASKCIIHDLAARNVL VLEDTNMTKIDFGLARDIHHIDYKTTNGRLPVKMAPEALFDRIYTHQSDVMVSGV LLWEIFTLGSGPYGVPMEELFKLLKEGHRMDKPTNCTNELYMMKDCWHAMPQSORT FNOLVEDLRLALSSNQEYLDLSMPVNYQSPCFPDRSRSTSCSGSDSMFSDHPLPDE PCLPKYSNGGLKKR" 2440. .3634 3'UTR misc_feature 2440. .2619 /note="translational inhibitory regulatory element contained within the 3' UTR" BASE COUNT 1015 a 827 c 806 g 986 t ORIGIN

translation inhibitory element in the 3' untranslated region Development 121 (6), 1775-1785 (1995) 95324403 3 (bases 1 to 3634) Musci,T.J. Direct Submission Submitted (11-APR-1995) Thomas J. Musci, Dept. of OB/GYN, University of California, San Francisco, Box 0556, San Francisco, CA 94143, USA On Jun 12, 1995 this sequence version replaced gi:214137. Location/Qualifiers source 1. .3634 /organism="Xenopus laevis" /db_xref="taxon:8355" CDS 1. .2439 /codon_start=1 /product="fibroblast growth factor receptor-1" /protein_id="AAA86868.1" /db_xref="GI:857678" /translation="MFSGRSLLLGWVLLGAALSVARPPSTLPDVEAPKTKTEVEPYSAPGCDRITLQCLREDVQSINWKNQVQLSETNTRITGEEIOISNAGPEDNGVYACVTNGSRITYVLCVNVSDALPSAEDDDDDSSSEKAENSKPNRPLSHPEKMEKKLHAPAAKTVKFCRPAANGTPTPLRLWLNKRRAFQQDQRIQGYKVRSTQWLSLIMDSVVP SDQGNVTCIVENKYGTINHTYQLDVVERSPHRPILOAGLPANTSVTGTAAEFSDAQO YTCLAANSIGISHSNAWLTIVKVEDNKPALLASPLQLEIIIIYCTGAAPVSAMVVTIIII FKMKHPSKKSDNSQLAVHKLAKSIPVRQVTVSGDSSMSGCVILVRRLSSGTPM LSGLSEVELPEDPRWEVARDRLILGKPLGEGCFQVVMFAEIGLDEKPNKVTQKAVK MLKSDASEKDLISSEMENMKIGKHKNIINLLGACTQDGPLYVIVETSKGNLREY LRRARRPAMEYTCVCPDQLLSFKDLVSCAYOVARGMDYLASKCIIHDLAARNVL VLEDTNMTKIDFGLARDIHHIDYKTTNGRLPVKMAPEALFDRIYTHQSDVMVSGV LLWEIFTLGSGPYGVPMEELFKLLKEGHRMDKPTNCTNELYMMKDCWHAMPQSORT FNOLVEDLRLALSSNQEYLDLSMPVNYQSPCFPDRSRSTSCSGSDSMFSDHPLPDE PCLPKYSNGGLKKR" 2440. .3634 3'UTR misc_feature 2440. .2619 /note="translational inhibitory regulatory element contained within the 3' UTR" BASE COUNT 1015 a 827 c 806 g 986 t ORIGIN

Query Match 5.7%; Score 27; DB 5; Length 3634; Best Local Similarity 100.0%; Pred. No. 0.00039; Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 69 aaagtgcacccagagacctgctgc 95
|||||
Db 1833 AAGTGCATCCACAGACCTGGCTGC 1859

RESULT 22
LOCUS XELX1FGFR 3815 bp mRNA linear VRT 28-APR-1993
DEFINITION Xenopus laevis fibroblast growth factor receptor mRNA, complete cds.
ACCESSION M55163
VERSION M55163.1 GI:214893
KEYWORDS fibroblast growth factor receptor.
SOURCE xenopus laevis XTC cell line, cDNA to mRNA.
ORGANISM xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Piploidea; Pipidae;
Xenopodinae; Xenopus.
Friesel,R.E. and Dawid,I.B.
TITLE cDNA cloning and developmental expression of fibroblast growth factor receptors from Xenopus laevis
Mol. Cell. Biol. 11, 2481-2488 (1991)
JOURNAL MEDLINE REFERENCE 91203867
Location/Qualifiers source 1. .3815 /organism="Xenopus laevis"

/db_xref="taxon:8355"
/cell_line="XTC"
1. .3815
/gene="X1FGFR"
137. .2581
/gene="X1FGFR"
/codon_start=1
/product="fibroblast growth factor receptor"
/protein_id="AAA49990.1"
/db_xref="GI:214894"
/translation="MFSGRSLLLGWVLLGAALSVARPPSTLPDVEAPKTKTEVEPYSAPGCDRITLQCLREDVQSINWKNQVQLSETNTRITGEEIOISNAGPEDNGVYACVTNGSRITYVLCVNVSDALPSAEDDDDDSSSEKAENSKPNRPLSHPEKMEKKLHAPAAKTVKFCRPAANGTPTPLRLWLNKRRAFQQDQRIQGYKVRSTQWLSLIMDSVVP SDQGNVTCIVENKYGTINHTYQLDVVERSPHRPILOAGLPANTSVTGTAAEFSDAQO YTCLAANSIGISHSNAWLTIVKVEDNKPALLASPLQLEIIIIYCTGAAPVSAMVVTIIII FKMKHPSKKSDNSQLAVHKLAKSIPVRQVTVSGDSSMSGCVILVRRLSSGTPM LSGLSEVELPEDPRWEVARDRLILGKPLGEGCFQVVMFAEIGLDEKPNKVTQKAVK MLKSDASEKDLISSEMENMKIGKHKNIINLLGACTQDGPLYVIVETSKGNLREY LRRARRPAMEYTCVCPDQLLSFKDLVSCAYOVARGMDYLASKCIIHDLAARNVL VLEDTNMTKIDFGLARDIHHIDYKTTNGRLPVKMAPEALFDRIYTHQSDVMVSGV LLWEIFTLGSGPYGVPMEELFKLLKEGHRMDKPTNCTNELYMMKDCWHAMPQSORT FNOLVEDLRLALSSNQEYLDLSMPVNYQSPCFPDRSRSTSCSGSDSMFSDHPLPDE PCLPKYSNGGLKKR" 137. .199
sig_peptide
mat_peptide
/gene="X1FGFR"
200. .2578
/gene="X1FGFR"
/product="fibroblast growth factor receptor"
BASE COUNT 1030 a 879 c 881 g 1025 t ORIGIN

Query Match 5.7%; Score 27; DB 5; Length 3815; Best Local Similarity 100.0%; Pred. No. 0.00039; Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 69 aaagtgcacccagagacctgctgc 95
|||||
Db 1975 AAGTGCATCCACAGACCTGGCTGC 2001

RESULT 23
LOCUS AF402786 4254 bp mRNA linear ROD 11-OCT-2001
DEFINITION Rattus norvegicus receptor tyrosine kinase VEGFR-3kt (Vegfr3) mRNA, complete cds, alternatively spliced.
ACCESSION AF402786
VERSION AF402786.1 GI:16033529
KEYWORDS
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 4254)
AUTHORS Krishnan,J. and Sleeman,J.P.
TITLE Characterization of a novel alternatively spliced form of VEGFR-3
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 4254)
AUTHORS Krishnan,J. and Sleeman,J.P.
TITLE Direct Submission
Submitted (25-JUL-2001) Institut fuer Toxikologie und Genetik, Forschungszentrum Karlsruhe, Postfach 3640, Karlsruhe 76021, Germany
Location/Qualifiers source 1. .4254 /organism="Rattus norvegicus" /strain="Sprague-Dawley" /db_xref="taxon:10116" 1. .4254 /gene="Vegfr3"

CDS 1..3279
/gene="Vegfr3"
/note="kinase domain truncated form of VEGFR-3;
alternatively spliced"
/codon_start=1
/product="receptor tyrosine kinase VEGFR-3kt"
/protein_id="AAL13270.1"
/db_xref="GI:16033530"
/translation="MOPGAALNRRLWLCGLGLOGLANGYSWTPPTLNITEDSYVIDTG
DSLISCRGHPLEMTWRGAQEVLTGGKSESDTOVVDCEGTEARPYCKVLSLAQTH
ANNSTGYCYIKARIEGTTAASTYVVRDFEQPTINKPDTLLNVRKDSMMVPCLV
SIPGLNITLRSSQSVLHPDGOEVLMDRRGRVPTLLLRDALYLCQETTWGDDOFLSN
PFLVHITGNELYDQLYPKKSLELLVGEKLVNCTVMAEFDGVTFDMDYPGKOAERA
KWVPRSSOOTHTELSLTLTHVNSQHDLPYVCEANNGIQQFRESTEVIIVHEKPFIS
VENLKGVPLEATAGDEMVKLPVLAAYPPPEFQWYKDKKAVTGRHNPALVKEVTEA
SAGVYTLALNSAAGLRONTISLELVNVPVPHIHEKEASSPSIYSRHSRQTLTCTYGV
POPUSVQWHRPMTPKCTFAQRSLRRRQPDQMPQCRDKKEVTTQDAVNPIESLDTWT
ESVEGKNKTVSKLVIQDANVSAMTKVFNKVGQDERLIYFYVTTIPDGFSIESEPE
DPLEGQSVRLSCRADNTYIEHLRMYRLNLSLTHDAQGNPLLLDCKNVHLFATPLEANL
EEAEPGARHATLSLNIIPVAPEDGEDYVCEVQDRRSQDKHCKKYLVSQALFAPRLTQ
NLTDLLVNRVTSLEMRCPVAGAHVPSIWMYKDERLLEKESGIDLADSNQRLSIORVRE
EDAGRYLCSVCNAKGCNVSSAVAGESEDKGSMEIYLIGTVGVVFFVWVLLLIIFC
NMKRPAAHAIKTGYLSIIMDPGEVPLEEOCEYLSYDSQWMEFFPRERHLGRVLGHGAF
GKVVESAFGINKGSSCDTVAVKMLKEGATASEHRLMSELKILIHGNHLNVNLLG
ACTKPNGLPMVIVFCKYGNLSNFKVRETFDPAEKSPQRRFRAMVEGAKADRR
RLGSTDRALFTRFLMGKSARRAPFVQEAEDLWLSPLTMEDLVCSYQVARGMEFLAS
KVYTTOSDVMSFCVLLWEIFSLGASPYGVQINEEFCORLKDCTRMKHAPELATPAIRH
IMSCSGCDPKARPASDLVEIIGDLLQGGQWEEBEECHALSSQSEEDGPMOAST
TALHITDAEASSPPSHCHSLAARYNYVSPFGRVLRGTAKPGSSNMKTFTEELPMTP
TTYKASVDNQTDSCMVLASEEFOIESRHQEGSFSRKQDGHMDISRGHPDQGRRR
RPTQGAQGGKVFYNNYGEVSPQCTGDCGCPGSGTFFADSNT"
BASE COUNT 1008 a 1260 c 1259 g 833 t
ORIGIN
Query Match 5.7%; Score 27; DB 10; Length 4360;
Best Local Similarity 100.0%; Pred. No. 0.00039;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 79 cacagagacctgctgctcggaacatt 105
|||||
Db 3103 CACAGAGACCTGGCTGCTCGGAACATT 3129
RESULT 25
AF402785 4360 bp mRNA linear ROD 11-OCT-2001
LOCUS Rattus norvegicus receptor tyrosine kinase VEGFR-3 (Vegfr3) mRNA,
DEFINITION complete cds, alternatively spliced.
ACCESSION AF402785
VERSION AF402785.1 GI:16033526
KEYWORDS Norway rat.
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 4360)
AUTHORS Krishnan,J. and Sleeman,J.P.
TITLE Characterization of a novel alternatively spliced form of VEGFR-3
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 4360)
AUTHORS Krishnan,J. and Sleeman,J.P.
TITLE Direct Submission
JOURNAL Submitted (25-JUL-2001) Institut fuer Toxikologie und Genetik,
Forschungszentrum Karlsruhe, Postfach 3640, Karlsruhe 76021,
Germany
FEATURES Location/Qualifiers
1. 4360
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
1. 4360
/gene="Vegfr3"
1. 4092
/gene="Vegfr3"

CDS 989 a 1236 c 1224 g 805 t
ORIGIN
Query Match 5.7%; Score 27; DB 10; Length 4254;
Best Local Similarity 100.0%; Pred. No. 0.00039;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 79 cacagagacctgctgctcggaacatt 105
|||||
Db 3103 CACAGAGACCTGGCTGCTCGGAACATT 3129
RESULT 24
AF402785 4360 bp mRNA linear ROD 11-OCT-2001
LOCUS Rattus norvegicus receptor tyrosine kinase VEGFR-3 (Vegfr3) mRNA,
DEFINITION complete cds, alternatively spliced.
ACCESSION AF402785
VERSION AF402785.1 GI:16033526
KEYWORDS Norway rat.
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 4360)
AUTHORS Krishnan,J. and Sleeman,J.P.
TITLE Characterization of a novel alternatively spliced form of VEGFR-3
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 4360)
AUTHORS Krishnan,J. and Sleeman,J.P.
TITLE Direct Submission
JOURNAL Submitted (25-JUL-2001) Institut fuer Toxikologie und Genetik,
Forschungszentrum Karlsruhe, Postfach 3640, Karlsruhe 76021,
Germany
FEATURES Location/Qualifiers
1. 4360
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
1. 4360
/gene="Vegfr3"
1. 4092
/gene="Vegfr3"

*	114730	116364: contig of 1635 bp in length	/gene="MAPK" /codon_start=1 /product="mitogen-activated protein kinase (p42)" /protein_id="CAA41548.1" /db_xref="GI:53002" /db_xref="MGD:MGI:105919" /translation="MAAAGAGPMVRGVDFGPRYTNLSYIGEGAYGMVCSAYDNL KVRVAIKTISPFEHQYTCORTLEIKILLRFRHNTIGINDIIRAPTIEOMKDYIV QDMETDLYKLLKTOHLSNDHCYFLYOILRLGKYIHSANVLRDLKPSNLLNTTCD LKICDFGLARVADPDHDTGFLTEVATRWYRAPEIMLSKNGYTKSIDINWSVGCILAE MLSNRPFPCKKHVLDOLNHLILGILGSPQEDLNCIINKARNYLLSLPHKNKVPNRL FPNADSRALDLDLRLTFNPKRIEVEQALAHPLYEYDPSDEPTAEAPFKDFMELD DLPKEKLELIFEETARFQPGYRS"
	114730	116364: contig of 1635 bp in length	
*	116365	116464: gap of unknown length	BASE COUNT 339 a 313 c 285 g 319 t ORIGIN
*	116465	118200: contig of 1736 bp in length	
*	118201	118300: gap of unknown length	Query Match 5.5%; Score 26; DB 10; Length 1256; Best Local Similarity 100.0%; Pred. No. 0.0015; Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
*	118301	119330: contig of 1230 bp in length	
*	119331	119630: gap of unknown length	Oy 130 aagatctgtgacttggccttgcccg 155 Db 502 AAGATCTGTGACTTTGGCCTTGCCCG 527
*	119631	121318: contig of 1688 bp in length	
*	121319	121418: gap of unknown length	RESULT 27 AR016532 LOCUS AR016532 1467 bp DNA linear PAT 05-DEC-1998 DEFINITION Sequence 3 from patent US 5776751. ACCESSION AR016532 VERSION AR016532.1 GI:3972809 KEYWORDS SOURCE Unknown. ORGANISM Unclassified. REFERENCE 1 (bases 1 to 1467) AUTHORS Boulton,T.G., Cobb,M.H., Yancopoulos,G.D., Nye,S. and Panayotatos,N. TITLE Family of MAP2 protein kinases JOURNAL Patent: US 5776751-A 3 07-JUL-1998; FEATURES Location/Qualifiers 1. .1467 source /organism="unknown" BASE COUNT 365 a 382 c 355 g 365 t ORIGIN
*	121419	122620: contig of 1202 bp in length	
*	122621	122720: gap of unknown length	Query Match 5.5%; Score 26; DB 6; Length 1467; Best Local Similarity 100.0%; Pred. No. 0.0015; Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
*	124128	124128: contig of 1408 bp in length	
*	124129	124228: gap of unknown length	Oy 130 aagatctgtgacttggccttgcccg 155 Db 655 AAGATCTGTGACTTTGGCCTTGCCCG 680
*	124229	126159: contig of 1931 bp in length	
*	126160	126259: gap of unknown length	RESULT 28 AR036245 LOCUS AR036245 1467 bp DNA linear PAT 29-SEP-1999 DEFINITION Sequence 3 from patent US 5872006. ACCESSION AR036245 VERSION AR036245.1 GI:5952913 KEYWORDS SOURCE Unknown. ORGANISM Unclassified. REFERENCE 1 (bases 1 to 1467) AUTHORS Boulton,T.G., Cobb,M.H., Yancopoulos,G.D., Nye,S. and Panayotatos,N. TITLE Family of MAP2 protein kinases JOURNAL Patent: US 5872006-A 3 16-FEB-1999;
*	126260	128394: contig of 2135 bp in length	
*	128395	128494: gap of unknown length	Query Match 5.7%; Score 27; DB 2; Length 161580; Best Local Similarity 100.0%; Pred. No. 0.00038; Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
*	128495	130496: contig of 2002 bp in length	
*	130497	130596: gap of unknown length	Oy 79 cacagagacctggctgcgaacatt 105 Db 25724 CACAGAGACTGGCTGCTCGGAACATT 25698
*	130597	132111: contig of 1515 bp in length	
*	132112	132211: gap of unknown length	RESULT 26 MMAPK42 LOCUS MMAPK42 1256 bp mRNA linear ROD 02-FEB-1999 DEFINITION Mouse MAPK mRNA for mitogen-activated protein kinase (p42). ACCESSION X58712 VERSION X58712.1 GI:53001 KEYWORDS mitogen-activated protein kinase; protein kinase. SOURCE Mus musculus house mouse. ORGANISM Mus musculus REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 1256) Her,J.J.H. Direct Submission Submitted (03-APR-1991) J.H. Her, University of Virginia, Dept of Microbiology and, Cancer Center Box 441, School of Medicine, Charlottesville VA 22908, USA 2 (bases 1 to 1256) Her,J.H., Wu,J., Rall,T.B., Sturgill,T.W. and Weber,M.J. Sequence of pp42/MAP kinase, a serine/threonine kinase regulated by tyrosine phosphorylation Nucleic Acids Res. 19 (13), 3743 (1991)
*	132212	132294: contig of 1083 bp in length	
*	132295	133394: gap of unknown length	source 1. .1256 /organism="Mus musculus" /strain="swiss" /db_xref="taxon:10090" /cell_line="3T3" /tissue_type="fibroblast" /clone_lib="lambda gt10" 1. .1256 /gene="MAPK" /evidence=experimental 1. .1256 /gene="MAPK" 19. .1095
*	133395	134851: contig of 1457 bp in length	
*	134852	134951: gap of unknown length	mrna gene CDS
*	134952	136002: contig of 1051 bp in length	
*	136003	136102: gap of unknown length	

FEATURES
source Location/Qualifiers
1..1467
/organism="unknown"
BASE COUNT 365 a 382 c 355 g 365 t
ORIGIN

Query Match 5.5%; Score 26; DB 6; Length 1467;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 aagatctgtgactttggccttgcccg 155
|||||
DB 655 AAGATCTGTGACTTTGGCCTTGCCCG 680

RESULT 29

LOCUS ARI171291 1467 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 3 from patent US 6297035.
ACCESSION ARI171291
VERSION ARI171291.1 GI:17910241
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1467)
AUTHORS Boulton,T.G., Cobb,M.H., Yancopoulos,G.D., Nye,S. and Panayotatos,N.
TITLE ERK1 MAP2 protein kinase
JOURNAL Patent: US 6297035-A 3 02-OCT-2001;
FEATURES Location/Qualifiers
source 1..1467
/organism="unknown"
BASE COUNT 365 a 382 c 355 g 365 t
ORIGIN

Query Match 5.5%; Score 26; DB 6; Length 1467;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 aagatctgtgactttggccttgcccg 155
|||||
DB 655 AAGATCTGTGACTTTGGCCTTGCCCG 680

RESULT 30

LOCUS ARI172792 1467 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 3 from patent US 6303359.
ACCESSION ARI172792
VERSION ARI172792.1 GI:17912283
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1467)
AUTHORS Boulton,T.G., Cobb,M.H., Yancopoulos,G.D., Nye,S. and Panayotatos,N.
TITLE ERK3 MAP2 protein kinase
JOURNAL Patent: US 6303359-A 3 16-OCT-2001;
FEATURES Location/Qualifiers
source 1..1467
/organism="unknown"
BASE COUNT 365 a 382 c 355 g 365 t
ORIGIN

Query Match 5.5%; Score 26; DB 6; Length 1467;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130

aagatctgtgactttggccttgcccg 155
|||||
DB 655 AAGATCTGTGACTTTGGCCTTGCCCG 680

RESULT 31

LOCUS I34200 1467 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 3 from patent US 5595904.
ACCESSION I34200
VERSION I34200.1 GI:1824991
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1467)
AUTHORS Boulton,T.G., Cobb,M.H., Yancopoulos,G.D., Nye,S. and Panayotatos,N.
TITLE Family of map2 protein kinases
JOURNAL Patent: US 5595904-A 3 21-JAN-1997;
FEATURES Location/Qualifiers
source 1..1467
/organism="unknown"
BASE COUNT 365 a 382 c 355 g 365 t
ORIGIN

Query Match 5.5%; Score 26; DB 6; Length 1467;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 aagatctgtgactttggccttgcccg 155
|||||
DB 655 AAGATCTGTGACTTTGGCCTTGCCCG 680

RESULT 32

RATERK2
LOCUS Rat extracellular signal-related kinase (ERK2) mRNA ROD 27-APR-1993
DEFINITION M64300
ACCESSION M64300
VERSION M64300.1 GI:204055
KEYWORDS extracellular signal-related kinase; protein kinase; protein serine/threonine kinase.
SOURCE Rat adult brain, cDNA to mRNA.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 1467)
AUTHORS Boulton,T.G., Nye,S.H., Robbins,D.J., Ip,N.Y., Radziejewska,E., Morgenbesser,S.D., Depinho,R.A., Panayotatos,N., Cobb,M.H. and Yancopoulos,G.D.
TITLE ERKs: A family of protein-serine/threonine kinases that are activated and tyrosine phosphorylated in response to insulin and NGF
JOURNAL Cell 65, 663-675 (1991)
MEDLINE 91235302
FEATURES Location/Qualifiers
source 1..1467
/organism="Rattus norvegicus"
/db_xref="taxon:10116"
/tissue_type="brain"
/dev_stage="adult"
/tissue_lib="lambda-ZAP2"
1..1467
/gene="ERK2"
172..1248
/gene="ERK2"
/note="presumed coding region"
/codon_start=1
/product="extracellular signal-related kinase 2"
/protein_id="AAA41124.1"

```

/db_xref="GI:204056"
/translation="MAAAAAAGPEMVRGVDFDVGPRYTNLSTYIGEGAYGMVCSAYDNL
NKVRVAIKTISPEHQTQRTREIKILLRFRHENIGINDIRAPTEQMKDVTIV
QDLMETDLYLKLTQHSNDHICYFLYQILRGLKYIHSANVLHRLKPSNLLNTTCD
LKICDFGLARVADPDHDTGFLTEYVATRWYRAPEIMLNSKGYTKSIDTWSVCILAE
MLSNRPIFCCKHYLDOLNHLTGLGSPSOEDLNCIINLKARNYLLSLPHKNKVPWNRLL
FPNADSKALDLDLKKMLTFNPHKRIEVEQALAIUPLYEQYDPSDEPIAEAFKDFMELD
DLPKELKELIFEETARFPQYRS"
BASE COUNT      365 a      382 c      355 g      365 t
ORIGIN

Query Match      5.5%; Score 26; DB 10; Length 1467;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 130 aagatctgtgacttggccttgccg 155
|||||
Db 655 AAGATCTGTGACTTTGGCCTTGCCCG 680

RESULT 33
S65207 LOCUS      1534 bp      mRNA      linear      VRT 02-NOV-1993
DEFINITION      endothelial kinase Quek2-vascular endothelial growth factor
receptor homolog [Coturnix coturnix-queals, ssp. japonica, E4
embryo, mRNA Partial, 1534 nt].
ACCESSION      S65207.1 GI:410682
VERSION        1
KEYWORDS
SOURCE
ORGANISM
common quail E4 embryo ssp. japonica.
Coturnix coturnix
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Coturnix.
1 (bases 1 to 1534)
Eichmann,A., Marcelle,C., Breant,C. and Le Douarin,N.M.
Two molecules related to the VEGF receptor are expressed in early
endothelial cells during avian embryonic development
Mech. Dev. 42 (1-2), 33-48 (1993)
93378866
GenBank staff at the National Library of Medicine created this
entry [NCBI gibbsq 137164] from the original journal article.
This sequence comes from Fig. 2.
FEATURES
source      1..1534
Location/Qualifiers
/organism="Coturnix coturnix"
/db_xref="taxon:9091"
1..1534
/partial
/gene="endothelial kinase Quek2"
1..1104
/partial
/gene="endothelial kinase Quek2"
/note="vascular endothelial growth factor receptor
homolog; human vascular endothelial growth factor receptor
homolog; ; This sequence comes from Fig. 2"
/codon_start=1
/product="endothelial kinase Quek2"
/protein_id="AAB28128.1"
/db_xref="GI:410683"
/translation="WMDLQWSPLTMEDLICYSFQVARGMEFLASRKCIRHDLAARNIL
LSENNVYKICDFGLARDIYKDPDYVRKSGARLPLKMWAPESIFDKVYTTQSDVMSLGV
LLWEIFSLGASPGVQIINEFCQRFKDGTRMRAPETTAETAIYRIMLSCHWGGPKERP
TFSDLVLEILLNLOENVOOEKDYIPLNDSHSSDDGFSQVPSQAQNSDEEDFDRI
RCHSLAARYNCVSPFGLCGNOIRCSSRIKTFEFPMTHTMKAPDNQDTSGMVL
GESEFEIENNRKRGFCSSKGNPRTAELSAEQSDLRGCRPSYGSQVGGQTFYNSEY
GEIUSEHSEDRSCTPPAEAGSPPALHASFFSEQY"
BASE COUNT      388 a      417 c      389 g      340 t
ORIGIN

Query Match      5.5%; Score 26; DB 5; Length 1534;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 64 tccgaaagtgcattccacagagacct 89
|||||
Db 88 TCCCGAAGTGCATCCACAGAGACCT 113

RESULT 34
MUSERK2 LOCUS      1747 bp      mRNA      linear      ROD 03-FEB-1999
DEFINITION      Mouse mRNA for ERK2, complete cds.
ACCESSION      D10939
VERSION        D10939.1 GI:220994
KEYWORDS
SOURCE
Mus musculus (strain C57 black B6) brain (cell line mouse whole
brain) cDNA to mRNA, clone G1A.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Takishima,K.
1 (bases 1 to 1747)
Direct Submission
Submitted (10-APR-1993) Kunito Takishima, National Defense Medical
College; Namiki 3-2, Tokorozawa, Saitama 359, Japan
(Tel:0429-95-1211(ex.2294), Fax:0429-95-0638)
2 (bases 1 to 1747)
Her,J.H., Wu,J., Hall,T.B., Sturgill,T.W. and Weber,M.J.
Sequence of pp42/MAP kinase, a serine/threonine kinase regulated by
tyrosine phosphorylation
Nucleic Acids Res. 19 (13), 3743 (1991)
91305126
3 (bases 1 to 1747)
Takishima,K.
unpublished (1992)
Submitted (10-Apr-1993) to DDBJ by:
Kunito Takishima
National Defence Medical College
3-2 Namiki
Tokorozawa, Saitama 359
Japan
Phone: 0429-95-1211 x2294
Fax: 0429-95-0638.
FEATURES
source      1..1747
Location/Qualifiers
/organism="Mus musculus"
/strain="C57 black B6"
/db_xref="taxon:10090"
/cell_line="mouse whole brain"
/tissue_type="Brain"
/dev_stage="Adult"
61..1137
/codon_start=1
/product="ERK2"
/protein_id="BAA01733.1"
/db_xref="GI:286076"
/translation="MAAAAAAGPEMVRGVDFDVGPRYTNLSTYIGEGAYGMVCSAYDNL
NKVRVAIKTISPEHQTQRTREIKILLRFRHENIGINDIRAPTEQMKDVTIV
QDLMETDLYLKLTQHSNDHICYFLYQILRGLKYIHSANVLHRLKPSNLLNTTCD
LKICDFGLARVADPDHDTGFLTEYVATRWYRAPEIMLNSKGYTKSIDTWSVCILAE
MLSNRPIFCCKHYLDOLNHLTGLGSPSOEDLNCIINLKARNYLLSLPHKNKVPWNRLL
FPNADSKALDLDLKKMLTFNPHKRIEVEQALAIUPLYEQYDPSDEPIAEAFKDFMELD
DLPKELKELIFEETARFPQYRS"
BASE COUNT      502 a      364 c      413 g      468 t
ORIGIN

Query Match      5.5%; Score 26; DB 10; Length 1747;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 130 aagatctgtgacttggccttgccg 155

```

```
|||||
Db 544 AAGATCTGACTTTGGCCTTGCCCG 569

RESULT 35
A84443
LOCUS A84443 1815 bp DNA linear PAT 21-JAN-2000
DEFINITION Sequence 58 from Patent W09845704.
ACCESSION A84443
VERSION A84443.1 GI:67333362
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE A METHOD FOR EXTRACTING QUANTITATIVE INFORMATION RELATING TO AN
JOURNAL INFLUENCE ON A CELLULAR RESPONSE
TULLIN SOEREN (DK); KASPER ALMHOLT (DK)
FEATURES
Source 1..1815
Location/Qualifiers
/organism="unidentified"
/db_xref="taxon:32644"
CDS
1..1815
/note="unnamed protein product"
/codon_start=1
/db_xref="GI:67333363"
/translocation="MAAAAGAPMVRGQVDFGPRYTNLSYIGAGYGMVCSAYDNL
NKVRVAIKKISPEHOYQORTLEIKILLRFRHNIIGINDIIRAPTIQMKDVIIV
QDLMEITLKLKTLQHLSDHICFYLYQILRLGLKYIHSANVLHRDLKPSNLLNTTCD
LKICDFGLARVADPDHDHGTGLTEYVATRWRAPEIMLSKSGVTKSIDISVGCILAE
MLSNRPFPCKHYLDOLNHLILGILGSPSQEDLNCIINLKARNYLLSLPHKNKVPWNL
FPNADKALDLQKMLTFNPKHRIEVEQALAHPLYEQYDPSDEPIAEAFKFDMLD
DLPEKKELIFETARFQCGYSMDPPVATNVSKEGEELFTGVVPIVLVDGVNGHK
FVSQGEGBGATYQKLFKFTTGLKLPVWPTLVTTLTYGVQCFSRYPDHMKOHDF
KSAMPEGYVIMADQKNGIRVNFIRHNIEDGSGVOLADHYQOONTPIGDPVLLPDNHY
LSTQSAKSPDNKRDHMLVLEFVTAAGITLGMDELYK"
BASE COUNT 480 a 506 c 451 g 378 t
ORIGIN

Query Match 5.5%; Score 26; DB 6; Length 1815;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 130 aagatctgtgactttggccttgcccg 155
|||||
Db 484 AAGATCTGACTTTGGCCTTGCCCG 509

RESULT 36
A84425
LOCUS A84425 1818 bp DNA linear PAT 21-JAN-2000
DEFINITION Sequence 40 from Patent W09845704.
ACCESSION A84425
VERSION A84425.1 GI:67333344
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE A METHOD FOR EXTRACTING QUANTITATIVE INFORMATION RELATING TO AN
JOURNAL INFLUENCE ON A CELLULAR RESPONSE
TULLIN SOEREN (DK); KASPER ALMHOLT (DK)
FEATURES
Source 1..1818
Location/Qualifiers
/organism="unidentified"
/db_xref="taxon:32644"
```

```
CDS
1..1818
/note="unnamed protein product"
/codon_start=1
/protein_id="CAB69292.1"
/db_xref="GI:67333345"
/translocation="MVSKEGEELFTGVVPIVLVDGVNGHKFSVSGEGGDATYGLKT
LKFICTGTLKLPVWPTLVTTLTYGVQCFSRYPDHMKOHDFPKSAMPEGYVQERTIFPK
DQGNKYTRAEVAFEGDTLVNRIELKIGIDFKEDGNILGHKLEYNYSNHYIIMADKQKH
GKVNFKIRHNIEDGSGVOLADHYQOONTPIGDPVLLPDNHYLSTQSAKSPDNKRDH
MYLLEEVTAAGITLGMDELYKSGLSRSVTMAAAAGAPMVRGQVDFGPRYTNLSYI
GEGAGYGMVCSAYDNLKNKRVAKKISPEHOYQORTLEIKILLRFRHNIIGINDIIR
APTIQMKDVIIVODLMETDLYKLLKTOHLSNDHICFYLYQILRLGLKYIHSANVLH
ROKPSNLLNTTCDLKICDFGLARVADPDHDHGTGLTEYVATRWRAPEIMLSKSGV
TKSIDISVGCILAEMLSNRPFPCKHYLDOLNHLILGILGSPSQEDLNCIINLKARNY
LTLSPHKNKVPWNLFPNADKALDLQKMLTFNPKHRIEVEQALAHPLYEQYDPSD
EPIAEAFKFDMLDLPKEKELIFETARFQCGYS"
BASE COUNT 482 a 505 c 451 g 380 t
ORIGIN

Query Match 5.5%; Score 26; DB 6; Length 1818;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 130 aagatctgtgactttggccttgcccg 155
|||||
Db 1225 AAGATCTGACTTTGGCCTTGCCCG 1250

RESULT 37
CCQUEK2 4617 bp mRNA linear VRT 03-DEC-1996
LOCUS C. coturnix Quek2 mRNA for vascular endothelial growth factor
DEFINITION
ACCESSION X83287
VERSION X83287.1 GI:619865
KEYWORDS growth factor receptor; Quek2 gene.
SOURCE common quail.
ORGANISM C. coturnix
REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
TITLES Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Coturnix.
JOURNAL 1 (bases 1 to 4617)
MEDLINE Elchmann,A., Marcelle,C., Breat,C. and Le Douarin,N.M.
AUTHORS Molecular cloning of Quek 1 and 2, two quail vascular endothelial
TITLES growth factor (VEGF) receptor-like molecules
JOURNAL Gene 174 (1), 3-8 (1996)
REFERENCE 97017121
MEDLINE 2 (bases 1 to 4617)
AUTHORS Marcelle,C.A.
TITLES Direct Submission
JOURNAL Submitted (02-DEC-1994) C.A. Marcelle, Univ. of California, Irvine.,
Dept. of Developmental and Cell Biology, Irvine, California 92717,
USA

FEATURES
Source Location/Qualifiers
1..4617
/organism="Coturnix coturnix"
/sub_species="japonica"
/db_xref="taxon:9091"
/tissue_type="whole embryo"
/dev_stage="embryo, 4 day"
/gene="Quek2"
49..4188
/gene="Quek2"
/codon_start=1
/product="vascular endothelial growth factor receptor"
/protein_id="CAA58267.1"
/db_xref="GI:1707416"
/translocation="MKRVCTLPWLWLGVISADLVSSYSMTPTLSITEEBHIINAK
DTLITCRGQHPLSNWPCARWTPVEGRRNWSQPOORPVGAGNPEEDCEGTGTPYC
KVLVLTSQANDTGYHCYKYIDAKIEGTAVSAYIFVRDFEQFPINKPELLISKK"
```

ENTWVPCIVSLIPDLNVTLLISONSLIHPRDKTIFPDNKKGVQVPTQLIRDSLVQCEVY
IDNKVFSNFTIIHAGIELYDIOLIFPKAMELLVGERKLVNLCVTWAEFNSGVRFQMT
YQKOMQRAVIESRSRQTHTESSILTLHNVSQQDLGRYTCATNAGQAOMLESTDV
IYHEKPEINVRKGPVIEATGAEVKLPVKVYVPPQDFQWYKAGKLIPKQSQSSM
QIKDVAEHGACTYTLVLRNLVGLKELISLQILVNVPPRIHEKETSPSIYSRSPQA
LTCVYGPAPVIEOWWRPMPCRMFSRSLNSRRAARRHORMRPECKDMKDVSR
ODAVNPYESIDTWVEFVEGRNKTYSKLAIOEANYSAMVKTASNKVGRDRLIYFYVT
TIPOGFELOSPESEPIEGQDLQLSNADNYTYENLOWYRLNLSKLHDEGNPLVLDC
KNVHYATKMOGELRPODSDNATLLTIPNISLGEEDYVCEVONRRTREKCHCKY
ISVQALEPRLKQNLTDIWNVSDSIEMRCKVGNHVPDIOSWYKDEKLVEVSGSIDIA
DFNQLYSIQRVEDAGLYLCSVNAKGVNSASVSVEGSDDKTNVEIILIGTVI
AVFFWILLIIFCNIKRPAHADIKTGYLSIIMDPGEVPLEEOCAIYLDQSKMFFPD
RHLGNLVNLLGACTKPNGLMVIYBECKYGNLSNVLRTKREGFSYREKSPRLIO
HIGHKLVGHGAFKVEASAFGINKNSCTVAAKMLKEGATASEOKALMSLKJLI
VOSIVEAVRDRRSRGTSDSAIFNRLMHKSQVQPIQEVDDVLQPLMEDLTCIS
PLKVMGMEFLASRCKIHRDLAARNLILSENNAVKICDFGLARDIYKDPDYVRKGSARL
RAPEYTTAEIYRIKMTQSDVMVSEFVLLWEIFSLGASPYPGVQINEFCORFKDGTSM
SEDDGFQSPVASQONSDIEDFDMIRIRCHSLAARYNCVSFPGCLTGNGNTRCSSLIK
TFEEFPMTHTWYKAHPNODTDSGMVLASEEPIERTENRRKEGGSFKGPNRTAELSAE
QSDLRGCRPSYSGVSGQTYNSEYGELSHSESDRSTCTPAGASPPALHASFSEQ
Y"

misc_feature 49..2411
/gene="Quek2"
/note="extracellular domain"
misc_feature 2412..2481
/gene="Quek2"
/note="transmembrane domain"
misc_feature 2614..3579
/gene="Quek2"
/note="tyrosine kinase domain"
BASE COUNT 1187 a 1233 c 1241 g 956 t
ORIGIN

Query Match 5.5%; Score 26; DB 5; Length 4617;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 64 tcccaaaagtcatcacagagacct 89
|||||
Db 3172 TCCCGAAGTGCATCACAGAGACCT 3197

RESULT 38
RATIGIRT
LOCUS Rattus norvegicus insulin-like growth factor I receptor mRNA, complete cds.
DEFINITION Rattus norvegicus insulin-like growth factor I receptor mRNA, complete cds.
ACCESSION L29232.1 GI:460333
VERSION L29232.1
KEYWORDS Norway rat.
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 4696)
Du,J. and Delafontaine,P.
AUTHORS Inhibition of vascular smooth muscle cell growth through antisense transcription of a rat insulin-like growth factor I receptor cDNA
TITLE Circ. Res. 76 (6), 963-972 (1995)
JOURNAL 95277910
MEDLINE 7758167
PUBMED
COMMENT On Mar 15, 1994 this sequence version replaced gi:459940.
FEATURES Location/Qualifiers
source 1..4696
/organism="Rattus norvegicus"
/db_xref="taxon:10116"
/tissue_type="brain"
/dev_stage="adult"
46..4158
/note="bp 136-2256: alpha subunit; bp 2257-2268: putative

protein cleavage site, RRRR; bp 2269-4158: beta subunit;
bp 2857-2907: putative trans-membrane domain; bp
3055-3825: putative tyrosine kinase domain; bp 658-838:
cysteine rich domain"
/codon_start=1
/product="insulin-like growth factor 1 receptor precursor"
/protein_id="AAA41392.1"
/db_xref="GI:460334
/translation="MKSGSGSGPTSLWGLVFLSAALSMLWPTSGEICGPGIDIRNDYO
QKRLNCTVIEGFLHILLISGAEDYSRFPKLTIVTEYLLLFVAGLESGLDFPN
LTVIRGKFLYALVIFEMTNLKDICGLYLRNITRGAIIRKNAADLCYLSLIDWLSL
LTVASNNYIVGNKPPKVEGDLCTLEEKPMCEKTTINNEYNYRMTNRCQKCPSL
CDRACTENNECCHEPCSCHTPDONTTCVACRHYVYKGVCPACPGYRFEQWRC
VDRFCANTPAESSDSDGPIVHDGCMQCSGFIINSTQSMYCIPECGPCPKVCGD
EERKTKTIDVTSQMLQGTILKLNLLINIRGNIIASELENFMGLIEVYTVYKIR
HSHALVSLFKNLRLILBEEQLEGNYFYVLDNQNLQQLDWNHNTLTIVRSQMMYFA
FNPKLCVSEIYRMEVETGTRQSGKIDINRNGRASCESDVLRTSTTWTKNRILII
TWIRYRPDPYDLISFTYVYKEAFKNVTEYDQDAGCSNMMNDVDLPNKEGEPG
ILLHLGKPMTOYAYVYKAVITWVNDHIRGAKSEILYIRTNASVPSIPLDVLSASNS
SSOLIVKWNPTLPNGNLVYIVRQROPDQGYLFRHNYCSKDIPIRKVADCTIDVE
EVTENKTEVCGGDKGPCACPKTEAKOAEKEAEYRKVEFNHLSIIVPSPERRR
RDVLQVANTMSSRNTVADTYNITDPEETETETPFESRVDNKERTVISNLRPFT
LYRIDTHSCNHEAEKLGCSASNFVARTMPAEGADDIPGVTWEPRPENSIFLKMPEP
ENPNGLILMYEIKYQVEDQRECVSRQYKYGGAKNLNLNFCNTARLQATLSGN
GSWTDVPFFVYPAKTYVNPDMHLIIALPVAIILTVGLVIMLYVFFHKKRNSRLGCV
LYASVNPYESAADVYVPDEMEVAREKITMNRLEGQSGFQVYEGVAKGVKDEPETR
VALKTVNEAASMRERIEFLNEASVMKEFNCHVVRLLGVVYSGOPTLVINELMTRGD
KSLRLSRPEVENNLLIPSLSKMTQAGEIADGHAYLNANKFVRDLAARNCMVAE
DFTVKGDFQMTDRIDYDIYRKGGKLLPVRWMSPESLADGFTTHSDVNSGVVLM
EIALAPQYOGLSNEQVLRVMEGGLLDKPDNCMDMLFELMRMCHWOYNPKMRPSFLE
IIGSIKDEMEPSFOEVSFYVSEENKPEPEELEMELEPEENMESVPLDPSASSALP
LPERHSGHKAENGPGVLVLRASFDERQPYAHMNGRANERALPLQSSSTC"
46..135
sig_peptide 136..4155
mac_peptide
3'UTR 4159..4696
BASE COUNT 1149 a 1270 c 1241 g 1036 t
ORIGIN

Query Match 5.5%; Score 26; DB 10; Length 4696;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 77 tccacagagacctgctcgctcggaac 102
|||||
Db 3443 TCCACAGAGACCTGCTCGTCTCGGAAC 3468

RESULT 39
D87264S4
LOCUS D87264S4 786 bp DNA linear ROD 14-APR-2000
DEFINITION Mus musculus DNA for ERK2, exon 4.
ACCESSION D87267
VERSION D87267.1 GI:2506068
KEYWORDS Erk2; extracellular signal-regulated kinase 2.
SEGMENT 4 of 8
SOURCE Mus musculus DNA.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (sites)
Sugiura,N., Suga,T., Ozeki,Y., Mamiya,G. and Takishima,K.
AUTHORS The mouse extracellular signal-regulated kinase 2 gene. Gene
TITLE structure and characterization of the promoter
J. Biol. Chem. 272 (34), 21575-21581 (1997)
JOURNAL 97407954
MEDLINE 2 (bases 1 to 786)
REFERENCE Takishima,K.
AUTHORS Direct Submission
TITLE Submitted (21-AUG-1996) Kunio Takishima, National Defense Medical
JOURNAL College, Department of Biochemistry I; Namiki 3-2, Tokorozawa,
Saitama 359, Japan (Tel:0429-95-1373, Fax:0429-96-5189)

FEATURES
source Location/Qualifiers
1. .786
/organism="Mus musculus"
/db_xref="taxon:10090"
intron <1..197
/number=3
exon 198..314
/number=4
intron 315..>786
/number=4
BASE COUNT 207 a 165 c 162 g 252 t
ORIGIN

Query Match 5.3%; Score 25; DB 10; Length 786;
Best Local Similarity 100.0%; Pred. No. 0.0057;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 131 agatctgtgacttggccttgcgcg 155
|||||
Db 196 AGATCTGTGACTTGGCCTTGCCTG 220
|||||

RESULT 40
AR062728 159 bp DNA linear PAT 29-SEP-1999
LOCUS
DEFINITION Sequence 19 from patent US 5843749.
ACCESSION AR062728
VERSION AR062728.1 GI:5990419
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 159)
AUTHORS Maisonnier,P.C., Masiakowski,P. and Yancopoulos,G.D.
TITLE Enh and Ror tyrosine kinases
JOURNAL Patent: US 5843749-A 19 01-DEC-1998;
LOCATION/Qualifiers
FEATURES
source 1..159
/organism="unknown"
BASE COUNT 38 a 36 c 51 g 34 t
ORIGIN

Query Match 4.9%; Score 23; DB 6; Length 159;
Best Local Similarity 100.0%; Pred. No. 0.085;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 124 gtggtgaagatctgtgactttgg 146
|||||
Db 22 GTGCTGAAGATCTGTGACTTTGG 44
|||||

RESULT 41
D50001S13 272 bp DNA linear PRI 14-APR-2000
LOCUS
DEFINITION Human DNA for alpha-platelet-derived growth factor receptor, exon 18.
ACCESSION D50013
VERSION D50013.1 GI:767793
KEYWORDS alpha-platelet-derived growth factor receptor; PDGFRA.
SEGMENT 13 of 17
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (sites)
AUTHORS Kawagishi,J., Kumabe,T., Yoshimoto,T. and Yamamoto,T.
TITLE Structure, organization, and transcription units of the human alpha-platelet-derived growth factor receptor gene, PDGFRA
JOURNAL Genomics 30 (2), 224-232 (1995)
MEDLINE 96163874
REFERENCE 2 (bases 1 to 272)

AUTHORS Kawagishi,J.
JOURNAL Unpublished (1996)
REFERENCE 3 (bases 1 to 272)
AUTHORS Kawagishi,J.
TITLE Direct Submission
JOURNAL Submitted (03-APR-1995) Jun Kawagishi, Tohoku University, Gene Research Center; 1-1 Tsutsumidouri-Anamiyamachi, Aobaku, Sendai, Miyagi 981, Japan (Tel:022-272-4321(ex.388, 389), Fax:022-263-9295)
FEATURES
source Location/Qualifiers
1..272
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="4"
/map="4q11-q13"
/tissue_type="blood"
intron <1..92
/gene="PDGFRA"
/number=17
exon 93..215
/gene="PDGFRA"
/number=18
intron 216..>272
/gene="PDGFRA"
/number=18
BASE COUNT 63 a 75 c 61 g 73 t
ORIGIN

Query Match 4.9%; Score 23; DB 9; Length 272;
Best Local Similarity 100.0%; Pred. No. 0.085;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 127 gtgaagatctgtgactttgcct 149
|||||
Db 147 GTGAAGATCTGTGACTTTGCCT 169
|||||

RESULT 42
MUS3RTK 429 bp mRNA linear ROD 30-DEC-1996
LOCUS
DEFINITION Mus musculus (clone FTS) receptor tyrosine kinase type III (did) mRNA, partial cds.
ACCESSION L36163
VERSION L36163.1 GI:537334
KEYWORDS receptor tyrosine kinase; tyrosine kinase.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 429)
AUTHORS Rosnet,O., Mattei,M.G., Marchetto,S. and Birnbaum,D.
TITLE Isolation and chromosomal localization of a novel FMS-like tyrosine kinase gene
JOURNAL Genomics 9, 380-385 (1991)
MEDLINE 91169547
FEATURES
source Location/Qualifiers
1..429
/organism="Mus musculus"
/strain="BALB/c"
/sub_species="domesticus"
/db_xref="taxon:10090"
/clone="FTS"
/tissue_type="testis"
/dev_stage="adult"
<1..>429
/note="domain 2"
/codon_start=1
/product="receptor tyrosine kinase"
/protein_id="AAB39407.1"
/db_xref="GI:537335"
/translation="EFLEFKSCVHRDLAARNVLVTHGKVKIKCDFGLARDILSDSSYV
VRGNARLPVKWNAPESLFEGITYIKSDVMSYGLLWEIFSLGVNPPGIPVDANFYKL
TQSGFKMEQPFYATEGIYFVMQSWAFDSKRKPSFPNLISF"

```

BASE COUNT      101 a      107 c      114 g      107 t
ORIGIN

Query Match      4.9%; Score 23; DB 10; Length 429;
Best Local Similarity 100.0%; Pred. No. 0.085;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 gtggtgaagatctgtgactttgg 146
|||||
Db 73 GTGGTGAAGATCTGTGACTTTGG 95

RESULT 43
LOCUS      AF178759      1525 bp      mRNA      linear      VRT 01-OCT-1999
DEFINITION Danio rerio flt4 protein mRNA, partial cds.
ACCESSION  AF178759
VERSION     AF178759.2 GI:6006041
KEYWORDS   .
SOURCE     zebrafish
ORGANISM   Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE  1 (bases 1 to 1525)
AUTHORS   Thompson,M.A., Ransom,D.G., Pratt,S.J., MacLennan,H., Kieran,M.W.,
            Detrich,H.W. III, Vail,B., Huber,T.L., Paw,B., Brownlie,A.J.,
            Oates,A.C., Fritz,A., Gates,M.A., Amores,A., Bahary,N.,
            Talbot,W.S., Her,H., Beier,D.R., Postlethwait,J.H. and Zon,L.I.
TITLE     The cloche and spadetail genes differentially affect hematopoiesis
            and vasculogenesis
JOURNAL   Dev. Biol. (NY) 197, 248-269 (1998)
REFERENCE  2 (bases 1 to 1525)
AUTHORS   Thompson,M.A., Ransom,D.G., Pratt,S.J., MacLennan,H., Kieran,M.W.,
            Detrich,H.W. III, Vail,B., Huber,T.L., Paw,B., Brownlie,A.J.,
            Oates,A.C., Fritz,A., Gates,M.A., Amores,A., Bahary,N.,
            Talbot,W.S., Her,H., Beier,D.R., Postlethwait,J.H. and Zon,L.I.
TITLE     Direct Submission
JOURNAL   Submitted (18-AUG-1999) Hematology/Oncology, Children's Hospital,
            300 Longwood Ave, Boston, MA 02115, USA
COMMENT   On Oct 1, 1999 this sequence version replaced gi:5917727.
FEATURES   Location/Qualifiers
            source      1..1525
                        /organism="Danio rerio"
                        /db_xref="taxon:7955"
                        /chromosome="14"
                        <!. .1216
                        /codon_start=2
                        /product="flt4 protein"
                        /protein_id="AAD56011.2"
                        /db_xref="GI:6006042"
                        /translation="GNLSNFLRAKREFFFLPYRDRSPKTSQVRRMIAGQASQSEHQP
                        STSTNPRVTVDLMKTPLTIEDLCYSQVARGMEFLASRKCIIHRDLAARNILUSE
                        NNVKICDFGLARDIYKDPYVRKGNARLPKWMAPESIFDKVYTSQSDVSFQVLLW
                        EIFSLSPGQIDEDCKRLKDGTRMRAPNASPEIYIGIMLACWQGEPRPRPTFP
                        ALVEILGDLQENSLPEIPFNVSOSSEDDGFSOASSRPPSQEETRLACNTLPTRYNC
                        VPFAGCVMGVSPSTCHSRVKTFEELPMEMTSKHTQHDSDTDSGMVLASDELEFEKH
                        RGMALTTATTGOSTDRILISCPVSVSSGSGGLLRVPVFTOLSGOTFYNNYGHLSSEG
                        VSYFSSDDAQ"
BASE COUNT      442 a      376 c      352 g      355 t
ORIGIN

Query Match      4.9%; Score 23; DB 5; Length 1525;
Best Local Similarity 100.0%; Pred. No. 0.084;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 gtggtgaagatctgtgactttgg 146
|||||
Db 314 GTGGTGAAGATCTGTGACTTTGG 336

BASE COUNT      101 a      107 c      114 g      107 t
ORIGIN

Query Match      4.9%; Score 23; DB 6; Length 1894;
Best Local Similarity 100.0%; Pred. No. 0.084;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 gtggtgaagatctgtgactttgg 146
|||||
Db 976 GTGGTGAAGATCTGTGACTTTGG 998

RESULT 45
LOCUS      AC2TKSEA      2538 bp      ss-RNA      linear      VRL 27-APR-1993
DEFINITION Avian retrovirus proviral tyrosine kinase (ENV-SEA oncogene), 3'
            end.
ACCESSION  M25158
VERSION     M25158.1 GI:209658
KEYWORDS   c-myc proto-oncogene; long terminal repeat (LTR); tyrosine kinase.
            Avian retrovirus (isolate SI3) RNA, from a chicken, passed in rat
            cells.
ORGANISM   Avian carcinoma virus
            Viruses; Retroid viruses; Retroviridae; Alpharetrovirus.
REFERENCE  1 (bases 1 to 2538)
AUTHORS   Smith,D.R., Vogt,P.K. and Hayman,M.J.
TITLE     The SEA oncogene of avian retrovirus SI3; A new member of the
            protein tyrosine kinase gene family
JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 86, 5291-5295 (1989)
MEDLINE   89315783
COMMENT   Draft entry and computer-readable sequence for [1] kindly provided
            by M.J.Hayman, 02-JUN-1989.
FEATURES   Location/Qualifiers
            source      1..2538
                        /organism="Avian carcinoma virus"
                        /db_xref="taxon:11958"
                        <!. .1791
                        /note="ARV polyprotein"
                        /codon_start=1
                        /protein_id="AAA42392.1"
                        /translation="KLTMLAPNHTDLKVLANSRRTGIRRKNTSHLDDTCSDVOLM
                        GPTARIFASILAPGVAATQALREIERLACKSVKQANLTSLGDLDDVTSIRHAVLQ
                        NRAAIDFLLAHGHGCEIAGMCCFNLSHSESIOKKFOLMKKHVNKIGVSDPIGSM
                        LRGLFGIGEWAVHLLKGLLGLVILLVCLPCLLOFVSSSIRKMI DNSLGYREC
                        RKLOEANRADSPGLARPHAFHASAGADAGGSPYLLLLRTTSCCLDLRPELLEVKD
                        ILIPERLITHRSRVIGRHFSGSVTHGTMDPLLNLCARCAVSLSHRITYLEEVFELR
                        EGLVMKGFHPQVLSLLGVCLPRHGLPVLVLYPMRHGDLRHFVRAQERSPTVKELIGF
                        GLQVALGMEYLAQKFEVRLAARNCLMDELTITVKVADFLGRADVEFGKEYYSIRQHRH
                        AKLPVRMALESQTOKFTTKSDVMSFGLVMMELLTRGASPYPEVDPYDMARYLLRGR
                        RLPOPCPDITLYGVMLSCWAPTPEERPSFGLVLCLELRLVSLASLEGEHYINMAVTYN
                        LESGPPFPAPRGOLPDSDEDEEEVAE"
                        <!. .678
                        /product="envelope protein"
                        679..1788
            mat_peptide
            mat_peptide
```

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 16, 2002, 02:57:00 ; Search time 808.35 Seconds
(without alignments)
2.105 Million cell updates/sec

Title: US-09-375-248-1_COPY_2588_2588

Perfect score: 1

Sequence: 1 g 1

Scoring table: OLIGO_NUC
Gapop 60.0 , Capext 60.0

Searched: 1163369 seqs, 850982142 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2326738

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Pending_Patents_NA_New:*

- 1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:*
- 2: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*
- 3: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*
- 4: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
- 5: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*
- 6: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:*
- 7: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	100.0	1	2	6	US-10-027-632-51869
C 2	100.0	1	2	6	US-10-027-632-52280
C 3	100.0	1	2	6	US-10-027-632-52357
C 4	100.0	1	2	6	US-10-027-632-53003
C 5	100.0	1	2	6	US-10-027-632-58305
C 6	100.0	1	2	6	US-10-027-632-175312
7	100.0	1	2	6	US-10-027-632-175337
8	100.0	1	2	6	US-10-027-632-175354
9	100.0	1	2	6	US-10-027-632-175401
10	100.0	1	2	6	US-10-027-632-175403
11	100.0	1	2	6	US-10-027-632-175415
12	100.0	1	2	6	US-10-027-632-175419
13	100.0	1	2	6	US-10-027-632-175426
14	100.0	1	2	6	US-10-027-632-175433
15	100.0	1	2	6	US-10-027-632-175849
16	100.0	1	2	6	US-10-027-632-176848
17	100.0	1	2	6	US-10-027-632-176849
18	100.0	1	2	6	US-10-027-632-176880
19	100.0	1	2	6	US-10-027-632-178420
20	100.0	1	2	6	US-10-027-632-178440
21	100.0	1	2	6	US-10-027-632-178440
22	100.0	1	2	6	US-10-027-632-178617
23	100.0	1	2	6	US-10-027-632-178640
C 24	100.0	1	3	1	PCT-US02-00351-20
C 25	100.0	1	3	6	US-10-027-632-52136
C 26	100.0	1	3	6	US-10-027-632-52402

C 27	100.0	3	6	US-10-027-632-52403	Sequence 52403, A
C 28	100.0	3	6	US-10-027-632-52404	Sequence 52404, A
C 29	100.0	3	6	US-10-027-632-52410	Sequence 52410, A
C 30	100.0	3	6	US-10-027-632-52417	Sequence 52417, A
C 31	100.0	3	6	US-10-027-632-52418	Sequence 52418, A
C 32	100.0	3	6	US-10-027-632-52419	Sequence 52419, A
C 33	100.0	3	6	US-10-027-632-52425	Sequence 52425, A
C 34	100.0	3	6	US-10-027-632-52491	Sequence 52491, A
C 35	100.0	3	6	US-10-027-632-52495	Sequence 52495, A
C 36	100.0	3	6	US-10-027-632-52496	Sequence 52496, A
C 37	100.0	3	6	US-10-027-632-52508	Sequence 52508, A
C 38	100.0	3	6	US-10-027-632-52512	Sequence 52512, A
C 39	100.0	3	6	US-10-027-632-52513	Sequence 52513, A
C 40	100.0	3	6	US-10-027-632-52615	Sequence 52615, A
C 41	100.0	3	6	US-10-027-632-52633	Sequence 52633, A
C 42	100.0	3	6	US-10-027-632-52651	Sequence 52651, A
C 43	100.0	3	6	US-10-027-632-52753	Sequence 52753, A
C 44	100.0	3	6	US-10-027-632-52758	Sequence 52758, A
C 45	100.0	3	6	US-10-027-632-52761	Sequence 52761, A

ALIGNMENTS

RESULT 1

US-10-027-632-51869/c
; Sequence 51869, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51869
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-51869

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 2 G 2

RESULT 2

US-10-027-632-52280/c
; Sequence 52280, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51869
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-51869


```
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52280
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52280
```

```
Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 g 1
Db 2 G 2
```

```
RESULT 3
US-10-027-632-52357/c
; Sequence 52357, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52357
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52357
```

```
Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 g 1
```

```
Db 2 G 2
RESULT 4
US-10-027-632-53003/c
; Sequence 53003, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53003
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-53003
```

```
Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 g 1
Db 2 G 2
```

```
RESULT 5
US-10-027-632-58305/c
; Sequence 58305, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58305
```

; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-58305

Query Match 100.0%; Score 1: DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 1 G 1

RESULT 6
US-10-027-632-175312
; Sequence 175312, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175312
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175312

Query Match 100.0%; Score 1: DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 1 G 1

RESULT 7
US-10-027-632-175337
; Sequence 175337, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29

; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175337
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175337

Query Match 100.0%; Score 1: DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 1 G 1

RESULT 8
US-10-027-632-175354
; Sequence 175354, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175354
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175354

Query Match 100.0%; Score 1: DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 1 G 1

RESULT 9
US-10-027-632-175401
; Sequence 175401, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.

; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175401
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175401

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 1 g 1

RESULT 10
US-10-027-632-175403
; Sequence 175403, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175403
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175403

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 1 g 1

RESULT 11
US-10-027-632-175415
; Sequence 175415, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175415
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175415

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 1 g 1

RESULT 12
US-10-027-632-175419
; Sequence 175419, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175419
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175419

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 1 g 1

RESULT 13
US-10-027-632-175426
; Sequence 175426, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175426
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175426

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 1 g 1

RESULT 14
US-10-027-632-175433
; Sequence 175433, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20

; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175433
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175433

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 1 g 1

RESULT 15
US-10-027-632-175849
; Sequence 175849, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175849
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175849

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 1 g 1

RESULT 16
US-10-027-632-176848
; Sequence 176848, Application US/10027632

```
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 176848
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-176848
```

```
Query Match          100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 g 1
        |
Db      1 g 1
```

```
RESULT 17
US-10-027-632-176849
; Sequence 176849, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 176849
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-176849
```

```
Query Match          100.0%; Score 1; DB 6; Length 2;
```

```
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 g 1
        |
Db      1 g 1

RESULT 18
US-10-027-632-176880
; Sequence 176880, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 176880
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-176880
```

```
Query Match          100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 g 1
        |
Db      1 g 1
```

```
RESULT 19
US-10-027-632-178420
; Sequence 178420, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
```

; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 178420
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-178420

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
|
Db 1 g 1

RESULT 20
US-10-027-632-178440
; Sequence 178440, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 178440
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-178440

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
|
Db 1 g 1

RESULT 21
US-10-027-632-178440/c
; Sequence 178440, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12

; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 178440
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-178440

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
|
Db 2 g 2

RESULT 22
US-10-027-632-178617
; Sequence 178617, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 178617
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-178617

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
|
Db 2 g 2

RESULT 23

US-10-027-632-178640
; Sequence 178640, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 178640
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-178640

Query Match 100.0% Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 2 g 2

RESULT 24
PCT-US02-00351-20/c
; Sequence 20, Application PC/TUS0200351
; GENERAL INFORMATION:
; APPLICANT: Chet, Ilan
; APPLICANT: Viterbo, Ada
; TITLE OF INVENTION: RECOMBINANT FUNGAL CHITINASES, POLYNUCLEOTIDE SEQUENCES ENCODING
; FILE REFERENCE: 02/23682
; CURRENT APPLICATION NUMBER: PCT/US02/00351
; CURRENT FILING DATE: 2002-05-05
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: motif found in the URSs of both ech42 and prbl genes
PCT-US02-00351-20

Query Match 100.0% Score 1; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 3 G 3

RESULT 25

US-10-027-632-52136
; Sequence 52136, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52136
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52136

Query Match 100.0% Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 3 g 3

RESULT 26
US-10-027-632-52402/c
; Sequence 52402, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52402
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52402

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 2 G 2

RESULT 27

US-10-027-632-52403/c
; Sequence 52403, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 52403
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52403

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 2 G 2

RESULT 28

US-10-027-632-52404/c
; Sequence 52404, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358

; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 52404
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52404

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 2 G 2

RESULT 29

US-10-027-632-52410/c
; Sequence 52410, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 52410
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52410

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 3 G 3

RESULT 30

US-10-027-632-52417/c
; Sequence 52417, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30

;
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52417
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52417

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 2 G 2

RESULT 31
US-10-027-632-52418/c
; Sequence 52418, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52418
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52418

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 2 G 2

RESULT 32
US-10-027-632-52419/c
; Sequence 52419, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52419
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52419

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 2 G 2

RESULT 33
US-10-027-632-52425/c
; Sequence 52425, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52425
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human

US-10-027-632-52425

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 3 g 3

RESULT 34

US-10-027-632-52491
; Sequence 52491, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52491
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52491

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 2 g 2

RESULT 35

US-10-027-632-52495/c
; Sequence 52495, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363

; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52495
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52495

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 3 g 3

RESULT 36

US-10-027-632-52496
; Sequence 52496, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52496
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52496

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 2 g 2

RESULT 37

US-10-027-632-52508
; Sequence 52508, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129

; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52508
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52508

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 2 g 2

RESULT 38
US-10-027-632-52512/c
; Sequence 52512, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52512
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52512

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|

Db 3 G 3
RESULT 39
US-10-027-632-52513
; Sequence 52513, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52513
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52513

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 2 g 2

RESULT 40
US-10-027-632-52615
; Sequence 52615, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52615
; LENGTH: 3

; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52615

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 2 g 2

RESULT 41

US-10-027-632-52633
; Sequence 52633, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52633
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52633

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 2 g 2

RESULT 42

US-10-027-632-52651
; Sequence 52651, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218

; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52651
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52651

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 2 g 2

RESULT 43

US-10-027-632-52753
; Sequence 52753, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52753
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52753

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 2 g 2

RESULT 44

US-10-027-632-52758/c
; Sequence 52758, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52758
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52758

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
Db 1 g 1

RESULT 45
US-10-027-632-52761
; Sequence 52761, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52761
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52761

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
Db 1 g 1

Search completed: July 16, 2002, 02:57:00
Job time: 24558 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 15, 2002, 20:07:36 ; Search time 7067.1 Seconds
(without alignments)
1.910 Million cell updates/sec

Title: US-09-375-248-1_COPY_2588_2588
Perfect score: 1
Sequence: 1 g 1

Scoring table: OLIGO_NUC
Gap 60.0 , Gapext 60.0

Searched: 13736207 seqs, 6748477542 residues

Word size : 0

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

EST:*

- 1: em_estba:*
- 2: em_esthum:*
- 3: em_estin:*
- 4: em_estm:*
- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_hic:*
- 9: gb_est1:*
- 10: gb_est2:*
- 11: gb_hic:*
- 12: gb_gss:*
- 13: em_gss_hum:*
- 14: em_gss_inv:*
- 15: em_gss_pln:*
- 16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	1	100.0	2	2 HSM003817	AL039341 Homo sapi
C 2	1	100.0	2	2 HSM007187	AL042337 Homo sapi
C 3	1	100.0	2	2 HSM008709	AL043859 Homo sapi
C 4	1	100.0	2	2 HSM011919	AL047069 Homo sapi
C 5	1	100.0	2	10 B1817789	B1817789 G3-G22 Ax
C 6	1	100.0	2	10 C55081	C55081 C55081 Yujl
C 7	1	100.0	2	10 BE351920	BE351920 894053D07
C 8	1	100.0	2	12 AZ463604	AZ463604 1M0272J05
C 9	1	100.0	3	9 AW672605	AW672605 2xA Expla
C 10	1	100.0	3	12 AZ438202	AZ438202 1M0228I08
C 11	1	100.0	3	12 CNS00KCV	AL077515 Drosophil
C 12	1	100.0	4	2 BG926576	BG926576 HNC56-1-A
C 13	1	100.0	4	2 BG926576	BG926576 HNC56-1-A
C 14	1	100.0	4	2 HSM003901	AL039425 Homo sapi
C 15	1	100.0	4	2 HSM010467	AL045617 Homo sapi
C 16	1	100.0	4	2 HSM010467	AL045617 Homo sapi
C 17	1	100.0	4	9 AW672622	AW672622 73C Expla

C 18	1	100.0	4	12 CNS004RB	AL054121 Drosophil
C 19	1	100.0	5	2 HSM007310	AL042460 Homo sapi
C 20	1	100.0	5	2 HSM007835	AL042985 Homo sapi
C 21	1	100.0	5	2 HSM011053	AL046203 Homo sapi
C 22	1	100.0	6	2 BG927410	BG927410 HNC1-1-G7
C 23	1	100.0	6	2 HSM003844	AL039368 Homo sapi
C 24	1	100.0	6	2 HSM004423	AL039947 Homo sapi
C 25	1	100.0	6	2 HSM007334	AL042484 Homo sapi
C 26	1	100.0	6	2 HSM007683	AL042833 Homo sapi
C 27	1	100.0	6	2 HSM008014	AL043184 Homo sapi
C 28	1	100.0	6	2 HSM010918	AL046068 Homo sapi
C 29	1	100.0	6	2 HSM010918	AL046068 Homo sapi
C 30	1	100.0	6	10 BE726686	BE726686 894095011
C 31	1	100.0	6	10 BE726686	BE726686 894095011
C 32	1	100.0	7	2 BG997546	BG997546 HOA14-1-H
C 33	1	100.0	7	2 BG997546	BG997546 HOA14-1-H
C 34	1	100.0	7	2 HSM007412	AL042562 Homo sapi
C 35	1	100.0	7	2 HSM007412	AL042562 Homo sapi
C 36	1	100.0	7	2 HSM007502	AL042652 Homo sapi
C 37	1	100.0	7	2 HSM007502	AL042652 Homo sapi
C 38	1	100.0	7	10 C58888	C58888 C58888 Yujl
C 39	1	100.0	8	2 HSM001420	AL037095 Homo sapi
C 40	1	100.0	8	2 HSM001743	AL037413 Homo sapi
C 41	1	100.0	8	2 HSM004451	AL039975 Homo sapi
C 42	1	100.0	8	2 HSM004451	AL039975 Homo sapi
C 43	1	100.0	8	2 HSM007277	AL042427 Homo sapi
C 44	1	100.0	8	2 HSM007277	AL042427 Homo sapi
C 45	1	100.0	8	2 HSM007323	AL042473 Homo sapi

ALIGNMENTS

RESULT 1

HS0003817/C standard; RNA; EST; 2 BP.

AC AL039341;

SV AL039341.1

DT 12-MAR-1999 (Rel. 59, Created)

DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)

DE Homo sapiens mRNA; EST DKFZp434F2010_r1 (from clone DKFZp434F2010)

DE EST; expressed sequence tag.

DE Homo sapiens (human)

DE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

XX [1]

XX 1-2

XX Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;

XX Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.

XX MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY

XX Clone from S. Wiemann, sequenced by Qiagen within the cDNA

XX sequencing consortium of the German Genome Project

XX No sl sequence available

XX This clone is available at the RZPD in Berlin

XX Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

XX Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

XX key Location/Qualifiers

XX source 1..2

XX /db_xref="taxon:9606"

XX /organism="Homo sapiens"

XX /clone="DKFZp434F2010"

XX /clone_lib="434 (synonym: htes3). Vector pSport1; host

```

FT      DH10B; sites NotI + SalI"
FT      /dev_stage="adult"
FT      /tissue_type="testis"
XX
SQ      Sequence 2 BP; 0 A; 1 C; 0 G; 1 T; 0 Other;

      Query Match      100.0%; Score 1; DB 2; Length 2;
      Best Local Similarity 100.0%; Pred. No. 0;
      Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 g 1
Db      2 G 2

RESULT 2
HSM007187/c
ID      HSM007187 standard; RNA; EST; 2 BP.
XX
AC      AL042337;
XX
SV      AL042337.1
XX
DT      12-MAR-1999 (Rel. 59, Created)
DT      12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE      Homo sapiens mRNA; EST DKFZp43400820_r1 (from clone DKFZp43400820)
XX
KW      EST; expressed sequence tag.
XX
OS      Homo sapiens (human)
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC      Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN      [1]
RP      1-2
RA      Bloeker H., Boecker M., Brandt P., Mewes W., Gassenhuber J., Wiemann S.;
RT      ;
RL      Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL      MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC      Clone from S. Wiemann, sequenced by GBF within the cDNA
CC      sequencing consortium of the German Genome Project
CC      No SI sequence available
CC      This clone is available at the RZPD in Berlin
CC      Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC      Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH      Key      Location/Qualifiers
FH      source      1..2
FT      /db_xref="taxon:9606"
FT      /organism="Homo sapiens"
FT      /clone="DKFZp43400820"
FT      /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT      DH10B; sites NotI + SalI"
FT      /dev_stage="adult"
FT      /tissue_type="testis"
XX
SQ      Sequence 2 BP; 0 A; 1 C; 0 G; 1 T; 0 Other;

      Query Match      100.0%; Score 1; DB 2; Length 2;
      Best Local Similarity 100.0%; Pred. No. 0;
      Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 g 1
Db      2 G 2

RESULT 4
HSM011919/c
ID      HSM011919 standard; RNA; EST; 2 BP.
XX
AC      AL047069;
XX
SV      AL047069.1
XX
DT      12-MAR-1999 (Rel. 59, Created)
DT      12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE      Homo sapiens mRNA; EST DKFZp586P0517_r1 (from clone DKFZp586P0517)
XX
KW      EST; expressed sequence tag.
XX
OS      Homo sapiens (human)
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC      Eutheria; Primates; Catarrhini; Hominidae; Homo.

```



```

XX  [1]
KN  Koehrer K., Beyer A., Mewes W., Gassenhuber J., Wiemann S.;
RP  1-2
RA  ;
RT  Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL  MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC  Clone from S. Wiemann, sequenced by BMFZ within the cDNA
CC  sequencing consortium of the German Genome Project
CC  No sl sequence available
CC  This clone is available at the RZPD in Berlin
CC  Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC  Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH  Key Location/Qualifiers
FT  source
FT  1..2
FT  /db_xref="taxon:9606"
FT  /organism="Homo sapiens"
FT  /clone="DKFZp586P0517"
FT  /clone_lib="586 (synonym: hutel). Vector pSport1; host
FT  DH10B; sites NotI + SalI/MluI"
FT  /dev_stage="adult"
FT  /tissue_type="uterus"
XX
SQ  Sequence 2 BP: 0 A: 1 C: 0 G: 1 T: 0 other;

Query Match 100.0%; Score 1; DB 2; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 2 G 2

RESULT 5
BI817789/c
LOCUS
DEFINITION G3-C22 Axolotl Lambda Zap Library Ambystoma mexicanum cDNA similar
to putative ribosomal protein S2, mRNA sequence.
ACCESSION BI817789
VERSION BI817789.1 GI:15951401
KEYWORDS EST.
SOURCE axolotl.
ORGANISM Ambystoma mexicanum
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Caudata; Salamandroldea; Ambystomatidae;
Ambystoma.
REFERENCE 1 (bases 1 to 2)
AUTHORS Voss,S.R., King,D., Maness,N., Smith,J.J., Rondet,M., Bryant,S.V.,
Gardiner,D.M. and Parichy,D.M.
TITLE Expressed sequence tags from an axolotl limb regeneration library
JOURNAL Unpublished (2001)
COMMENT Contact: Voss SR
Department of Biology
Colorado State University
Fort Collins, CO 80523, USA
Tel: 970 491 4869
Fax: 970 491 0649
Email: svross@lanar.colostate.edu
Single pass sequence from 5' end. Low quality sequence was trimmed
from the ends (PHRED error rate = 5%). Trace file available:
svross@lanar.colostate.edu.
Location/Qualifiers
1..2
/organism="Ambystoma mexicanum"
/db_xref="taxon:8296"
/clone_lib="Axolotl Lambda Zap Library"
/tissue_type="Regenerating forelimb"
/dev_stage="Medium-bud blastema"

FEATURES
source
1..2
/organism="Caenorhabditis elegans"
/strain="CB1489 him-8(e1489)"
/db_xref="taxon:6239"
/clone="yk350c9"
/clone_lib="Yuji Kohara unpublished cDNA"
/sex="hermaphrodite, male"
/tissue_type="whole animal"
/dev_stage="varied"

BASE COUNT 1 a 1 c 0 g 0 t
ORIGIN
Query Match 100.0%; Score 1; DB 10; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 2 G 2

RESULT 7
BE351920
LOCUS
DEFINITION BE351920.y1 C. reinhardtii CC-1690, normalized, Lambda Zap II
Chlamydomonas reinhardtii cDNA, mRNA sequence.
ACCESSION BE351920
VERSION BE351920.1 GI:9263773
KEYWORDS EST.
SOURCE Chlamydomonas reinhardtii.
ORGANISM Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
REFERENCE 1 (bases 1 to 2)

```

```

BASE COUNT 0 a 1 c 0 g 1 t
ORIGIN
Query Match 100.0%; Score 1; DB 10; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 1 G 1

RESULT 6
C55081/c
LOCUS
DEFINITION C55081 Yuji Kohara unpublished cDNA Caenorhabditis elegans cDNA
clone yk350c9 3', mRNA sequence.
ACCESSION C55081
VERSION C55081.1 GI:2399682
KEYWORDS EST.
SOURCE Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae
; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE 1 (bases 1 to 2)
AUTHORS Kohara,Y., Motohashi,T., Tabara,H., Watanabe,H., Sugimoto,A., Sano
,M., Miyata,A. and Nishigaki,A.
TITLE Expression map of the C.elegans genome
JOURNAL Unpublished (1996)
COMMENT Contact: Yuji Kohara
Genome Biology Lab.
National Institute of Genetics
Yata 111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp.
Location/Qualifiers
1..2
/organism="Caenorhabditis elegans"
/strain="CB1489 him-8(e1489)"
/db_xref="taxon:6239"
/clone="yk350c9"
/clone_lib="Yuji Kohara unpublished cDNA"
/sex="hermaphrodite, male"
/tissue_type="whole animal"
/dev_stage="varied"

BASE COUNT 1 a 1 c 0 g 0 t
ORIGIN
Query Match 100.0%; Score 1; DB 10; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 2 G 2

RESULT 7
BE351920
LOCUS
DEFINITION BE351920.y1 C. reinhardtii CC-1690, normalized, Lambda Zap II
Chlamydomonas reinhardtii cDNA, mRNA sequence.
ACCESSION BE351920
VERSION BE351920.1 GI:9263773
KEYWORDS EST.
SOURCE Chlamydomonas reinhardtii.
ORGANISM Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
REFERENCE 1 (bases 1 to 2)

```

AUTHORS Grossman, A., Davies, J., Federspiel, N., Harris, E., Lefebvre, P., McDermott, J. P., Silflow, C., Stern, D. and Surzycki, R.
TITLE Analyses of the Chlamydomonas reinhardtii Genome: A Model, Unicellular System for Analyzing Gene Function and Regulation in Vascular Plants: project phase 2
JOURNAL Unpublished (2000)
COMMENT Contact: Elizabeth H. Harris
 DCMB Box 91000
 Duke University
 Durham, NC 27708-1000, USA
 Tel: 919 613 8164
 Fax: 919 613 8177
 Email: chlamy@duke.edu.

FEATURES source
 1. .2
 Location/Qualifiers
 /organism="Chlamydomonas reinhardtii"
 /strain="CC-1690 wild type mt+ 21gr"
 /db_xref="taxon:3055"
 /clone_lib="C. reinhardtii CC-1690, normalized, Lambda Zap II"
 /note="Vector: pBluescript II SK-; Site_1: EcoRI; site_2: XhoI; This library, constructed by John Davies and Jeffrey McDermott, combines cDNAs from CC-1690 cells grown to mid-log phase in TAP (acetate-containing) medium in the light, TAP medium in the dark, HS (minimal) medium in ambient levels of CO₂ and HS medium bubbled with 5% CO₂. PolyA mRNA was purified from each sample, pooled and cDNA synthesized. The cDNA was directionally cloned into lambda Zap II (Stratagene) in the EcoRI (5') and XhoI (3') sites. pBluescript II SK- plasmids were excised from the lambda Zap clones by superinfection with ExAssist (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al (1996) Genome Research 6: 791-806."

BASE COUNT 0 a 0 c 2 g 0 t
ORIGIN

Query Match 100.0%; Score 1; DB 10; Length 2;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
 Db 1 G 1

RESULT 8
AZ463604
LOCUS 1M0272J05R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0272J05 R, DNA sequence.
DEFINITION AZ463604
ACCESSION AZ463604.1 GI:10621729
VERSION GSS.
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 1 (bases 1 to 2)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177

REFERENCE AUTHORS
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0272 row: J column: 05
 Seq primer: CACACAGGAAACACGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 451.
 Location/Qualifiers
 1. .2

FEATURES source
 1. .2
 Location/Qualifiers
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone_lib="UUGC1M0272J05"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 0 c 1 g 1 t
ORIGIN

Query Match 100.0%; Score 1; DB 12; Length 2;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
 Db 1 G 1

RESULT 9
AW672605
LOCUS 2XA Explanted metanephric mesenchyme induced to differentiate into epithelial structures of the nephron ex vivo. Rattus norvegicus cDNA similar to similar to: gb|AF022811.1|AF022811 Mus musculus cornichon mRNA, mRNA sequence.
DEFINITION AW672605
ACCESSION AW672605.1 GI:7541085
VERSION EST.
KEYWORDS Norway rat.
SOURCE Rattus norvegicus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 1 (bases 1 to 3)
 Plisov, S.Y., Ivanov, S.V., Yoshino, K., Dove, L.F., Plisova, T.M., Higginbotham, K.G., Karavanova, I., Lerman, M. and Perantoni, A.O.
 Mesenchymal-epithelial transition in the developing metanephric kidney: gene expression study by differential display
 Genesis 27 (1), 22-31 (2000)
 20321327
 Contact: Plisov S.Y.
 Laboratory of Comparative Carcinogenesis
 National Cancer Institute
 FCRDC, Bldg. 538, Room 205, Frederick, MD 21702, USA

REFERENCE AUTHORS
TITLE Mesenchymal-epithelial transition in the developing metanephric kidney: gene expression study by differential display
JOURNAL Genesis 27 (1), 22-31 (2000)
MEDLINE 20321327
COMMENT Contact: Plisov S.Y.
 Laboratory of Comparative Carcinogenesis
 National Cancer Institute
 FCRDC, Bldg. 538, Room 205, Frederick, MD 21702, USA

Tel: 301 846 1242
Fax: 301 846 4956
Email: pilsov@mail.ncifcrf.gov

PCR Primers

FORWARD: ctctgagctccgctc

BACKWARD: ttaagcttttttttttc

Insert Length: 350 Std Error: 0.00

Seq primer: SP6

High quality sequence stop: 261.

Location/Qualifiers

FEATURES

source

1. .3
/organism="Rattus norvegicus"
/db_xref="taxon:10116"
/clone.lib="Explanted metanephric mesenchyme induced to differentiate into epithelial structures of the nephron ex vivo."
/tissue_type="Metanephric mesenchyme"
/cell_type="Mesenchymal/Epithelial"
/dev_stage="13 dpc-16dpc"
/lab_host="JMI09"
/note="Organ: Kidney; Vector: pGEM-T-Easy (Promega); Restriction Enzymes 1: ApaI, AatII, SphI, NcoI, BstZI, NotI, SacII, and EcoRI; SpeI, EcoRI, NotI, BstZI, PstI, SalI, NdeI, SacI, BstXI, and NsiI cDNA fragment PCR-amplified in mRNA differential display analysis; cloned in pGEM-T-Easy (Promega); its expression is developmentally regulated during mesenchymal-epithelial conversion in the metanephric kidney."
1 a 0 c 2 g 0 t

BASE COUNT

ORIGIN

Query Match 100.0%; Score 1; DB 9; Length 3;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1

|

Db 1 g 1

RESULT 10

AZ438202/c

LOCUS

DEFINITION AZ438202 3 bp DNA linear GSS 03-OCT-2000

clone UUCG1M0228108 F, DNA sequence.

ACCESSION AZ438202

VERSION AZ438202.1 GI:10562215

KEYWORDS GSS.

SOURCE house mouse.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 3)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly

,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.

and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112 USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0228 row: 1 column: 08

Seq primer: CGTTGTAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 302.

Location/Qualifiers

source

1. .3

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUCG1M0228108"

/clone.lib="Mouse 10kb plasmid UUCG1M library"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/note="Vector: pMD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pMD42 (gil4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid p1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

1 a 1 c 0 g 1 t

BASE COUNT

ORIGIN

Query Match 100.0%; Score 1; DB 12; Length 3;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1

|

Db 1 g 1

RESULT 11

CNS00KCV

LOCUS

DEFINITION CNS00KCV 3 bp DNA linear GSS 03-JUN-1999

Drosophila melanogaster genome survey sequence TET3 end of BAC:

BACR17D19 of RPCI-98 library from Drosophila melanogaster (fruit

fly), genomic survey sequence.

AL077515

AL077515.1 GI:4956992

GSS.

SOURCE fruit fly.

ORGANISM Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 3)

Genoscope.

Direct Submission

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a

collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila

melanogaster genome using these BACs. For further information

please see <http://www.fruitfly.org> The BDGP Drosophila

melanogaster BAC library was prepared by Kazutoyo Osoegawa and

Aaron Mammose in Pieter de Jong's laboratory in the Department of

Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,

NY. The library is named RPCI-98 and was constructed by partial

ECORI digestion of Drosophila DNA provided by the BDGP from the

isogenic strain y2: cn bw sp, the same strain used for the BDGP's

Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES

source
1..3
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACRI7D19"
/note="end : TET3"

BASE COUNT 0 a 0 c 3 g 0 t
ORIGIN

Query Match 100.0%; Score 1; DB 12; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
Db 1 G 1

RESULT 12

BG926576 standard; RNA; EST; 4 BP.

XX AC BG926576;

XX SV BG926576.1

XX 09-JUN-2001 (Rel. 68, Created)

DT 14-NOV-2001 (Rel. 69, Last updated, Version 2)

XX HNC56-1-A10.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
DE sequence.

XX KW EST.

OS Homo sapiens (human)

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia;

OC Eutheria; Primates; Catarrhini; Hominidae; Homo.

XX [1]

RP 1-4
RX MEDLINE; 21482651.

RX PUBMED; 11597177.

RA Kumar S., Connor J.R., Dodds R.A., Halsey W., Van Horn M., Mao J.,
Sathe G.M., Mui P., Agarwal P., Badger A.M., Lee J.C., Gowen M., Lark M.W.;

RT "Identification and initial characterization of 5000 expressed sequenced
tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA
libraries";

RL Osteoarthritis Cartilage 9(7):641-653(2001).

XX Contact: Sanjay Kumar

CC UW2109

CC GlaxoSmithKline

CC 709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA

CC Tel: 610-270-7245

CC Fax: 610-270-5598

CC Email: sanjay.kumar-1@gsk.com

CC Seq primer: T7.

XX Key

FH Location/Qualifiers

FH 1..4

FT /db_xref="taxon:9606"

FT /note="Vector: pSPORT 1; Site_1: SalI; Site_2: NotI;

FT Directional"

FT /organism="Homo sapiens"

FT /clone_lib="HNC (Human Normal Cartilage)"

FT /tissue_type="cartilage"

FT

FT /lab_host="E.coli DH10 B"

XX Sequence 4 BP; 1 A; 1 C; 1 G; 1 T; 0 other;

SQ

Query Match 100.0%; Score 1; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1

Db 4 G 4

RESULT 13

BG926576/c

ID BG926576 standard; RNA; EST; 4 BP.

XX AC BG926576;

XX SV BG926576.1

XX 09-JUN-2001 (Rel. 68, Created)

DT 14-NOV-2001 (Rel. 69, Last updated, Version 2)

XX HNC56-1-A10.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
DE sequence.

XX KW EST.

OS Homo sapiens (human)

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia;

OC Eutheria; Primates; Catarrhini; Hominidae; Homo.

XX [1]

RP 1-4
RX MEDLINE; 21482651.

RX PUBMED; 11597177.

RA Kumar S., Connor J.R., Dodds R.A., Halsey W., Van Horn M., Mao J.,
Sathe G.M., Mui P., Agarwal P., Badger A.M., Lee J.C., Gowen M., Lark M.W.;

RT "Identification and initial characterization of 5000 expressed sequenced
tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA
libraries";

RL Osteoarthritis Cartilage 9(7):641-653(2001).

XX Contact: Sanjay Kumar

CC UW2109

CC GlaxoSmithKline

CC 709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA

CC Tel: 610-270-7245

CC Fax: 610-270-5598

CC Email: sanjay.kumar-1@gsk.com

CC Seq primer: T7.

XX Key

FH Location/Qualifiers

FH 1..4

FT /db_xref="taxon:9606"

FT /note="Vector: pSPORT 1; Site_1: SalI; Site_2: NotI;

FT Directional"

FT /organism="Homo sapiens"

FT /clone_lib="HNC (Human Normal Cartilage)"

FT /tissue_type="cartilage"

FT

FT /lab_host="E.coli DH10 B"

XX Sequence 4 BP; 1 A; 1 C; 1 G; 1 T; 0 other;

SQ

Query Match 100.0%; Score 1; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1

Db 4 G 4

RESULT 13

BG926576/c

ID BG926576 standard; RNA; EST; 4 BP.

XX AC BG926576;

XX SV BG926576.1

XX 09-JUN-2001 (Rel. 68, Created)

DT 14-NOV-2001 (Rel. 69, Last updated, Version 2)

XX HNC56-1-A10.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
DE sequence.

XX KW EST.

OS Homo sapiens (human)

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia;

OC Eutheria; Primates; Catarrhini; Hominidae; Homo.

XX [1]

RP 1-4
RX MEDLINE; 21482651.

RX PUBMED; 11597177.

RA Kumar S., Connor J.R., Dodds R.A., Halsey W., Van Horn M., Mao J.,
Sathe G.M., Mui P., Agarwal P., Badger A.M., Lee J.C., Gowen M., Lark M.W.;

RT "Identification and initial characterization of 5000 expressed sequenced
tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA
libraries";

RL Osteoarthritis Cartilage 9(7):641-653(2001).

XX Contact: Sanjay Kumar

CC UW2109

CC GlaxoSmithKline

CC 709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA

CC Tel: 610-270-7245

CC Fax: 610-270-5598

CC Email: sanjay.kumar-1@gsk.com

CC Seq primer: T7.

XX Key

FH Location/Qualifiers

FH 1..4

FT /db_xref="taxon:9606"

FT /note="Vector: pSPORT 1; Site_1: SalI; Site_2: NotI;

FT Directional"

FT /organism="Homo sapiens"

FT /clone_lib="HNC (Human Normal Cartilage)"

FT /tissue_type="cartilage"

FT

```

Db          1
            3 G 3

RESULT 14
HSM003901
ID HSM003901 standard; RNA; EST; 4 BP.
XX
AC AL039425;
XX
SV AL039425.1
XX
DT 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE Homo sapiens mRNA; EST DKFZp34L0810_s1 (from clone DKFZp34L0810)
XX
KW EST; expressed sequence tag.
XX
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN [1]
RP 1-4
KA Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
; Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by Qiagen within the cdna
CC sequencing consortium of the German Genome Project
CC r1 sequence also available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH Key Location/Qualifiers
FH source
FT 1..4
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp34L0810"
FT /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"
XX
SQ Sequence 4 BP; 2 A; 0 C; 1 G; 0 T; 1 other;

Query Match 100.0%; Score 1; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 4 G 4

RESULT 15
HSM010467
ID HSM010467 standard; RNA; EST; 4 BP.
XX
AC AL045617;
XX
SV AL045617.1
XX
DT 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE Homo sapiens mRNA; EST DKFZp34O245_r1 (from clone DKFZp34O245)
XX
KW EST; expressed sequence tag.
XX
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN [1]
RP 1-4
KA Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
; Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by Qiagen within the cdna
CC sequencing consortium of the German Genome Project
CC No s1 sequence available
CC This clone is available at the RZPD in Berlin

```

```

KW EST; expressed sequence tag.
XX
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN [1]
RP 1-4
KA Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
; Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by Qiagen within the cdna
CC sequencing consortium of the German Genome Project
CC No s1 sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH Key Location/Qualifiers
FH source
FT 1..4
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp34O245"
FT /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"
XX
SQ Sequence 4 BP; 0 A; 2 C; 1 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 4 G 4

RESULT 16
HSM010467/C
ID HSM010467 standard; RNA; EST; 4 BP.
XX
AC AL045617;
XX
SV AL045617.1
XX
DT 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE Homo sapiens mRNA; EST DKFZp34O245_r1 (from clone DKFZp34O245)
XX
KW EST; expressed sequence tag.
XX
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN [1]
RP 1-4
KA Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
; Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by Qiagen within the cdna
CC sequencing consortium of the German Genome Project
CC No s1 sequence available
CC This clone is available at the RZPD in Berlin

```

```

CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
XX Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
FH Key Location/Qualifiers
FT source 1..4
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKF2p340245"
FT /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"
XX
SQ Sequence 4 BP; 0 A; 2 C; 1 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 2 G 2

RESULT 17
LOCUS AW672622
DEFINITION 73C Explanted metanephric mesenchyme induced to differentiate into
cDNA similar to similar to: embIAL049970.1|HSM800317 Homo sapiens
mRNA: cDNA DKF2p564B102 (from clone DKF2p564B102);, mRNA sequence.
ACCESSION AW672622
VERSION AW672622.1 GI:7541102
KEYWORDS EST.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1 (bases 1 to 4)
AUTHORS Plisov,S.Y., Ivanov,S.V., Yoshino,K., Dove,L.F., Plisova,T.M.,
Higginbotham,K.G., Karavanova,I., Lerman,M. and Perantoni,A.O.
TITLE Mesenchymal-epithelial transition in the developing metanephric
kidney: gene expression study by differential display
JOURNAL Genesis 27 (1), 22-31 (2000)
MEDLINE 20321327
COMMENT Contact: Plisov S.Y.
Laboratory of Comparative Carcinogenesis
National Cancer Institute
FCRDC, Bldg. 538, Room 205, Frederick, MD 21702, USA
Tel: 301 846 1242
Fax: 301 846 4956
Email: plisov@mail.ncicfcr.gov
PCR PRIMERS
FORWARD: ctccagctccgcg
BACKWARD: ttaagctttttttttg
Insert Length: 262 Std Error: 0.00
Seq primer: Sp6
High quality sequence stop: 262
POLYA=Yes.

FEATURES
source Location/Qualifiers
1..4
/organism="Rattus norvegicus"
/db_xref="taxon:10116"
/clone_lib="Explanted metanephric mesenchyme induced to
differentiate into epithelial structures of the nephron ex
vivo."
/tissue_type="Metanephric mesenchyme"
/cell_type="Mesenchymal/Epithelial"
/dev_stage="13 dpc-16dpc"
/lab_host="JMI09"

```

```

/note="Organ: Kidney; Vector: pGEM-Teasy (Promega).;
Restriction Enzymes 1: ApaI, AatII, SphI, NcoI, BstXI,
NotI, SacII, and EcoRI SpeI, EcoRI, NotI, BstXI, PstI,
SalI, NdeI, SacI, BstXI, and NsiI cDNA fragment
PCR-amplified in mRNA differential display analysis;
cloned in pGEM-Teasy (Promega); its expression is
developmentally regulated during mesenchymal-epithelial
conversion in the metanephric kidney."
BASE COUNT 1 a 3 g 0 c
ORIGIN

Query Match 100.0%; Score 1; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 1 G 1

RESULT 18
LOCUS CNS004RB/c
DEFINITION Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR10A06 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION AL054121
VERSION AL054121.1 GI:4931932
KEYWORDS GSS.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 4)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see http://www.fruitfly.org The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osoegawa and
Aaron Mamoser in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain y2; cn bw sp, the same strain used for the BDGP's
PI and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES
source Location/Qualifiers
1..4
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR10A06"
/note="end : TET3"
BASE COUNT 1 a 1 c 0 g 2 t
ORIGIN

Query Match 100.0%; Score 1; DB 12; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 1 G 1

```

```

Db          4 G 4

RESULT 19
HSM007310
ID HSM007310 standard; RNA; EST; 5 BP.
XX
AC AL042460;
XX
SV AL042460.1
XX
DT 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE Homo sapiens mRNA; EST DKFZp434E1821_r1 (from clone DKFZp434E1821)
XX
KW EST; expressed sequence tag.
XX
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN [1]
RP 1-5
RA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by LMU within the cDNA
CC sequencing consortium of the German Genome Project
CC No.s1 sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH Key Location/Qualifiers
FH source 1..5
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp434E1821"
FT /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"
XX
SQ Sequence 5 BP; 2 A; 0 C; 1 G; 2 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 g 1
Db 1 G 1

RESULT 20
HSM007835/c
ID HSM007835 standard; RNA; EST; 5 BP.
XX
AC AL042985;
XX
SV AL042985.1
XX
DT 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE Homo sapiens mRNA; EST DKFZp434N1522_r1 (from clone DKFZp434N1522)
XX
KW EST; expressed sequence tag.

```

```

XX Homo sapiens (human)
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN [1]
RP 1-5
RA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by LMU within the cDNA
CC sequencing consortium of the German Genome Project
CC No.s1 sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH Key Location/Qualifiers
FH source 1..5
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp434N1522"
FT /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"
XX
SQ Sequence 5 BP; 2 A; 1 C; 0 G; 0 T; 2 other;

Query Match 100.0%; Score 1; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 g 1
Db 5 G 5

RESULT 21
HSM011053
ID HSM011053 standard; RNA; EST; 5 BP.
XX
AC AL046203;
XX
SV AL046203.1
XX
DT 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE Homo sapiens mRNA; EST DKFZp434D137_r1 (from clone DKFZp434D137)
XX
KW EST; expressed sequence tag.
XX
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN [1]
RP 1-5
RA Koehrer K., Beyer A., Mewes W., Gassenhuber J., Wiemann S.;
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by BMFZ within the cDNA
CC sequencing consortium of the German Genome Project
CC No.s1 sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

```

CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

FH Key Location/Qualifiers

FT source 1..5

FT /db_xref="taxon:9606"

FT /organism="Homo sapiens"

FT /clone="DKFZp434D137"

FT /clone_lib="434 (synonym: htes3). Vector pSport1; host

FT DH10B; sites NotI + SalI"

FT /dev_stage="adult"

FT /tissue_type="testis"

XX Sequence 5 BP; 2 A; 0 C; 1 G; 2 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1

Db 1 G 1

RESULT 22

BC927410/G standard; RNA; EST; 6 BP.

XX AC BG927410;

XX SV BG927410.1

XX 09-JUN-2001 (Rel. 68, Created)

DT 14-NOV-2001 (Rel. 69, Last updated, Version 2)

XX HNC1-1-G7-R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA sequence.

XX EST.

XX Homo sapiens (human)

OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia;

OC Eutheria; Primates; Catarrhini; Hominidae; Homo.

XX [1]

RN 1-6

RP MEDLINE; 21482651.

RX PUBMED; 11597177.

RA Kumar S., Connor J.R., Dodds R.A., Halsey W., Van Horn M., Mao J.,

RA Sathe G.M., Mui P., Agarwal P., Badger A.M., Lee J.C., Cowen M., Lark M.W.;

RT "Identification and initial characterization of 5000 expressed sequenced

tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA

libraries";

RT Osteoarthritis Cartilage 9(7):641-653(2001).

XX Contact: Sanjay Kumar

CC UW2109

CC GlaxoSmithKline

CC 709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA

CC Tel: 610-270-7245

CC Fax: 610-270-5598

CC Email: sanjay_kumar-legsk.com

CC Seq primer: T7.

XX Key Location/Qualifiers

FH source 1..6

FT /db_xref="taxon:9606"

FT /note="Vector: pSPORT 1; Site_1: SalI; Site_2: NotI;

FT Directional"

FT /organism="Homo sapiens"

FT /clone_lib="HNC (Human Normal Cartilage)"

FT /tissue_type="cartilage"

FT /lab_host="E.coli DH10 B"

SQ Sequence 6 BP; 0 A; 5 C; 0 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 6;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1

Db 6 G 6

RESULT 23

HSM003844 standard; RNA; EST; 6 BP.

XX AC AL039368;

XX SV AL039368.1

XX 12-MAR-1999 (Rel. 59, Created)

DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)

XX Homo sapiens mRNA; EST DKFZp434I0110_r1 (from clone DKFZp434I0110)

XX EST; expressed sequence tag.

XX Homo sapiens (human)

OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia;

OC Eutheria; Primates; Catarrhini; Hominidae; Homo.

XX [1]

RN 1-6

RP Duesterhoeft A., Lauber J., Newes W., Gassenhuber J., Wiemann S.;

RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.

RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY

XX Clone from S. Wiemann, sequenced by Qiagen within the cDNA

sequencing consortium of the German Genome Project

CC No sl sequence available

CC This clone is available at the RZPD in Berlin

CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

XX Key Location/Qualifiers

FH source 1..6

FT /db_xref="taxon:9606"

FT /organism="Homo sapiens"

FT /clone="DKFZp434I0110"

FT /clone_lib="434 (synonym: htes3). Vector pSport1; host

FT DH10B; sites NotI + SalI"

FT /dev_stage="adult"

FT /tissue_type="testis"

XX SQ Sequence 6 BP; 2 A; 0 C; 2 G; 2 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 6;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1

Db 1 G 1

RESULT 24

HSM004423 standard; RNA; EST; 6 BP.


```

XX AC AL039947;
XX XX
SV SV
XX 12-MAR-1999 (Rel. 59, Created)
DT DT
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX XX
DE Homo sapiens mRNA; EST DKFZp434J0112_r1 (from clone DKFZp434J0112)
XX XX
KW EST: expressed sequence tag.
XX XX
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX [1]
RN 1-6
RA Duisterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
RT ;
RL Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX XX
CC Clone from S. Wiemann, sequenced by Qiagen within the cDNA
CC sequencing consortium of the German Genome Project
CC No si sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX XX
FH Key Location/Qualifiers
FH source
FT 1..6
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp434J0112"
FT /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"
XX XX
SQ Sequence 6 BP; 2 A; 0 C; 2 G; 2 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 g 1
DB 1 G 1

RESULT 25
HSM007334
ID HSM007334 standard; RNA; EST; 6 BP.
AC AC
XX AL042484.1
SV AL042484.1
XX XX
DT 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX XX
DE Homo sapiens mRNA; EST DKFZp434F0321_r1 (from clone DKFZp434F0321)
XX XX
KW EST: expressed sequence tag.
XX XX
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX [1]
RN 1-6
RA Duisterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
RT ;
RL Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX XX
CC Clone from S. Wiemann, sequenced by LMU within the cDNA
CC sequencing consortium of the German Genome Project
CC No si sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX XX
FH Key Location/Qualifiers
FH source
FT 1..6
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp434J0112"
FT /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"
XX XX
SQ Sequence 6 BP; 2 A; 0 C; 2 G; 2 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 g 1
DB 1 G 1

RESULT 26
HSM007683/c
ID HSM007683 standard; RNA; EST; 6 BP.
XX AC
XX AL042833;
XX SV AL042833.1
XX XX
DT 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX XX
DE Homo sapiens mRNA; EST DKFZp434G1622_r1 (from clone DKFZp434G1622)
XX XX
KW EST: expressed sequence tag.
XX XX
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX [1]
RN 1-6
RA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
RT ;
RL Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX XX
CC Clone from S. Wiemann, sequenced by LMU within the cDNA
CC sequencing consortium of the German Genome Project
CC No si sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX XX
FH Key Location/Qualifiers
FH source
FT 1..6
FT /db_xref="taxon:9606"

```

```

FT      /organism="Homo sapiens"
FT      /clone="DKF2p434G1622"
FT      /clone_lib="434 (synonym: htes3)}. Vector pSport1; host
FT      DH10B; sites Noti + Sali"
FT      /dev_stage="adult"
FT      /tissue_type="testis"
XX      Sequence 6 BP; 2 A; 2 C; 0 G; 2 T; 0 other;

Query Match      100.0%; Score 1; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 g 1
Db      6 G 6

RESULT 27
HSM008014/C
ID      HSM008014 standard; RNA; EST; 6 BP.
XX      AC AL043164;
XX      SV AL043164.1
XX      12-MAR-1999 (Rel. 59, Created)
DT      12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX      DE Homo sapiens mRNA; EST DKF2p434F1123_s1 (from clone DKF2p434F1123)
XX      KW EST; expressed sequence tag.
XX      OS Homo sapiens (human)
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC      Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX      RN [1]
RP      1-6
RA      Poustka A., Klein M., Mewes W., Gassenhuber J., Wiemann S.;
RT      Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL      MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX      CC Clone from S. Wiemann, sequenced by LMU within the cDNA
CC      sequencing consortium of the German Genome Project
CC      r1 sequence also available
CC      This clone is available at the RZPD in Berlin
CC      Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC      Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX      PH Key Location/Qualifiers
FH      source 1..6
FT      /db_xref="taxon:9606"
FT      /organism="Homo sapiens"
FT      /clone="DKF2p434F1123"
FT      /clone_lib="434 (synonym: htes3)}. Vector pSport1; host
FT      DH10B; sites Noti + Sali"
FT      /dev_stage="adult"
FT      /tissue_type="testis"
XX      SQ Sequence 6 BP; 2 A; 2 C; 0 G; 3 T; 0 other;

Query Match      100.0%; Score 1; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 g 1
Db      5 G 5

/organism="Homo sapiens"
/clone="DKF2p434G1622"
/clone_lib="434 (synonym: htes3)}. Vector pSport1; host
DH10B; sites Noti + Sali"
dev_stage="adult"
tissue_type="testis"

Sequence 6 BP; 1 A; 2 C; 0 G; 3 T; 0 other;

Query Match      100.0%; Score 1; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 g 1
Db      5 G 5

```

```

RESULT 28
HSM010918 standard; RNA; EST; 6 BP.
XX      ID HSM010918 standard; RNA; EST; 6 BP.
XX      AC AL046068;
XX      SV AL046068.1
XX      12-MAR-1999 (Rel. 59, Created)
DT      12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX      DE Homo sapiens mRNA; EST DKF2p434F1672_r1 (from clone DKF2p434F1672)
XX      KW EST; expressed sequence tag.
XX      OS Homo sapiens (human)
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC      Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX      RN [1]
RP      1-6
RA      Poustka A., Klein M., Mewes W., Gassenhuber J., Wiemann S.;
RT      Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL      MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX      CC Clone from S. Wiemann, sequenced by DKF2 within the cDNA
CC      sequencing consortium of the German Genome Project
CC      No s1 sequence available
CC      This clone is available at the RZPD in Berlin
CC      Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC      Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX      PH Key Location/Qualifiers
FH      source 1..6
FT      /db_xref="taxon:9606"
FT      /organism="Homo sapiens"
FT      /clone="DKF2p434F1672"
FT      /clone_lib="434 (synonym: htes3)}. Vector pSport1; host
FT      DH10B; sites Noti + Sali"
FT      /dev_stage="adult"
FT      /tissue_type="testis"
XX      SQ Sequence 6 BP; 0 A; 2 C; 2 G; 0 T; 2 other;

Query Match      100.0%; Score 1; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 g 1
Db      1 G 1

RESULT 29
HSM010918/C
ID      HSM010918 standard; RNA; EST; 6 BP.
XX      AC AL046068;
XX      SV AL046068.1
XX      12-MAR-1999 (Rel. 59, Created)
DT      12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX      DE Homo sapiens mRNA; EST DKF2p434F1672_r1 (from clone DKF2p434F1672)
XX      KW EST; expressed sequence tag.
XX

```

```

OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP 1-6
RA Poustka A., Klein M., Mewes W., Gassenhuber J., Wiemann S.;
RT :
RL Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferspitze 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by DKFZ within the cDNA
CC sequencing consortium of the German Genome Project
CC No SI sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH Key Location/Qualifiers
FH
FH 1. .6
FH /db_xref="taxon:9606"
FH /organism="Homo sapiens"
FH /clone="DKFZp434F1672"
FH /clone_lib="434 (synonym: htes)}. Vector pSport1; host
FH DH10B; sites NotI + SalI"
FH /dev_stage="adult"
FH /tissue_type="testis"
XX
SQ Sequence 6 BP; 0 A; 2 C; 2 G; 0 T; 2 other;

      Query Match      100.0%; Score 1; DB 2; Length 6;
      Best Local Similarity 100.0%; Pred. No. 0;
      Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
   |
Db 5 G 5

RESULT 30
BE726686
LOCUS      6 bp mRNA linear EST 14-SEP-2000
DEFINITION Chlamydomonas reinhardtii cDNA, mRNA sequence.
ACCESSION BE726686
VERSION BE726686.1 GI:10128110
KEYWORDS EST.
SOURCE Chlamydomonas reinhardtii.
ORGANISM Chlamydomonas reinhardtii.
REFERENCE 1 (bases 1 to 6)
AUTHORS Grossman,A., Davies,J., Federspiel,N., Harris,E., Lefebvre,P.,
McDermott,J.P., Silflow,C., Stern,D. and Surzycki,R.
ANALYSES OF THE CHLAMYDOMONAS REINHARDTII GENOME: A MODEL,
UNICELLULAR SYSTEM FOR ANALYZING GENE FUNCTION AND REGULATION IN
VASCULAR PLANTS; project phase 2
JOURNAL Unpublished (2000)
COMMENT Contact: Charles Hauser
DCMB Box 91000
Duke University
Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
Email: chauser@duke.edu.
FEATURES
Location/Qualifiers
1. .6
/organism="Chlamydomonas reinhardtii"
/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690, normalized, Lambda Zap
II"
II"
/Note="Vector: pBluescript II SK-; Site.1: EcoRI; Site.2:
XhoI; This library, constructed by John Davies and Jeffrey
McDermott, combines cDNAs from CC-1690 cells grown to
mid-log phase in TAP (acetate-containing) medium in the
light, TAP medium in the dark, HS (minimal) medium in
ambient levels of CO2 and HS medium bubbled with 5% CO2.
polyA mRNA was purified from each sample, pooled and cDNA
synthesized. The cDNA was directionally cloned into Lambda
ZAP II (Stratagene) in the EcoRI (5') and XhoI (3') sites.
pBluescript II SK- plasmids were excised from the lambda
ZAP clones by superinfection with ExAssist (Stratagene)
phage. The library was normalized using method 4 described
in Bonaldo et al (1996) Genome Research 6: 791-806."

```

```

II"
/Note="Vector: pBluescript II SK-; Site.1: EcoRI; Site.2:
XhoI; This library, constructed by John Davies and Jeffrey
McDermott, combines cDNAs from CC-1690 cells grown to
mid-log phase in TAP (acetate-containing) medium in the
light, TAP medium in the dark, HS (minimal) medium in
ambient levels of CO2 and HS medium bubbled with 5% CO2.
polyA mRNA was purified from each sample, pooled and cDNA
synthesized. The cDNA was directionally cloned into Lambda
ZAP II (Stratagene) in the EcoRI (5') and XhoI (3') sites.
pBluescript II SK- plasmids were excised from the lambda
ZAP clones by superinfection with ExAssist (Stratagene)
phage. The library was normalized using method 4 described
in Bonaldo et al (1996) Genome Research 6: 791-806."

BASE COUNT      0 a      1 c      5 g      0 t
ORIGIN

      Query Match      100.0%; Score 1; DB 10; Length 6;
      Best Local Similarity 100.0%; Pred. No. 0;
      Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
   |
Db 1 G 1

RESULT 31
BE726686/c
LOCUS      6 bp mRNA linear EST 14-SEP-2000
DEFINITION Chlamydomonas reinhardtii cDNA, mRNA sequence.
ACCESSION BE726686
VERSION BE726686.1 GI:10128110
KEYWORDS EST.
SOURCE Chlamydomonas reinhardtii.
ORGANISM Chlamydomonas reinhardtii.
REFERENCE 1 (bases 1 to 6)
AUTHORS Grossman,A., Davies,J., Federspiel,N., Harris,E., Lefebvre,P.,
McDermott,J.P., Silflow,C., Stern,D. and Surzycki,R.
ANALYSES OF THE CHLAMYDOMONAS REINHARDTII GENOME: A MODEL,
UNICELLULAR SYSTEM FOR ANALYZING GENE FUNCTION AND REGULATION IN
VASCULAR PLANTS; project phase 2
JOURNAL Unpublished (2000)
COMMENT Contact: Charles Hauser
DCMB Box 91000
Duke University
Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
Email: chauser@duke.edu.
FEATURES
Location/Qualifiers
1. .6
/organism="Chlamydomonas reinhardtii"
/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690, normalized, Lambda Zap
II"
II"
/Note="Vector: pBluescript II SK-; Site.1: EcoRI; Site.2:
XhoI; This library, constructed by John Davies and Jeffrey
McDermott, combines cDNAs from CC-1690 cells grown to
mid-log phase in TAP (acetate-containing) medium in the
light, TAP medium in the dark, HS (minimal) medium in
ambient levels of CO2 and HS medium bubbled with 5% CO2.
polyA mRNA was purified from each sample, pooled and cDNA
synthesized. The cDNA was directionally cloned into Lambda
ZAP II (Stratagene) in the EcoRI (5') and XhoI (3') sites.
pBluescript II SK- plasmids were excised from the lambda
ZAP clones by superinfection with ExAssist (Stratagene)
phage. The library was normalized using method 4 described
in Bonaldo et al (1996) Genome Research 6: 791-806."

```

```
BASE COUNT      0 a      1 c      5 g      0 t
ORIGIN

Query Match      100.0%; Score 1; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
   |
Db 2 G 2

RESULT 32
BG897546      standard; RNA; EST; 7 BP.
XX BG897546
AC BG897546;
XX
SV BG897546.1
XX
XX 09-JUN-2001 (Rel. 68, Created)
DT 14-NOV-2001 (Rel. 69, Last updated, Version 2)
XX
DE HOA14-1-H11 HOA (Human Osteoarthritic Cartilage) Homo sapiens cDNA, mRNA
DE sequence.
XX
XX EST.
XX
XX Homo sapiens (human)
OS
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
XX [1]
RN
RP 1-7
RX MEDLINE: 21482651.
RX PUBMED: 11597177.
RA Kumar S., Connor J.R., Dodds R.A., Halsey W., Van Horn M., Mao J.,
RA Sathe G.M., Mui P., Agarwal P., Badger A.M., Lee J.C., Gowen M., Lark M.W.;
RA "Identification and initial characterization of 5000 expressed sequenced
RT tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA
RT libraries";
RT Osteoarthriti Cartilage 9(7):641-653(2001).
RL
XX
XX Contact: Sanjay Kumar
CC UW2109
CC GlaxoSmithKline
CC 709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
CC Tel: 610-270-7245
CC Fax: 610-270-5598
CC Email: sanjay_kumar-legsk.com
CC Seq primer: T7.
XX
XX Key      Location/Qualifiers
FH
FH source      1..7
FT      /db_xref="taxon:9606"
FT      /note="Vector: pSPORT 1; Site_1: SalI; Site_2: NotI;
FT      Directional"
FT      /organism="Homo sapiens"
FT      /clone_lib="HOA (Human Osteoarthritic Cartilage)"
FT      /tissue_type="cartilage"
FT      /lab_host="E.coli DH10 B"
XX
SQ      Sequence 7 BP; 1 A; 3 C; 1 G; 2 T; 0 other;

Query Match      100.0%; Score 1; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
   |
Db 7 G 7

RESULT 34
HSM007412
XX HSM007412      standard; RNA; EST; 7 BP.
XX
XX AL042562;
XX
SV AL042562.1
```

```

XX 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE Homo sapiens mRNA; EST DKF2p434J1721_r1 (from clone DKF2p434J1721)
XX
KW EST; expressed sequence tag.
XX
US Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
XX [1]
RP 1-7
RA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
RL Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
XX Clone from S. Wiemann, sequenced by LMU within the cDNA
CC sequencing consortium of the German Genome Project
CC No SI sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
XX Key Location/Qualifiers
FH
FH source 1..7
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKF2p434J1721"
FT /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"
XX
XX Sequence 7 BP; 2 A; 1 C; 2 G; 2 T; 0 other;
SQ
Query Match 100.0%; Score 1; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. NO. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 g 1
Db 2 G 2
RESULT 35
HSM007412/c
ID HSM007412 standard; RNA; EST; 7 BP.
XX
XX AL042562;
XX
XX AL042562.1
XX
XX 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
XX Homo sapiens mRNA; EST DKF2p434J1721_r1 (from clone DKF2p434J1721)
XX
XX EST; expressed sequence tag.
XX
XX Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
XX [1]
RP 1-7
RA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
RL Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.

```

```

RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
XX Clone from S. Wiemann, sequenced by LMU within the cDNA
CC sequencing consortium of the German Genome Project
CC No SI sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
XX Key Location/Qualifiers
FH
FH source 1..7
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKF2p434J1721"
FT /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"
XX
XX Sequence 7 BP; 2 A; 1 C; 2 G; 2 T; 0 other;
SQ
Query Match 100.0%; Score 1; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. NO. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 g 1
Db 1 G 1
RESULT 36
HSM007502
ID HSM007502 standard; RNA; EST; 7 BP.
XX
XX AL042652;
XX
XX AL042652.1
XX
XX 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
XX Homo sapiens mRNA; EST DKF2p434N1921_r1 (from clone DKF2p434N1921)
XX
XX EST; expressed sequence tag.
XX
XX Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
XX [1]
RP 1-7
RA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
RL Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
XX Clone from S. Wiemann, sequenced by LMU within the cDNA
CC sequencing consortium of the German Genome Project
CC No SI sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
XX Key Location/Qualifiers
FH
FH source 1..7
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKF2p434N1921"
FT /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT DH10B; sites NotI + SalI"

```

```

FT      /dev_stage="adult"
XX      /tissue_type="testis"
SQ      Sequence 7 BP; 0 A; 1 C; 3 G; 3 T; 0 other;

Query Match      100.0%; Score 1; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 g 1
Db      2 G 2

RESULT 37
HSM007502/C
ID      HSM007502 standard; RNA; EST; 7 BP.
XX
AC      AL042652;
XX
SV      AL042652.1
XX
DT      12-MAR-1999 (Rel. 59, Created)
DT      12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE      Homo sapiens mRNA; EST DKFZp434N1921_r1 (from clone DKFZp434N1921)
XX
KW      EST; expressed sequence tag.
XX
OS      Homo sapiens (human)
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC      Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
[1]
RA      Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
RT      ;
RL      Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL      MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC      Clone from S. Wiemann, sequenced by LMU within the cDNA
CC      sequencing consortium of the German Genome Project
CC      No sl sequence available
CC      This clone is available at the RZPD in Berlin
CC      Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC      Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH      Key      Location/Qualifiers
FT      source
FT      1..7
FT      /db_xref="taxon:9606"
FT      /organism="Homo sapiens"
FT      /clone="DKFZp434N1921"
FT      /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT      DH10B; sites NotI + SalI"
FT      /dev_stage="adult"
FT      /tissue_type="testis"
XX
SQ      Sequence 7 BP; 0 A; 1 C; 3 G; 3 T; 0 other;

Query Match      100.0%; Score 1; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 g 1
Db      1 G 1

RESULT 38
C58888

```

```

LOCUS      C58888      7 bp      mRNA      linear      EST 22-SEP-1997
DEFINITION clone Yk383a7 3', mRNA sequence.
ACCESSION  C58888
VERSION    C58888
KEYWORDS   EST.
SOURCE     Caenorhabditis elegans.
ORGANISM   Caenorhabditis elegans.
REFERENCE  1 (bases 1 to 7)
AUTHORS    Kohara,Y., Motohashi,T., Tabara,H., Watanabe,H., Sugimoto,A., Sano
            ,M., Miyata,A. and Nishigaki,A.
TITLE      Expression map of the C.elegans genome
JOURNAL    Unpublished (1996)
COMMENT    Contact: Yuji Kohara
            Genome Biology Lab.
            National Institute of Genetics
            Yata 1111, Mishima, Shizuoka 411, Japan
            Tel: 81-559-81-6854
            Fax: 81-559-81-6855
            Email: ykohara@lab.nig.ac.jp.
FEATURES   Location/Qualifiers
            1..7
            /organism="Caenorhabditis elegans"
            /strain="CB1489 him-8(e1489)"
            /db_xref="taxon:6239"
            /clone="yk383a7"
            /clone_lib="Yuji Kohara unpublished cDNA"
            /sex="hermaphrodite, male"
            /tissue_type="whole animal"
            /dev_stage="varied"
BASE COUNT  2 a      0 c      1 g      3 t      1 others
ORIGIN
Query Match      100.0%; Score 1; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 g 1
Db      7 G 7

RESULT 39
HSM001420/C
ID      HSM001420 standard; RNA; EST; 8 BP.
XX
AC      AL037095;
XX
SV      AL037095.1
XX
DT      12-MAR-1999 (Rel. 59, Created)
DT      12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE      Homo sapiens mRNA; EST DKFZp564L2064_r1 (from clone DKFZp564L2064)
XX
KW      EST; expressed sequence tag.
XX
OS      Homo sapiens (human)
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC      Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
[1]
RA      Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
RT      ;
RL      Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL      MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC      Clone from S. Wiemann, sequenced by Qiagen within the cDNA
CC      sequencing consortium of the German Genome Project

```

CC No sl sequence available
 CC This clone is available at the RZPD in Berlin
 CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
 CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

XX Key Location/Qualifiers

FH source

FT 1. .8
 FT /db_xref="taxon:9606"
 FT /organism="Homo sapiens"
 FT /clone="DKFZp564L2064"
 FT /clone_lib="564 (synonym: hfbr2). Vector pAMP1; host
 FT Xl-2blue; sites NotI + SalI"
 FT /dev_stage="fetal"
 FT /tissue_type="brain"

XX Sequence 8 BP; 2 A; 3 C; 0 G; 3 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1

Db 7 G 7

RESULT 40

HS0001743/c

ID HSM001743 standard; RNA; EST; 8 BP.

XX AC AL037413;

XX SV AL037413.1

XX 12-MAR-1999 (Rel. 59, Created)

DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)

XX Homo sapiens mRNA; EST DKFZp564L0771_s1 (from clone DKFZp564L0771)

XX EST; expressed sequence tag.

XX Homo sapiens (human)

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;

OC Eutheria; Primates; Catarrhini; Hominidae; Homo.

XX [1]

RA Bloeker H., Boescher M., Brandt P., Mewes W., Gassenhuber J., Wiemann S.;

RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.

RL MIPS, Am Klopferspitze 18a D-82152 Martinsried, GERMANY

XX Clone from S. Wiemann, sequenced by GBF within the cDNA

CC sequencing consortium of the German Genome Project

CC No sl sequence available

CC This clone is available at the RZPD in Berlin

CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

XX Key Location/Qualifiers

FH source

FT 1. .8
 FT /db_xref="taxon:9606"
 FT /organism="Homo sapiens"
 FT /clone="DKFZp564L0771"
 FT /clone_lib="564 (synonym: hfbr2). Vector pAMP1; host
 FT Xl-2blue; sites NotI + SalI"
 FT /dev_stage="fetal"
 FT /tissue_type="brain"

XX Sequence 8 BP; 1 A; 7 C; 0 G; 0 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1

Db 7 G 7

RESULT 41

HS0004451

ID HSM004451 standard; RNA; EST; 8 BP.

XX AC AL039975;

XX SV AL039975.1

XX 12-MAR-1999 (Rel. 59, Created)

DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)

XX Homo sapiens mRNA; EST DKFZp434K0712_r1 (from clone DKFZp434K0712)

XX EST; expressed sequence tag.

XX Homo sapiens (human)

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;

OC Eutheria; Primates; Catarrhini; Hominidae; Homo.

XX [1]

RA Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;

RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.

RL MIPS, Am Klopferspitze 18a D-82152 Martinsried, GERMANY

XX Clone from S. Wiemann, sequenced by Qiagen within the cDNA

CC sequencing consortium of the German Genome Project

CC No sl sequence available

CC This clone is available at the RZPD in Berlin

CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

XX Key Location/Qualifiers

FH source

FT 1. .8
 FT /db_xref="taxon:9606"
 FT /organism="Homo sapiens"
 FT /clone="DKFZp434K0712"
 FT /clone_lib="434 (synonym: htes3). Vector pSport1; host
 FT DH10B; sites NotI + SalI"
 FT /dev_stage="adult"
 FT /tissue_type="testis"

XX Sequence 8 BP; 2 A; 2 C; 2 G; 2 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1

Db 1 G 1

RESULT 42

HS0004451/c

ID HSM004451 standard; RNA; EST; 8 BP.

XX AC AL039975;

```

SV AL039975.1
XX 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE Homo sapiens mRNA; EST DKFZp434K0712_r1 (from clone DKFZp434K0712)
XX
KW EST; expressed sequence tag.
XX
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN [1]
RP 1-8
RA Dueterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
RT ;
RL Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RI MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by Qiagen within the cDNA
CC sequencing consortium of the German Genome Project
CC No sl sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH Key Location/Qualifiers
FT source 1..8
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp434K0712"
FT /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"
XX
SQ Sequence 8 BP; 2 A; 2 C; 2 G; 2 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 8 G 8

RESULT 43
HSM007277
ID HSM007277 standard; RNA; EST; 8 BP.
XX
AC AL042427;
SV AL042427.1
XX
DT 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE Homo sapiens mRNA; EST DKFZp434C2421_r1 (from clone DKFZp434C2421)
XX
KW EST; expressed sequence tag.
XX
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN [1]
RP 1-8
RA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
RT ;
RL Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RI MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by LMU within the cDNA
CC sequencing consortium of the German Genome Project
CC No sl sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH Key Location/Qualifiers
FT source 1..8
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp434C2421"
FT /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"
XX
SQ Sequence 8 BP; 2 A; 2 C; 2 G; 2 T; 0 other;

```

```

RL Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by LMU within the cDNA
CC sequencing consortium of the German Genome Project
CC No sl sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH Key Location/Qualifiers
FT source 1..8
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp434C2421"
FT /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"
XX
SQ Sequence 8 BP; 2 A; 2 C; 2 G; 2 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 1 G 1

RESULT 44
HSM007277/c
ID HSM007277 standard; RNA; EST; 8 BP.
XX
AC AL042427;
XX
SV AL042427.1
XX
DT 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE Homo sapiens mRNA; EST DKFZp434C2421_r1 (from clone DKFZp434C2421)
XX
KW EST; expressed sequence tag.
XX
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN [1]
RP 1-8
RA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
RT ;
RL Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RI MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by LMU within the cDNA
CC sequencing consortium of the German Genome Project
CC No sl sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH Key Location/Qualifiers
FT source 1..8
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp434C2421"
FT /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"
XX
SQ Sequence 8 BP; 2 A; 2 C; 2 G; 2 T; 0 other;

```


Search completed: July 15, 2002, 20:07:36
Job time: 14494 sec

```

FT      DH10B; sites NotI + Sall"
FT      /dev_stage="adult"
FT      /tissue_type="testis"
XX
SQ      Sequence 8 BP; 2 A; 2 C; 2 G; 2 T; 0 other;

Query Match      100.0%; Score 1; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 g 1
        |
Db      8 G 8

RESULT 45
HSM007323
ID      HSM007323 standard; RNA; EST; 8 BP.
XX
AC      AL042473;
XX
SV      AL042473.1
XX
DT      12-MAR-1999 (Rel. 59, Created)
DT      12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE      Homo sapiens mRNA; EST DKFZp434F012l_r1 (from clone DKFZp434F012l)
XX
KW      EST; expressed sequence tag.
XX
OS      Homo sapiens (human)
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC      Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN      [1]
RP      1-8
RT      ;
RL      Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL      MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC      Clone from S. Wiemann, sequenced by LMU within the cDNA
CC      sequencing consortium of the German Genome Project
CC      No sl sequence available
CC      This clone is available at the RZPD in Berlin
CC      Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC      Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH      Key      Location/Qualifiers
FH      source      1..8
FH      /db_xref="taxon:9606"
FH      /organism="Homo sapiens"
FH      /clone="DKFZp434F012l"
FH      /clone_lib="434 (synonym: htes3). Vector pSport1; host
FH      DH10B; sites NotI + Sall"
FH      /dev_stage="adult"
FH      /tissue_type="testis"
XX
SQ      Sequence 8 BP; 2 A; 2 C; 2 G; 2 T; 0 other;

Query Match      100.0%; Score 1; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 g 1
        |
Db      1 G 1

```

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 16, 2002, 02:50:26 : Search time 12941.8 seconds
(without alignments)
1.672 Million cell updates/sec

Title: US-09-375-248-1_COPY_2588_2588

Perfect score: 1
Sequence: 1 g 1

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 21979536 seqs, 10817449327 residues

Word size : 0

Total number of hits satisfying chosen parameters: 43959072

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Pending_Patents_NA_Main:*

- 1: /cgn2_6/ptodata/2/pna/PCTUS_COMB.seq:*
- 2: /cgn2_6/ptodata/2/pna/US06_COMB.seq:*
- 3: /cgn2_6/ptodata/2/pna/US07_COMB.seq:*
- 4: /cgn2_6/ptodata/2/pna/US080_COMB.seq:*
- 5: /cgn2_6/ptodata/2/pna/US081_COMB.seq:*
- 6: /cgn2_6/ptodata/2/pna/US082_COMB.seq:*
- 7: /cgn2_6/ptodata/2/pna/US083_COMB.seq:*
- 8: /cgn2_6/ptodata/2/pna/US084_COMB.seq:*
- 9: /cgn2_6/ptodata/2/pna/US085_COMB.seq:*
- 10: /cgn2_6/ptodata/2/pna/US086_COMB.seq:*
- 11: /cgn2_6/ptodata/2/pna/US087_COMB.seq:*
- 12: /cgn2_6/ptodata/2/pna/US088_COMB.seq:*
- 13: /cgn2_6/ptodata/2/pna/US089_COMB.seq:*
- 14: /cgn2_6/ptodata/2/pna/US090_COMB.seq:*
- 15: /cgn2_6/ptodata/2/pna/US091_COMB.seq:*
- 16: /cgn2_6/ptodata/2/pna/US092_COMB.seq:*
- 17: /cgn2_6/ptodata/2/pna/US093_COMB.seq:*
- 18: /cgn2_6/ptodata/2/pna/US094_COMB.seq:*
- 19: /cgn2_6/ptodata/2/pna/US095A_COMB.seq:*
- 20: /cgn2_6/ptodata/2/pna/US095B_COMB.seq:*
- 21: /cgn2_6/ptodata/2/pna/US095C_COMB.seq:*
- 22: /cgn2_6/ptodata/2/pna/US095D_COMB.seq:*
- 23: /cgn2_6/ptodata/2/pna/US096A_COMB.seq:*
- 24: /cgn2_6/ptodata/2/pna/US096B_COMB.seq:*
- 25: /cgn2_6/ptodata/2/pna/US096C_COMB.seq:*
- 26: /cgn2_6/ptodata/2/pna/US096D_COMB.seq:*
- 27: /cgn2_6/ptodata/2/pna/US096E_COMB.seq:*
- 28: /cgn2_6/ptodata/2/pna/US097A_COMB.seq:*
- 29: /cgn2_6/ptodata/2/pna/US097B_COMB.seq:*
- 30: /cgn2_6/ptodata/2/pna/US097C_COMB.seq:*
- 31: /cgn2_6/ptodata/2/pna/US098A_COMB.seq:*
- 32: /cgn2_6/ptodata/2/pna/US098B_COMB.seq:*
- 33: /cgn2_6/ptodata/2/pna/US098C_COMB.seq:*
- 34: /cgn2_6/ptodata/2/pna/US099A_COMB.seq:*
- 35: /cgn2_6/ptodata/2/pna/US099B_COMB.seq:*
- 36: /cgn2_6/ptodata/2/pna/US099C_COMB.seq:*
- 37: /cgn2_6/ptodata/2/pna/US100_COMB.seq:*
- 38: /cgn2_6/ptodata/2/pna/US101_COMB.seq:*
- 39: /cgn2_6/ptodata/2/pna/US6000_COMB.seq:*
- 40: /cgn2_6/ptodata/2/pna/US6001_COMB.seq:*
- 41: /cgn2_6/ptodata/2/pna/US6002_COMB.seq:*
- 42: /cgn2_6/ptodata/2/pna/US6003_COMB.seq:*
- 43: /cgn2_6/ptodata/2/pna/US6004_COMB.seq:*

- 44: /cgn2_6/ptodata/2/pna/US6005_COMB.seq:*
- 45: /cgn2_6/ptodata/2/pna/US6006_COMB.seq:*
- 46: /cgn2_6/ptodata/2/pna/US6007_COMB.seq:*
- 47: /cgn2_6/ptodata/2/pna/US6008_COMB.seq:*
- 48: /cgn2_6/ptodata/2/pna/US6009_COMB.seq:*
- 49: /cgn2_6/ptodata/2/pna/US6010_COMB.seq:*
- 50: /cgn2_6/ptodata/2/pna/US6011_COMB.seq:*
- 51: /cgn2_6/ptodata/2/pna/US6012_COMB.seq:*
- 52: /cgn2_6/ptodata/2/pna/US6013_COMB.seq:*
- 53: /cgn2_6/ptodata/2/pna/US6014_COMB.seq:*
- 54: /cgn2_6/ptodata/2/pna/US6015_COMB.seq:*
- 55: /cgn2_6/ptodata/2/pna/US6016_COMB.seq:*
- 56: /cgn2_6/ptodata/2/pna/US6017_COMB.seq:*
- 57: /cgn2_6/ptodata/2/pna/US6018_COMB.seq:*
- 58: /cgn2_6/ptodata/2/pna/US6019_COMB.seq:*
- 59: /cgn2_6/ptodata/2/pna/US6020_COMB.seq:*
- 60: /cgn2_6/ptodata/2/pna/US6021_COMB.seq:*
- 61: /cgn2_6/ptodata/2/pna/US6022_COMB.seq:*
- 62: /cgn2_6/ptodata/2/pna/US6023_COMB.seq:*
- 63: /cgn2_6/ptodata/2/pna/US6024_COMB.seq:*
- 64: /cgn2_6/ptodata/2/pna/US6025_COMB.seq:*
- 65: /cgn2_6/ptodata/2/pna/US6026_COMB.seq:*
- 66: /cgn2_6/ptodata/2/pna/US6027_COMB.seq:*
- 67: /cgn2_6/ptodata/2/pna/US6028_COMB.seq:*
- 68: /cgn2_6/ptodata/2/pna/US6029_COMB.seq:*
- 69: /cgn2_6/ptodata/2/pna/US6030_COMB.seq:*
- 70: /cgn2_6/ptodata/2/pna/US6031_COMB.seq:*
- 71: /cgn2_6/ptodata/2/pna/US6032_COMB.seq:*
- 72: /cgn2_6/ptodata/2/pna/US6033_COMB.seq:*
- 73: /cgn2_6/ptodata/2/pna/US6034_COMB.seq:*
- 74: /cgn2_6/ptodata/2/pna/US6035_COMB.seq:*
- 75: /cgn2_6/ptodata/2/pna/US6036_COMB.seq:*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1	100.0	2	3	US-07-934-385-14
2	1	100.0	2	5	US-08-107-721-46
3	1	100.0	2	5	US-08-107-721B-46
4	1	100.0	2	15	US-09-172-828-15
5	1	100.0	2	16	US-09-284-725-201
6	1	100.0	2	17	US-09-306-333A-32
7	1	100.0	2	17	US-09-306-333A-32
8	1	100.0	2	17	US-09-387-777-2
9	1	100.0	2	17	US-09-387-777-3
10	1	100.0	2	17	US-09-387-777-5
11	1	100.0	2	17	US-09-387-777-6
12	1	100.0	2	17	US-09-387-777-7
13	1	100.0	2	17	US-09-387-777-7
14	1	100.0	2	17	US-09-387-777-8
15	1	100.0	2	17	US-09-387-777-9
16	1	100.0	2	17	US-09-387-777-10
17	1	100.0	2	17	US-09-387-777-10
18	1	100.0	2	17	US-09-387-777-11
19	1	100.0	2	17	US-09-387-777-12
20	1	100.0	2	17	US-09-387-777-14
21	1	100.0	2	17	US-09-387-777-15
22	1	100.0	2	18	US-09-472-035A-19
23	1	100.0	2	18	US-09-472-035A-20
24	1	100.0	2	24	US-09-634-306B-51869
25	1	100.0	2	24	US-09-634-306B-52280
26	1	100.0	2	24	US-09-634-306B-52357
27	1	100.0	2	24	US-09-634-306B-53003
28	1	100.0	2	24	US-09-634-306B-58305
29	1	100.0	2	24	US-09-634-306B-175312
30	1	100.0	2	24	US-09-634-306B-175337
31	1	100.0	2	24	US-09-634-306B-175354

32 1 100.0 2 24 US-09-634-306B-175401 Sequence 175401,
33 1 100.0 2 24 US-09-634-306B-175403 Sequence 175403,
34 1 100.0 2 24 US-09-634-306B-175415 Sequence 175415,
35 1 100.0 2 24 US-09-634-306B-175419 Sequence 175419,
36 1 100.0 2 24 US-09-634-306B-175426 Sequence 175426,
37 1 100.0 2 24 US-09-634-306B-175433 Sequence 175433,
38 1 100.0 2 24 US-09-634-306B-175849 Sequence 175849,
39 1 100.0 2 24 US-09-634-306B-176848 Sequence 176848,
40 1 100.0 2 24 US-09-634-306B-176849 Sequence 176849,
41 1 100.0 2 24 US-09-634-306B-176880 Sequence 176880,
42 1 100.0 2 24 US-09-634-306B-178420 Sequence 178420,
43 1 100.0 2 24 US-09-634-306B-178440 Sequence 178440,
44 1 100.0 2 24 US-09-634-306B-178440 Sequence 178440,
45 1 100.0 2 24 US-09-634-306B-178617 Sequence 178617,

ALIGNMENTS

RESULT 1
US-07-934-385-14
; Sequence 14, Application US/07934385
; GENERAL INFORMATION:
; APPLICANT: LATHAM, JOHN
; APPLICANT: LEUNG, LAWRENCE
; TITLE OF INVENTION: APTAMERS SPECIFIC FOR BIOMOLECULES
; TITLE OF INVENTION: CONTAINING MODIFIED NUCLEOTIDE RESIDUES
; NUMBER OF SEQUENCES: 177
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/934,385
; FILING DATE: 19920821
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: GRACEY, NANCY J.
; REGISTRATION NUMBER: 28,216
; REFERENCE/DOCKET NUMBER: 24610-20022.22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: misc_difference
; LOCATION: replace(1,*)
; OTHER INFORMATION: /note= "This position is a
; biotin-17 nucleotide stretch of random sequences."
US-07-934-385-14

Query Match 100.0%; Score 1; DB 3; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 g 1
Db 2 G 2

RESULT 2
US-08-107-721-46
; Sequence 46, Application US/08107721
; GENERAL INFORMATION:
; APPLICANT: TOOLE, JOHN J.
; APPLICANT: GRIFFIN, LINDA C.
; APPLICANT: BOCK, LOUIS C.
; APPLICANT: LATHAM, JOHN A.
; APPLICANT: MUENCHAU, DARYL D.
; APPLICANT: KRAWCZYK, STEVEN
; TITLE OF INVENTION: APTAMERS SPECIFIC FOR BIOMOLECULES AND
; TITLE OF INVENTION: METHODS OF MAKING
; NUMBER OF SEQUENCES: 109
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GILEAD SCIENCES, INC.
; STREET: 344 LAKESIDE DRIVE
; CITY: FOSTER CITY
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/107,721
; FILING DATE: 20-AUG-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: GRACEY, NANCY J.
; REGISTRATION NUMBER: 28216
; REFERENCE/DOCKET NUMBER: 24610-20022.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)574-3000
; TELEFAX: (415)578-9264
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1
; OTHER INFORMATION: /note= "This is a biotin-17
; nucleotide stretch of abasic residues."
US-08-107-721-46
Query Match 100.0%; Score 1; DB 5; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 g 1
Db 2 G 2
RESULT 3
US-08-107-721B-46
; Sequence 46, Application US/08107721B
; GENERAL INFORMATION:
; APPLICANT: TOOLE, JOHN J.
; APPLICANT: GRIFFIN, LINDA C.
; APPLICANT: BOCK, LOUIS C.
; APPLICANT: LATHAM, JOHN A.
; APPLICANT: MUENCHAU, DARYL D.
; APPLICANT: KRAWCZYK, STEVEN
; TITLE OF INVENTION: APTAMERS SPECIFIC FOR BIOMOLECULES AND
; TITLE OF INVENTION: METHODS OF MAKING

;; PRIOR APPLICATION NUMBER: PCT/IB00/01607
;; PRIOR FILING DATE: 2000-11-06
;; NUMBER OF SEQ ID NOS: 122
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 32
;; LENGTH: 2
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-306-333A-32

Query Match 100.0%; Score 1; DB 17; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Caps 0;

Qy 1 q 1
Db 2 g 2

RESULT 7

US-09-306-333A-32/c
;; SEQUENCE 32, Application US/09306333A
;; GENERAL INFORMATION:
;; APPLICANT: Academy of Applied Science
;; TITLE OF INVENTION: BRCA1 and hMLH1 Gene Primer Sequences and Method for
;; FILE REFERENCE: BRCA1
;; CURRENT APPLICATION NUMBER: US/09/306,333A
;; CURRENT FILING DATE: 1999-05-06
;; PRIOR APPLICATION NUMBER: PCT/IB00/01607
;; PRIOR FILING DATE: 2000-11-06
;; NUMBER OF SEQ ID NOS: 122
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 32
;; LENGTH: 2
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-306-333A-32

Query Match 100.0%; Score 1; DB 17; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Caps 0;

Qy 1 q 1
Db 1 g 1

RESULT 8

US-09-387-777-2/c
;; SEQUENCE 2, Application US/0938777
;; GENERAL INFORMATION:
;; APPLICANT: Hadar Kless
;; TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
;; TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
;; TITLE OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS
;; NUMBER OF SEQUENCES: 88
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
;; STREET: 2001 Jefferson Davis Highway, Suite 207
;; CITY: Arlington
;; STATE: Virginia
;; COUNTRY: United States of America
;; ZIP: 22202
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
;; COMPUTER: Twinhead* Slimnote-890TX
;; OPERATING SYSTEM: MS DOS version 6.2,
;; SOFTWARE: Word for Windows version 2.0 converted
;; TO AN ASCII FILE

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/387,777
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Friedman, Mark M.
;; REGISTRATION NUMBER: 33,883
;; REFERENCE/DOCKET NUMBER: 34/40
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 972-3-5625553
;; TELEFAX: 972-3-5625554
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 2
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
US-09-387-777-2

Query Match 100.0%; Score 1; DB 17; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Caps 0;

Qy 1 q 1
Db 2 g 2

RESULT 9

US-09-387-777-3
;; SEQUENCE 3, Application US/0938777
;; GENERAL INFORMATION:
;; APPLICANT: Hadar Kless
;; TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
;; TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
;; TITLE OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS
;; NUMBER OF SEQUENCES: 88
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
;; STREET: 2001 Jefferson Davis Highway, Suite 207
;; CITY: Arlington
;; STATE: Virginia
;; COUNTRY: United States of America
;; ZIP: 22202
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
;; COMPUTER: Twinhead* Slimnote-890TX
;; OPERATING SYSTEM: MS DOS version 6.2,
;; SOFTWARE: Word for Windows version 2.0 converted
;; TO AN ASCII FILE
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/387,777
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Friedman, Mark M.
;; REGISTRATION NUMBER: 33,883
;; REFERENCE/DOCKET NUMBER: 34/40
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 972-3-5625553
;; TELEFAX: 972-3-5625554
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:

```

:      LENGTH: 2
:      TYPE: nucleic acid
:      STRANDEDNESS: single
:      TOPOLOGY: linear
US-09-387-777-3
Query Match      100.0%; Score 1; DB 17; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 2 G 2

RESULT 10
US-09-387-777-5/c
: Sequence 5, Application US/09387777
: GENERAL INFORMATION:
: APPLICANT: Hadar Kless
: TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
: TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
: NUMBER OF SEQUENCES: 88
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
: STREET: 2001 Jefferson Davis Highway, Suite 207
: CITY: Arlington
: STATE: Virginia
: COUNTRY: United States of America
: ZIP: 22202
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
: COMPUTER: Twinhead* Slimnote-890TX
: OPERATING SYSTEM: MS DOS version 6.2,
: SOFTWARE: Word for Windows version 3.11
: SOFTWARE: Word for Windows version 2.0 converted
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/387,777
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Friedman, Mark M.
: REGISTRATION NUMBER: 33,883
: REFERENCE/DOCKET NUMBER: 34/40
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 972-3-5625553
: TELEFAX: 972-3-5625554
: TELEX:
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
US-09-387-777-5
Query Match      100.0%; Score 1; DB 17; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 1 G 1

RESULT 11
US-09-387-777-6/c
: Sequence 6, Application US/09387777
: GENERAL INFORMATION:
: APPLICANT: Hadar Kless
: TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
: TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
: NUMBER OF SEQUENCES: 88
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
: STREET: 2001 Jefferson Davis Highway, Suite 207
: CITY: Arlington
: STATE: Virginia
: COUNTRY: United States of America
: ZIP: 22202
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
: COMPUTER: Twinhead* Slimnote-890TX
: OPERATING SYSTEM: MS DOS version 6.2,
: SOFTWARE: Word for Windows version 3.11
: SOFTWARE: Word for Windows version 2.0 converted
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/387,777
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Friedman, Mark M.
: REGISTRATION NUMBER: 33,883
: REFERENCE/DOCKET NUMBER: 34/40
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 972-3-5625553
: TELEFAX: 972-3-5625554
: TELEX:
: INFORMATION FOR SEQ ID NO: 6:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
US-09-387-777-6
Query Match      100.0%; Score 1; DB 17; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 2 G 2

RESULT 12
US-09-387-777-7
: Sequence 7, Application US/09387777
: GENERAL INFORMATION:
: APPLICANT: Hadar Kless
: TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
: TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
: NUMBER OF SEQUENCES: 88
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
: STREET: 2001 Jefferson Davis Highway, Suite 207
: CITY: Arlington
: STATE: Virginia
: COUNTRY: United States of America
: ZIP: 22202
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
```

; COMPUTER: Twinhead* Slimnote-890TX
; OPERATING SYSTEM: MS DOS version 6.2,
; SOFTWARE: Word for Windows version 3.11
; SOFTWARE: Word for Windows version 2.0 converted
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/387,777
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Friedmam, Mark M.
; REGISTRATION NUMBER: 33,883
; REFERENCE/DOCKET NUMBER: 34/40
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 972-3-5625553
; TELEFAX: 972-3-5625554
; TELEX:
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-387-777-7

Query Match 100.0%; Score 1; DB 17; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 2 G 2

RESULT 13
US-09-387-777-7/c
; Sequence 7, Application US/09387777
; GENERAL INFORMATION:
; APPLICANT: Hadar Kless
; TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
; TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
; TITLE OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
; STREET: 2001 Jefferson Davis Highway, Suite 207
; CITY: Arlington
; STATE: Virginia
; COUNTRY: United States of America
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
; COMPUTER: Twinhead* Slimnote-890TX
; OPERATING SYSTEM: MS DOS version 6.2,
; SOFTWARE: Word for Windows version 3.11
; SOFTWARE: Word for Windows version 2.0 converted
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/387,777
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Friedmam, Mark M.
; REGISTRATION NUMBER: 33,883
; REFERENCE/DOCKET NUMBER: 34/40
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 972-3-5625553
; TELEFAX: 972-3-5625554
; TELEX:
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-387-777-7

Query Match 100.0%; Score 1; DB 17; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 q 1
Db 1 G 1

RESULT 14
US-09-387-777-8/c
; Sequence 8, Application US/09387777
; GENERAL INFORMATION:
; APPLICANT: Hadar Kless
; TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
; TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
; TITLE OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
; STREET: 2001 Jefferson Davis Highway, Suite 207
; CITY: Arlington
; STATE: Virginia
; COUNTRY: United States of America
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
; COMPUTER: Twinhead* Slimnote-890TX
; OPERATING SYSTEM: MS DOS version 6.2,
; SOFTWARE: Word for Windows version 3.11
; SOFTWARE: Word for Windows version 2.0 converted
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/387,777
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Friedmam, Mark M.
; REGISTRATION NUMBER: 33,883
; REFERENCE/DOCKET NUMBER: 34/40
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 972-3-5625553
; TELEFAX: 972-3-5625554
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-387-777-8

Query Match 100.0%; Score 1; DB 17; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1


```
Db      1 G 1

RESULT 15
US-09-387-777-9
; Sequence 9, Application US/09387777
; GENERAL INFORMATION:
; APPLICANT: Hadar Kless
; TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
; TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
; STREET: 2001 Jefferson Davis Highway, Suite 207
; CITY: Arlington
; STATE: Virginia
; COUNTRY: United States of America
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
; COMPUTER: Twinhead* Slimnote-890TX
; OPERATING SYSTEM: MS DOS version 6.2,
; SOFTWARE: Word for Windows version 2.0 converted
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/387,777
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Friedman, Mark M.
; REGISTRATION NUMBER: 33,883
; REFERENCE/DOCKET NUMBER: 34/40
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 972-3-562553
; TELEFAX: 972-3-562554
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-387-777-9

Query Match      100.0%; Score 1; DB 17; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 g 1
       |
Db      1 G 1

RESULT 16
US-09-387-777-10
; Sequence 10, Application US/09387777
; GENERAL INFORMATION:
; APPLICANT: Hadar Kless
; TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
; TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
; STREET: 2001 Jefferson Davis Highway, Suite 207
; CITY: Arlington
; STATE: Virginia
; COUNTRY: United States of America
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
; COMPUTER: Twinhead* Slimnote-890TX
; OPERATING SYSTEM: MS DOS version 6.2,
; SOFTWARE: Word for Windows version 2.0 converted
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/387,777
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Friedman, Mark M.
; REGISTRATION NUMBER: 33,883
; REFERENCE/DOCKET NUMBER: 34/40
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 972-3-562553
; TELEFAX: 972-3-562554
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-387-777-9

Query Match      100.0%; Score 1; DB 17; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 g 1
       |
Db      1 G 1

RESULT 17
US-09-387-777-10/c
; Sequence 10, Application US/09387777
; GENERAL INFORMATION:
; APPLICANT: Hadar Kless
; TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
; TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
; STREET: 2001 Jefferson Davis Highway, Suite 207
; CITY: Arlington
; STATE: Virginia
; COUNTRY: United States of America
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
; COMPUTER: Twinhead* Slimnote-890TX
; OPERATING SYSTEM: MS DOS version 6.2,
; SOFTWARE: Word for Windows version 2.0 converted
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/387,777
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Friedman, Mark M.
; REGISTRATION NUMBER: 33,883
; REFERENCE/DOCKET NUMBER: 34/40
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 972-3-562553
; TELEFAX: 972-3-562554
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-387-777-10
```

ATTORNEY/AGENT INFORMATION:
NAME: Friedman, Mark M.
REGISTRATION NUMBER: 33,883
REFERENCE/DOCKET NUMBER: 34/40
TELEPHONE: 972-3-562553
TELEFAX: 972-3-562554
TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 2
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-387-777-10

Query Match 100.0%; Score 1; DB 17; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
I
Db 2 G 2

RESULT 18
US-09-387-777-11
Sequence 11, Application US/0938777
GENERAL INFORMATION:
APPLICANT: Hadar Kless
TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
TITLE OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
STREET: 2001 Jefferson Davis Highway, Suite 207
CITY: Arlington
STATE: Virginia
COUNTRY: United States of America
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
COMPUTER: Twinhead* Slimnote-890TX
OPERATING SYSTEM: MS DOS version 6.2,
OPERATING SYSTEM: Windows version 3.11
SOFTWARE: Word for Windows version 2.0 converted
CURRENT APPLICATION DATA:
SOFTWARE: to an ASCII file
APPLICATION NUMBER: US/09/387.777
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Friedman, Mark M.
REGISTRATION NUMBER: 33,883
REFERENCE/DOCKET NUMBER: 34/40
TELEPHONE: 972-3-562553
TELEFAX: 972-3-562554
TELEX:
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 2
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-387-777-11

Query Match 100.0%; Score 1; DB 17; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 g 1
I
Db 1 G 1
RESULT 19
US-09-387-777-12
Sequence 12, Application US/0938777
GENERAL INFORMATION:
APPLICANT: Hadar Kless
TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
TITLE OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
STREET: 2001 Jefferson Davis Highway, Suite 207
CITY: Arlington
STATE: Virginia
COUNTRY: United States of America
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
COMPUTER: Twinhead* Slimnote-890TX
OPERATING SYSTEM: MS DOS version 6.2,
OPERATING SYSTEM: Windows version 3.11
SOFTWARE: Word for Windows version 2.0 converted
CURRENT APPLICATION DATA:
SOFTWARE: to an ASCII file
APPLICATION NUMBER: US/09/387.777
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Friedman, Mark M.
REGISTRATION NUMBER: 33,883
REFERENCE/DOCKET NUMBER: 34/40
TELEPHONE: 972-3-562553
TELEFAX: 972-3-562554
TELEX:
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 2
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-387-777-12

Query Match 100.0%; Score 1; DB 17; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
I
Db 1 G 1

RESULT 20
US-09-387-777-14/c
Sequence 14, Application US/0938777
GENERAL INFORMATION:
APPLICANT: Hadar Kless
TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
TITLE OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS

```
:
: NUMBER OF SEQUENCES: 88
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
: STREET: 2001 Jefferson Davis Highway, Suite 207
: CITY: Arlington
: STATE: Virginia
: COUNTRY: United States of America
: ZIP: 22202
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
: COMPUTER: Twinhead* Slimnote-890TX
: OPERATING SYSTEM: MS DOS version 6.2,
: OPERATING SYSTEM: Windows version 3.11
: SOFTWARE: Word for Windows version 2.0 converted
: SOFTWARE: to an ASCII file
: CURRENT APPLICATION DATA: US/09/387,777
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Friedman, Mark M.
: REGISTRATION NUMBER: 33,883
: REFERENCE/DOCKET NUMBER: 34/40
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 972-3-562553
: TELEFAX: 972-3-562554
: TELEX:
: INFORMATION FOR SEQ ID NO: 14:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: US-09-387-777-14

Query Match 100.0%; Score 1; DB 17; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 2 G 2

RESULT 21
US-09-387-777-15
: Sequence 15, Application US/0938777
: GENERAL INFORMATION:
: APPLICANT: Hadar Kless
: TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
: TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
: TITLE OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS
: NUMBER OF SEQUENCES: 88
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
: STREET: 2001 Jefferson Davis Highway, Suite 207
: CITY: Arlington
: STATE: Virginia
: COUNTRY: United States of America
: ZIP: 22202
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
: COMPUTER: Twinhead* Slimnote-890TX
: OPERATING SYSTEM: MS DOS version 6.2,
: OPERATING SYSTEM: Windows version 3.11
: SOFTWARE: Word for Windows version 2.0 converted
: SOFTWARE: to an ASCII file
: CURRENT APPLICATION DATA: US/09/387,777
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Friedman, Mark M.
: REGISTRATION NUMBER: 33,883
: REFERENCE/DOCKET NUMBER: 34/40
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 972-3-562553
: TELEFAX: 972-3-562554
: TELEX:
: INFORMATION FOR SEQ ID NO: 19:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2
```

```
:
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Friedman, Mark M.
: REGISTRATION NUMBER: 33,883
: REFERENCE/DOCKET NUMBER: 34/40
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 972-3-562553
: TELEFAX: 972-3-562554
: TELEX:
: INFORMATION FOR SEQ ID NO: 15:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: US-09-387-777-15

Query Match 100.0%; Score 1; DB 17; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 2 G 2

RESULT 22
US-09-472-035A-19
: Sequence 19, Application US/09472035A
: GENERAL INFORMATION:
: APPLICANT: Yechezkel Kashi et al.
: TITLE OF INVENTION: ABUNDANT, WELL DISTRIBUTED AND
: TITLE OF INVENTION: HYPERPOLYMORPHIC SIMPLE SEQUENCE REPEATS
: TITLE OF INVENTION: IN PROKARYOTE GENOMES AND USE OF SAME FOR
: TITLE OF INVENTION: PROKARYOTE CLASSIFICATION AND TYPING
: NUMBER OF SEQUENCES: 42
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
: STREET: 2001 Jefferson Davis Highway, Suite 207
: CITY: Arlington
: STATE: Virginia
: COUNTRY: United States of America
: ZIP: 22202
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
: COMPUTER: Twinhead* Slimnote-890TX
: OPERATING SYSTEM: MS DOS version 6.2,
: OPERATING SYSTEM: Windows version 3.11
: SOFTWARE: Word for Windows version 2.0 converted to
: SOFTWARE: an ASCII file
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/472,035A
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Friedman, Mark M.
: REGISTRATION NUMBER: 33,883
: REFERENCE/DOCKET NUMBER: 74/77
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 972-3-562553
: TELEFAX: 972-3-562554
: TELEX:
: INFORMATION FOR SEQ ID NO: 19:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2
```

;
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-09-472-035A-19

Query Match 100.0%; Score 1; DB 18; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 1 G 1

RESULT 23
US-09-472-035A-20/c
; Sequence 20, Application US/09472035A
; GENERAL INFORMATION:
; APPLICANT: Yechezkel kashi et al.
; TITLE OF INVENTION: ABUNDANT, WELL DISTRIBUTED AND
; TITLE OF INVENTION: HYPERPOLYMORPHIC SIMPLE SEQUENCE REPEATS
; TITLE OF INVENTION: IN PROKARYOTE GENOMES AND USE OF SAME FOR
; TITLE OF INVENTION: PROKARYOTE CLASSIFICATION AND TYPING
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
; STREET: 2001 Jefferson Davis Highway, Suite 207
; CITY: Arlington
; STATE: Virginia
; COUNTRY: United States of America
; ZIP: 22202

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
; COMPUTER: Twinhead* Slimnote-890TX
; OPERATING SYSTEM: MS DOS version 6.2,
; OPERATING SYSTEM: Windows version 3.11
; SOFTWARE: Word for Windows version 2.0 converted to
; SOFTWARE: an ASCII file
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/472,035A
; FILING DATE:

; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Friedman, Mark M.
; REGISTRATION NUMBER: 33,883
; REFERENCE/DOCKET NUMBER: 74/77
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 972-3-5625553
; TELEFAX: 972-3-5625554
; TELEX:

; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-09-472-035A-20

Query Match 100.0%; Score 1; DB 18; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 2 G 2

RESULT 24

US-09-634-306B-51869/c
; Sequence 51869, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 51869
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-51869

Query Match 100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 2 G 2

RESULT 25
US-09-634-306B-52280/c
; Sequence 52280, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 52280
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-52280

Query Match 100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 2 G 2

RESULT 26

US-09-634-306B-52357/c
; Sequence 52357, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52357
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-52357

Query Match 100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 2 G 2

RESULT 27

US-09-634-306B-53003/c
; Sequence 53003, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358

; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53003
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-53003

Query Match 100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 2 G 2

RESULT 28

US-09-634-306B-58305/c
; Sequence 58305, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58305
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-58305

Query Match 100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 1 G 1

RESULT 29

US-09-634-306B-175312
; Sequence 175312, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; CURRENT FILING DATE: 2002-02-21

; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175312
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-175312

Query Match 100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 1 g 1

RESULT 30
US-09-634-306B-175337
; Sequence 175337, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175337
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-175337

Query Match 100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 1 g 1

RESULT 31
US-09-634-306B-175354
; Sequence 175354, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175354
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-175354

Query Match 100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 1 g 1

RESULT 32
US-09-634-306B-175401
; Sequence 175401, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175401
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human

US-09-634-306B-175401

Query Match 100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 1 g 1

RESULT 33

US-09-634-306B-175403
; Sequence 175403, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175403
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human

US-09-634-306B-175403

Query Match 100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 1 g 1

RESULT 34

US-09-634-306B-175415
; Sequence 175415, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363

; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175415
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
; US-09-634-306B-175415

Query Match 100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 1 g 1

RESULT 35

US-09-634-306B-175419
; Sequence 175419, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175419
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human

US-09-634-306B-175419

Query Match 100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 1 g 1

RESULT 36

US-09-634-306B-175426
; Sequence 175426, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129

; CURRENT APPLICATION NUMBER: US/09/634,306B
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175426
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-175426

Query Match 100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 1 g 1

RESULT 37
US-09-634-306B-175433
; Sequence 175433, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175433
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-175433

Query Match 100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|

Db 1 g 1

RESULT 38
US-09-634-306B-175849
; Sequence 175849, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175849
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-175849

Query Match 100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 1 g 1

RESULT 39
US-09-634-306B-176848
; Sequence 176848, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 176848
; LENGTH: 2

; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-176848

Query Match 100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 1 g 1

RESULT 40

US-09-634-306B-176849
; Sequence 176849, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 176849
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-176849

Query Match 100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 1 g 1

RESULT 41

US-09-634-306B-176880
; Sequence 176880, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218

; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 176880
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-176880

Query Match 100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 1 g 1

RESULT 42

US-09-634-306B-178420
; Sequence 178420, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 178420
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-178420

Query Match 100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 1 g 1

RESULT 43

US-09-634-306B-178440
; Sequence 178440, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 178440
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-178440

Query Match 100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
|
Db 1 g 1

RESULT 44
US-09-634-306B-178440/c
; Sequence 178440, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 178440
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-178440

Query Match 100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
|
Db 2 g 2

RESULT 45
US-09-634-306B-178617
; Sequence 178617, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 178617
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-178617

Query Match 100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
|
Db 2 g 2

Search completed: July 16, 2002, 02:50:26
Job time: 31279 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run On: July 15, 2002, 23:07:38 ; Search time 223.79 Seconds

(without alignments)

1.098 Million cell updates/sec

Title: US-09-375-248-1_COPY_2588_2588

Perfect score: 1

Sequence: 1 g 1

Scoring table: OLIGO_NUC

Gapop 60.0 , Capext 60.0

Searched: 383533 seqs, 122816752 residues

Word size : 0

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents NA.*

- 1: /cgn2_6/ptodata/2/ina/5A_COMB.seq.*
- 2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*
- 3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*
- 4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*
- 5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq.*
- 6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1	100.0	2	1	US-08-268-679B-8
2	1	100.0	2	1	US-08-484-192-16
3	1	100.0	2	4	US-08-361-024-3
C 4	1	100.0	2	4	US-08-361-024-3
5	1	100.0	3	1	US-07-791-213D-46
C 6	1	100.0	3	1	US-07-791-213D-46
7	1	100.0	3	1	US-07-791-213D-62
C 8	1	100.0	3	1	US-07-791-213D-62
9	1	100.0	3	1	US-08-268-679B-7
10	1	100.0	3	1	US-08-602-036A-2
C 11	1	100.0	3	1	US-08-602-036A-2
12	1	100.0	3	1	US-08-293-150A-46
C 13	1	100.0	3	1	US-08-293-150A-46
14	1	100.0	3	1	US-08-293-150A-62
C 15	1	100.0	3	1	US-08-293-150A-62
16	1	100.0	3	2	US-08-502-374A-2
C 17	1	100.0	3	2	US-08-502-374A-2
18	1	100.0	3	2	US-08-642-407A-2
C 19	1	100.0	3	2	US-08-642-407A-2
20	1	100.0	3	3	US-08-873-709-9
21	1	100.0	3	3	US-09-032-365A-36
22	1	100.0	3	4	US-08-793-634B-12
23	1	100.0	3	4	US-08-973-568-55
24	1	100.0	4	1	US-07-755-462-2
C 25	1	100.0	4	1	US-07-755-462-2
26	1	100.0	4	1	US-08-169-950-6
C 27	1	100.0	4	1	US-08-169-950-6

28	1	100.0	4	1	US-07-630-288A-7	Sequence 7, Appl
29	1	100.0	4	1	US-07-630-288A-11	Sequence 11, Appl
C 30	1	100.0	4	1	US-07-630-288A-11	Sequence 11, Appl
31	1	100.0	4	1	US-07-630-288A-13	Sequence 13, Appl
32	1	100.0	4	1	US-07-630-288A-14	Sequence 14, Appl
C 33	1	100.0	4	1	US-07-630-288A-14	Sequence 14, Appl
34	1	100.0	4	1	US-07-630-288A-34	Sequence 34, Appl
C 35	1	100.0	4	1	US-07-630-288A-34	Sequence 34, Appl
36	1	100.0	4	1	US-08-126-594-25	Sequence 25, Appl
C 37	1	100.0	4	1	US-08-126-594-25	Sequence 25, Appl
38	1	100.0	4	1	US-08-188-943-1	Sequence 1, Appl
C 39	1	100.0	4	1	US-08-188-943-1	Sequence 1, Appl
40	1	100.0	4	1	US-08-188-943-2	Sequence 2, Appl
C 41	1	100.0	4	1	US-08-188-943-2	Sequence 2, Appl
42	1	100.0	4	1	US-08-465-811A-25	Sequence 25, Appl
C 43	1	100.0	4	1	US-08-465-811A-25	Sequence 25, Appl
44	1	100.0	4	1	US-08-199-317-2	Sequence 2, Appl
C 45	1	100.0	4	1	US-08-199-317-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-268-679B-8
: Sequence 8, Application US/08268679B
: Patent No. 5674729
: GENERAL INFORMATION:
: APPLICANT: WIMMER, ECKARD; MOLLA,
: APPLICANT: AKTERUZZAMAN; PAUL, ANIKO V.
: TITLE OF INVENTION: DE NOVO CELL-FREE
: TITLE OF INVENTION: SYNTHESIS PICORNAVIRUS
: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
: STREET: 345 PARK AVE.
: CITY: NEW YORK
: STATE: NEW YORK
: COUNTRY: USA
: ZIP: 10154
: COMPUTER READABLE FORM:
: MEDIUM TYPE: FLOPPY DISK
: COMPUTER: IBM PC COMPATIBLE
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: WORD PERFECT # 5.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/268, 679B
: FILING DATE: 30-JUN-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/846,914
: FILING DATE: 06-MAR-1992
: CLASSIFICATION: 435
: APPLICATION NUMBER: 07/719,761
: FILING DATE: 24-JUN-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: MARIA C.H. LIN
: REGISTRATION NUMBER: 29,323
: REFERENCE/DOCKET NUMBER: 0887-4095 US2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 758-4800
: TELEFAX: (212) 751-6849
: TELEX: 421792
: INFORMATION FOR SEQ ID NO: 8:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2
: TYPE: NUCLEIC ACID
: STRANDEDNESS: SINGLE
: TOPOLOGY: UNKNOWN
: MOLECULE TYPE:
: DESCRIPTION: OLIGONUCLEOTIDE
: HYPOTHETICAL: NO
: ANTI-SENSE: YES
: ORIGINAL SOURCE: N.A.

;
US-08-268-679B-8

POSITION IN GENOME: N.A.

Query Match 100.0%; Score 1; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 1 G 1

RESULT 2

US-08-484-192-16
; Sequence 16, Application US/08484192
; Patent No. 5756291
; GENERAL INFORMATION:
; APPLICANT: GRIFFIN, LINDA C.
; APPLICANT: ALBRECHT, GLENN
; APPLICANT: LATHAM, JOHN
; APPLICANT: LEUNG, LAWRENCE
; APPLICANT: VERMAAS, ERIC
; APPLICANT: TOOLE, JOHN J.
; TITLE OF INVENTION: APOTAMERS SPECIFIC FOR BIOMOLECULES AND
; TITLE OF INVENTION: METHODS OF MAKING
; NUMBER OF SEQUENCES: 181
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,192
FILING DATE:

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/934,387
FILING DATE: 21-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: GRACEY, NANCY J.
REGISTRATION NUMBER: 28,216
REFERENCE/DOCKET NUMBER: 246102002221
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-813-5600
TELEFAX: 415-494-0792
TELEX: 706141

INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 2 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: misc_difference
LOCATION: replace(1, "")
OTHER INFORMATION: /note= "This is a blotin-17
OTHER INFORMATION: nucleotide stretch of abasic residues."
US-08-484-192-16

Query Match 100.0%; Score 1; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1

Db 2 G 2

RESULT 3

US-08-361-024-3
; Sequence 3, Application US/08361024
; Patent No. 6207368
; GENERAL INFORMATION:
; APPLICANT: Adams, Craig W.
; TITLE OF INVENTION: Method, Reagent and Kit
; TITLE OF INVENTION: for Detection and
; TITLE OF INVENTION: Amplification of
; TITLE OF INVENTION: Nucleic Acid Sequence
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Beckman Instruments, Inc.
; STREET: 2500 Harbor Boulevard
; CITY: Fullerton
; STATE: California
; COUNTRY: USA
; ZIP: 92634
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch,
MEDIUM TYPE: 1.44 Mb
COMPUTER: IBM
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/361,024
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/925,059
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Burgoon, Richard P.
REGISTRATION NUMBER: 34,787
REFERENCE/DOCKET NUMBER: 128D-126
TELECOMMUNICATION INFORMATION:
TELEPHONE: (714) 773-7610
TELEFAX: (714) 773-7936
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: yes
ANTI-SENSE: no
US-08-361-024-3

Query Match 100.0%; Score 1; DB 4; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 1 G 1

RESULT 4

US-08-361-024-3/c
; Sequence 3, Application US/08361024
; Patent No. 6207368
; GENERAL INFORMATION:
; APPLICANT: Adams, Craig W.
; TITLE OF INVENTION: Method, Reagent and Kit
; TITLE OF INVENTION: for Detection and
; TITLE OF INVENTION: Amplification of
; TITLE OF INVENTION: Nucleic Acid Sequence

NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Beckman Instruments, Inc.
STREET: 2500 Harbor Boulevard
CITY: Fullerton
STATE: California
COUNTRY: USA
ZIP: 92634
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch,
MEDIUM TYPE: 1.44 Mb
COMPUTER: IBM
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/361,024
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/925,059
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Burgoon, Richard P.
REGISTRATION NUMBER: 34,787
REFERENCE/DOCKET NUMBER: 128D-126
TELECOMMUNICATION INFORMATION:
TELEPHONE: (714) 773-7610
TELEFAX: (714) 773-7936
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: yes
ANTI-SENSE: no
US-08-361-024-3

Query Match 100.0%; Score 1; DB 4; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
|
Db 2 G 2

RESULT 5
US-07-791-213D-46
; Sequence 46, Application US/07791213D
; Patent No. 5409895
; GENERAL INFORMATION:
; APPLICANT: MORISHITA, Hideaki
; APPLICANT: KANAMORI, Toshinori
; APPLICANT: NOBUHARA, Masahiro
; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
; TITLE OF INVENTION: TREATING USING THE SAME
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/791,213D
FILING DATE: 13-NOV-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-306745
FILING DATE: 13-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 029650-032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 3 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-07-791-213D-46

Query Match 100.0%; Score 1; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
|
Db 2 G 2

RESULT 6
US-07-791-213D-46/c
; Sequence 46, Application US/07791213D
; Patent No. 5409895
; GENERAL INFORMATION:
; APPLICANT: MORISHITA, Hideaki
; APPLICANT: KANAMORI, Toshinori
; APPLICANT: NOBUHARA, Masahiro
; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
; TITLE OF INVENTION: TREATING USING THE SAME
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/791,213D
FILING DATE: 13-NOV-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-306745
FILING DATE: 13-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 029650-032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021

; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-07-791-213D-46

Query Match 100.0%; Score 1; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 3 G 3

RESULT 7
US-07-791-213D-62
; Sequence 62, Application US/07791213D
; Patent No. 5409895
; GENERAL INFORMATION:
; APPLICANT: MORISHITA, Hideaki
; APPLICANT: KANAMORI, Toshinori
; APPLICANT: NOBUHARA, Masahiro
; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
; TITLE OF INVENTION: TREATING USING THE SAME
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/791,213D
; FILING DATE: 13-NOV-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-306745
; FILING DATE: 13-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 029650-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-07-791-213D-62

Query Match 100.0%; Score 1; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1

Db 2 G 2
|

RESULT 8
US-07-791-213D-62/c
; Sequence 62, Application US/07791213D
; Patent No. 5409895
; GENERAL INFORMATION:
; APPLICANT: MORISHITA, Hideaki
; APPLICANT: KANAMORI, Toshinori
; APPLICANT: NOBUHARA, Masahiro
; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
; TITLE OF INVENTION: TREATING USING THE SAME
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/791,213D
; FILING DATE: 13-NOV-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-306745
; FILING DATE: 13-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 029650-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-07-791-213D-62

Query Match 100.0%; Score 1; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 3 G 3

RESULT 9
US-08-268-679B-7
; Sequence 7, Application US/08268679B
; Patent No. 5674729
; GENERAL INFORMATION:
; APPLICANT: WIMMER, ECKARD; MOLLA,
; APPLICANT: AKTERUZZAMAN; PAUL, ANIKO V.
; TITLE OF INVENTION: DE NOVO CELL-FREE
; TITLE OF INVENTION: SYNTHESIS PICORNAVIRUS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVE.
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PERFECT # 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/268.679B
FILING DATE: 30-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07A846.914
FILING DATE: 06-MAR-1992
CLASSIFICATION: 435
APPLICATION NUMBER: 07\719.761
FILING DATE: 24-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: MARIA C. H. LIN
REGISTRATION NUMBER: 29.323
REFERENCE/DOCKET NUMBER: 0887-4095 US2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 3
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: UNKNOWN
MOLECULE TYPE: OLIGONUCLEOTIDE
DESCRIPTION: NO
HYPOTHETICAL: YES
ANTI-SENSE: YES
ORIGINAL SOURCE: N.A.
POSITION IN GENOME: N.A.
US-08-268-679B-7

Query Match 100.0%; Score 1; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 2 g 2

RESULT 10
US-08-602-036A-2
Sequence 2, Application US/08602036A
Patent No. 5789248
GENERAL INFORMATION:
APPLICANT: Oeystein, Fodstad
APPLICANT: Hovig, Eivind
APPLICANT: Engebraaten, Olav
APPLICANT: Maelandsmo, Gunhild H.
TITLE OF INVENTION: CAPL SPECIFIC OLIGONUCLEOTIDES AND
METHODS OF INHIBITING METASTATIC CANCER
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE AND DORR LLP
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: United States of America
ZIP: 02109
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602.036A
FILING DATE: 16-FEB-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HYZ-039CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-602-036A-2

Query Match 100.0%; Score 1; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 1 g 1

RESULT 11
US-08-602-036A-2/c
Sequence 2, Application US/08602036A
Patent No. 5789248
GENERAL INFORMATION:
APPLICANT: Oeystein, Fodstad
APPLICANT: Hovig, Eivind
APPLICANT: Engebraaten, Olav
APPLICANT: Maelandsmo, Gunhild H.
APPLICANT: Agrawal, Sudhir
TITLE OF INVENTION: CAPL SPECIFIC OLIGONUCLEOTIDES AND
METHODS OF INHIBITING METASTATIC CANCER
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE AND DORR LLP
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: United States of America
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602.036A
FILING DATE: 16-FEB-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HYZ-039CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 3 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-602-036A-2

Query Match 100.0%; Score 1; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 3 G 3

RESULT 12

US-08-293-150A-46
; Sequence 46, Application US/08293150A
; Patent No. 5792629

GENERAL INFORMATION:

APPLICANT: MORISHITA, Hideaki
APPLICANT: KANAMORI, Toshinori
APPLICANT: NOBUHARA, Masahiro

TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
TITLE OF INVENTION: TREATING USING THE SAME
NUMBER OF SEQUENCES: 110

CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. Box 1404
CITY: Alexandria

STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/293.150A
FILING DATE: 19-AUG-1994

CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/791,213
FILING DATE: 13-NOV-1990

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-306745
FILING DATE: 13-NOV-1990

ATTORNEY/AGENT INFORMATION:

NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 029650-049
TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:

LENGTH: 3 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-293-150A-46

Query Match 100.0%; Score 1; DB 1; Length 3;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 2 G 2

RESULT 13

US-08-293-150A-46/c
; Sequence 46, Application US/08293150A
; Patent No. 5792629

GENERAL INFORMATION:

APPLICANT: MORISHITA, Hideaki
APPLICANT: KANAMORI, Toshinori
APPLICANT: NOBUHARA, Masahiro

TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
TITLE OF INVENTION: TREATING USING THE SAME
NUMBER OF SEQUENCES: 110

CORRESPONDENCE ADDRESS:

ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. Box 1404
CITY: Alexandria

STATE: Virginia

COUNTRY: United States

ZIP: 22313-1404

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/293.150A
FILING DATE: 19-AUG-1994

CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/791,213
FILING DATE: 13-NOV-1990

ATTORNEY/AGENT INFORMATION:

NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 029650-049
TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:

LENGTH: 3 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-293-150A-46

Query Match 100.0%; Score 1; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 3 G 3

RESULT 14

US-08-293-150A-62
; Sequence 62, Application US/08293150A
; Patent No. 5792629

;
; GENERAL INFORMATION:
; APPLICANT: MORISHITA, Hideaki
; APPLICANT: KANAMORI, Toshinori
; APPLICANT: NOBUHARA, Masahiro
; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
; TITLE OF INVENTION: TREATING USING THE SAME
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/293,150A
; FILING DATE: 19-AUG-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/791,213
; FILING DATE: 13-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-306745
; FILING DATE: 13-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M.
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 029650-049
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-293-150A-62

Query Match 100.0%; Score 1; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 2 G 2

RESULT 15
US-08-293-150A-62/C
; Sequence 62, Application US/08293150A
; Patent No. 5792629
; GENERAL INFORMATION:
; APPLICANT: MORISHITA, Hideaki
; APPLICANT: KANAMORI, Toshinori
; APPLICANT: NOBUHARA, Masahiro
; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
; TITLE OF INVENTION: TREATING USING THE SAME
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404

;
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/293,150A
; FILING DATE: 19-AUG-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/791,213
; FILING DATE: 13-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-306745
; FILING DATE: 13-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M.
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 029650-049
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-293-150A-62

Query Match 100.0%; Score 1; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 3 G 3

RESULT 16
US-08-502-374A-2
; Sequence 2, Application US/08502374A
; Patent No. 5872007
; GENERAL INFORMATION:
; APPLICANT: Fodstad, Oeystein
; APPLICANT: Hovig, Eivind
; APPLICANT: Engebraaten, Olav
; APPLICANT: Maelandsmo, Gunhild H.
; APPLICANT: Agrawal, Sudhir
; TITLE OF INVENTION: CAPL-SPECIFIC OLIGONUCLEOTIDES AND
; TITLE OF INVENTION: METHODS OF INHIBITING METASTATIC CANCER
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hale and Dorr LLP
; STREET: 60 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/502,374A
; FILING DATE: 14-Jul-1995

CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HY2-039DV2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-526-6000
TELEFAX: 617-526-5000
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
HYPOTHETICAL: NO
ANTI-SENSE: YES
US-08-502-374A-2

Query Match 100.0%; Score 1; DB 2; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 1 G 1

RESULT 17
US-08-502-374A-2/c
; Sequence 2, Application US/08502374A
; Patent No. 5872007
; GENERAL INFORMATION:
; APPLICANT: Fodstad, Oeystein
; APPLICANT: Hovig, Eivind
; APPLICANT: Engebraaten, Olav
; APPLICANT: Maelandmo, Gunhild H.
; APPLICANT: Agrawal, Sudhir
; TITLE OF INVENTION: CAPL-SPECIFIC OLIGONUCLEOTIDES AND
; TITLE OF INVENTION: METHODS OF INHIBITING METASTATIC CANCER
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hale and Dorr LLP
; STREET: 60 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/502.374A
; FILING DATE: 14-Jul-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kerner, Ann-Louise
; REGISTRATION NUMBER: 33,523
; REFERENCE/DOCKET NUMBER: HY2-039DV2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-526-6000
; TELEFAX: 617-526-5000
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
; HYPOTHETICAL: NO

ANTI-SENSE: YES
US-08-502-374A-2

Query Match 100.0%; Score 1; DB 2; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 3 G 3

RESULT 18
US-08-642-407A-2
; Sequence 2, Application US/08642407A
; Patent No. 5877308
; GENERAL INFORMATION:
; APPLICANT: Oeystein, Fodstad
; APPLICANT: Hovig, Eivind
; APPLICANT: Engebraaten, Olav
; APPLICANT: Maelandmo, Gunhild H.
; APPLICANT: Agrawal, Sudhir
; TITLE OF INVENTION: CAPL-SPECIFIC OLIGONUCLEOTIDES AND
; TITLE OF INVENTION: METHODS OF INHIBITING METASTATIC CANCER
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hale and Dorr LLP
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: United States of America
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/642.407A
; FILING DATE: 03-May-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kerner, Ann-Louise
; REGISTRATION NUMBER: 33,523
; REFERENCE/DOCKET NUMBER: HY2-039CPDV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 526-6000
; TELEFAX: (617) 526-5000
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-642-407A-2

Query Match 100.0%; Score 1; DB 2; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 1 G 1

RESULT 19
US-08-642-407A-2/c
; Sequence 2, Application US/08642407A

; Patent No. 5877308
; GENERAL INFORMATION:
; APPLICANT: Oeystein, Fodstad
; APPLICANT: Hovig, Eivind
; APPLICANT: Engebraten, Olav
; APPLICANT: Maelandsmo, Gunhild H.
; APPLICANT: Agrawal, Sudhir
; TITLE OF INVENTION: CAPL SPECIFIC OLIGONUCLEOTIDES AND
; METHODS OF INHIBITING METASTATIC CANCER
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HALE AND DORR LLP
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: United States of America
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/642.407A
; FILING DATE: 03-May-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kerner, Ann-Louise
; REGISTRATION NUMBER: 33,523
; REFERENCE/DOCKET NUMBER: HY2-039CPDV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 526-6000
; TELEFAX: (617) 526-5000
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-642-407A-2

Query Match 100.0%; Score 1; DB 2; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 3 G 3

RESULT 20
US-08-873-709-9
; Sequence 9, Application US/08873709
; Patent No. 6037126
; GENERAL INFORMATION:
; APPLICANT: Grossman, Abraham
; TITLE OF INVENTION: COMPOSITIONS, METHODS, KITS AND
; APPARATUS FOR DETERMINING THE PRESENCE OR ABSENCE OF
; A PROTEIN COMPONENT OF TELOMERASE ENZYME
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abraham Grossman
; STREET: 666 Washington Avenue
; CITY: Pleasantville
; STATE: NY
; COUNTRY: USA
; ZIP: 10570
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/873,709
; FILING DATE: 12-JUN-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Janiuk, Anthony J.
; REGISTRATION NUMBER: 29,809
; REFERENCE/DOCKET NUMBER: Q001/002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 914-747-9108
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
US-08-873-709-9

Query Match 100.0%; Score 1; DB 3; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 1 G 1

RESULT 21
US-09-032-365A-36
; Sequence 36, Application US/09032365A
; Patent No. 6114502
; GENERAL INFORMATION:
; APPLICANT: No. 6114502th, Michael
; APPLICANT: Nishina, Patsy
; APPLICANT: Naggart, Juergen
; APPLICANT: No. 6114502en-Trauth, Konrad
; TITLE OF INVENTION: GENE FAMILY ASSOCIATED WITH
; NEUROSENSORY DEFECTS
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bozicevic & Reed, LLP
; STREET: 285 Hamilton Avenue, Suite 200
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/032,365A
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sherwood, Pamela J
; REGISTRATION NUMBER: 36,677
; REFERENCE/DOCKET NUMBER: SEQ-2CIP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-327-3400
; TELEFAX: 650 327-3231
; TELEX:
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:

;
; LENGTH: 3 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cna
US-09-032-365A-36

Query Match 100.0%; Score 1; DB 3; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 1 G 1

RESULT 22
US-08-793-634B-12
; Sequence 12, Application US/08793634B
; Patent No. 6211431
; GENERAL INFORMATION:
; APPLICANT: Boevink, Petra C.
; APPLICANT: Surin, Brian P.
; APPLICANT: Keese, Paul K.
; APPLICANT: Chu, Paul W.G.
; APPLICANT: Waterhouse, Peter M.
; APPLICANT: Khan, Rafiqul I.
; APPLICANT: Larkin, Philip J.
; APPLICANT: Taylor, William C.
; APPLICANT: Marchall, Jerry S.
; TITLE OF INVENTION: NOVEL PLANT PROMOTERS AND USES
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; City: Garden City
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 11530

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/793.634B
; FILING DATE: June 9, 1997
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 10530
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 516-742-4343
; TELEFAX: 516-742-4366
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-793-634B-12

Query Match 100.0%; Score 1; DB 4; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 2 G 2

RESULT 23
US-08-973-568-55
; Sequence 55, Application US/08973568B
; Patent No. 6277634
; GENERAL INFORMATION:
; APPLICANT: McCall, Maxine J.
; APPLICANT: Hendry, Philip
; APPLICANT: Lockett, Trevor
; TITLE OF INVENTION: OPTIMIZED MINIZYMES AND MINIRIBOZYMES AND USES THEREOF
; FILE REFERENCE: 47203bpcus
; CURRENT APPLICATION NUMBER: US/08/973.568B
; CURRENT FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Combined DNA/RNA Molecule:
; OTHER INFORMATION: Synthetic Ribozyme or portion thereof
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Ribozymes and
US-08-973-568-55

Query Match 100.0%; Score 1; DB 4; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 1 g 1

RESULT 24
US-07-755-462-2
; Sequence 2, Application US/07755462
; Patent No. 5273881
; GENERAL INFORMATION:
; APPLICANT: Sena, Elissa P.
; APPLICANT: Calhoun, Cornelia J.
; APPLICANT: Zarling, David A.
; TITLE OF INVENTION: Diagnostic Applications of Double-D-Loop
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Dehlinger
; STREET: 350 Cambridge Avenue, Suite 300
; City: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/755.462
; FILING DATE: 19910904
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/520,321
; FILING DATE: 07-MAY-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 4255-0001.30
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Cleavage site for DpnI
US-07-755-462-2

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 1 G 1

RESULT 25
US-07-755-462-2/c
; Sequence 2, Application US/07755462
; Patent No. 5273881
; GENERAL INFORMATION:
; APPLICANT: Sena, Elissa P.
; APPLICANT: Calhoun, Cornelia J.
; APPLICANT: Zarling, David A.
; TITLE OF INVENTION: Diagnostic Applications of Double-D-Loop
; TITLE OF INVENTION: Formation
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Dehlinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07755.462
FILING DATE: 19910904
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/520.321
FILING DATE: 07-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33.875
REFERENCE/DOCKET NUMBER: 4255-0001.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Cleavage site for DpnI
US-07-755-462-2

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 g 1
|
Db 4 G 4
RESULT 26
US-08-169-950-6
; Sequence 6, Application US/08169950
; Patent No. 5366882
; GENERAL INFORMATION:
; APPLICANT: LUNNEN, KEITH D.
; APPLICANT: WILSON, GEOFFREY G.
; TITLE OF INVENTION: METHOD FOR PRODUCING THE BglI
; TITLE OF INVENTION: RESTRICTION ENDONUCLEASE AND METHYLASE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSEE: CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/169,950
FILING DATE: 17-DEC-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RESNICK, DAVID S.
REGISTRATION NUMBER: 34235
REFERENCE/DOCKET NUMBER: 43959
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-3400
TELEFAX: (617) 523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
US-08-169-950-6

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 1 G 1

RESULT 27
US-08-169-950-6/c
; Sequence 6, Application US/08169950
; Patent No. 5366882
; GENERAL INFORMATION:
; APPLICANT: LUNNEN, KEITH D.
; APPLICANT: WILSON, GEOFFREY G.
; TITLE OF INVENTION: METHOD FOR PRODUCING THE BglI
; TITLE OF INVENTION: RESTRICTION ENDONUCLEASE AND METHYLASE

NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
ADDRESSEE: CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/169,950
FILING DATE: 17-DEC-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RESNICK, DAVID S.
REGISTRATION NUMBER: 34235
REFERENCE/DOCKET NUMBER: 43959
TELEPHONE: (617) 523-3400
TELEFAX: (617) 523-6440
TELEX: 200251 STRE UR
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
US-08-169-950-6

Query Match 100.0% Score 1; DB 1; Length 4;
Best Local Similarity 100.0% Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 g 1
|
Db 4 G 4

RESULT 28
US-07-630-288A-7
Sequence 7, Application US/07630288A
Patent No. 5472840
GENERAL INFORMATION:
APPLICANT: Stefano, James E.
TITLE OF INVENTION: Nucleic Acid Structures with Catalytic
TITLE OF INVENTION: and Autocatalytic Replicating Features and Methods of Use
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Joanne M. Glesser
STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.
CITY: Naperville
STATE: IL
COUNTRY: USA
ZIP: 60563
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/630,288A
FILING DATE: 17-DEC-1990
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/370,218
FILING DATE: 06-JUN-1989

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/252,243
FILING DATE: 30-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Glesser, Joanne M.
REGISTRATION NUMBER: 32,838
REFERENCE/DOCKET NUMBER: 58190 2
TELEPHONE: (708) 717-2443
TELEFAX: (708) 717-2430
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-07-630-288A-7

Query Match 100.0% Score 1; DB 1; Length 4;
Best Local Similarity 100.0% Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 g 1
|
Db 1 G 1

RESULT 29
US-07-630-288A-11
Sequence 11, Application US/07630288A
Patent No. 5472840
GENERAL INFORMATION:
APPLICANT: Stefano, James E.
TITLE OF INVENTION: Nucleic Acid Structures with Catalytic
TITLE OF INVENTION: and Autocatalytic Replicating Features and Methods of Use
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Joanne M. Glesser
STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.
CITY: Naperville
STATE: IL
COUNTRY: USA
ZIP: 60563
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/630,288A
FILING DATE: 17-DEC-1990
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/370,218
FILING DATE: 06-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/252,243
FILING DATE: 30-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Glesser, Joanne M.
REGISTRATION NUMBER: 32,838
REFERENCE/DOCKET NUMBER: 58190 2
TELEPHONE: (708) 717-2443
TELEFAX: (708) 717-2430
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid

; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-07-630-288A-11

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
|
Db 1 g 1

RESULT 30
US-07-630-288A-11/c
; Sequence 11, Application US/07630288A
; Patent No. 5472840
; GENERAL INFORMATION:
; APPLICANT: Stefano, James E.
; TITLE OF INVENTION: Nucleic Acid Structures with Catalytic
; and Autocatalytic Replicating Features and Methods of Use
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Joanne M. Giesler
; STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.
; CITY: Naperville
; STATE: IL
; COUNTRY: USA
; ZIP: 60563
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/630,288A
; FILING DATE: 17-DEC-1990
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/370,218
; FILING DATE: 06-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/252,243
; FILING DATE: 30-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Giesler, Joanne M.
; REGISTRATION NUMBER: 32,838
; REFERENCE/DOCKET NUMBER: 58190 2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (708) 717-2443
; TELEFAX: (708) 717-2430
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-07-630-288A-11

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
|

Db 4 G 4

RESULT 31
US-07-630-288A-13
; Sequence 13, Application US/07630288A
; Patent No. 5472840
; GENERAL INFORMATION:
; APPLICANT: Stefano, James E.
; TITLE OF INVENTION: Nucleic Acid Structures with Catalytic
; and Autocatalytic Replicating Features and Methods of Use
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Joanne M. Giesler
; STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.
; CITY: Naperville
; STATE: IL
; COUNTRY: USA
; ZIP: 60563
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/630,288A
; FILING DATE: 17-DEC-1990
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/370,218
; FILING DATE: 06-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/252,243
; FILING DATE: 30-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Giesler, Joanne M.
; REGISTRATION NUMBER: 32,838
; REFERENCE/DOCKET NUMBER: 58190 2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (708) 717-2443
; TELEFAX: (708) 717-2430
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-07-630-288A-13

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
|
Db 1 G 1

RESULT 32
US-07-630-288A-14
; Sequence 14, Application US/07630288A
; Patent No. 5472840
; GENERAL INFORMATION:
; APPLICANT: Stefano, James E.
; TITLE OF INVENTION: Nucleic Acid Structures with Catalytic
; and Autocatalytic Replicating Features and Methods of Use
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Joanne M. Giesler

STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.
CITY: Naperville
STATE: IL
COUNTRY: USA
ZIP: 60563
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/630,288A
FILING DATE: 17-DEC-1990
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/370,218
FILING DATE: 06-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/252,243
FILING DATE: 30-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Glesser, Joanne M.
REGISTRATION NUMBER: 32,838
REFERENCE/DOCKET NUMBER: 58190 2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708) 717-2443
TELEFAX: (708) 717-2430
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-07-630-288A-14

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
I
Db 1 G 1

RESULT 33
US-07-630-288A-14/c
Sequence 14, Application US/07630288A
Patent No. 5472840
GENERAL INFORMATION:
APPLICANT: Stefano, James E.
TITLE OF INVENTION: Nucleic Acid Structures with Catalytic
TITLE OF INVENTION: and Autocatalytic Replicating Features and Methods of Use
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Joanne M. Glesser
STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.
CITY: Naperville
STATE: IL
COUNTRY: USA
ZIP: 60563
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/630,288A
FILING DATE: 17-DEC-1990
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/370,218
FILING DATE: 06-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/252,243
FILING DATE: 30-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Glesser, Joanne M.
REGISTRATION NUMBER: 32,838
REFERENCE/DOCKET NUMBER: 58190 2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708) 717-2443
TELEFAX: (708) 717-2430
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-07-630-288A-14

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
I
Db 4 G 4

RESULT 34
US-07-630-288A-34
Sequence 34, Application US/07630288A
Patent No. 5472840
GENERAL INFORMATION:
APPLICANT: Stefano, James E.
TITLE OF INVENTION: Nucleic Acid Structures with Catalytic
TITLE OF INVENTION: and Autocatalytic Replicating Features and Methods of Use
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Joanne M. Glesser
STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.
CITY: Naperville
STATE: IL
COUNTRY: USA
ZIP: 60563
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/630,288A
FILING DATE: 17-DEC-1990
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/370,218
FILING DATE: 06-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/252,243
FILING DATE: 30-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Glesser, Joanne M.
REGISTRATION NUMBER: 32,838
REFERENCE/DOCKET NUMBER: 58190 2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708) 717-2443
TELEFAX: (708) 717-2430
INFORMATION FOR SEQ ID NO: 34:

SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-07-630-288A-34

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 2 g 2

RESULT 35

US-07-630-288A-34/C
Sequence 34, Application US/07630288A
Patent No. 5472840
GENERAL INFORMATION:
APPLICANT: Stefano, James E.
TITLE OF INVENTION: Nucleic Acid Structures with Catalytic
and Autocatalytic Replicating Features and Methods of Use
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Joanne M. Giesser
STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.
CITY: Naperville
STATE: IL
COUNTRY: USA
ZIP: 60563

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/630.288A
FILING DATE: 17-DEC-1990
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/370.218
FILING DATE: 06-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/252.243
FILING DATE: 30-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Giesser, Joanne M.
REGISTRATION NUMBER: 32,838
REFERENCE/DOCKET NUMBER: 58190 2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708) 717-2443
TELEFAX: (708) 717-2430
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-07-630-288A-34

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 4 g 4

RESULT 36

US-08-126-594-25
Sequence 25, Application US/08126594
Patent No. 5482845
GENERAL INFORMATION:
APPLICANT: Soares, M. Bento
APPLICANT: Efstratiadis, Algriris
TITLE OF INVENTION: METHOD FOR CONSTRUCTION OF NORMALIZED
TITLE OF INVENTION: CDNA LIBRARIES
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White, c/o Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/126,594
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 42840/JPW/AKC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-126-594-25

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 3 g 3

RESULT 37

US-08-126-594-25/c
Sequence 25, Application US/08126594
Patent No. 5482845
GENERAL INFORMATION:
APPLICANT: Soares, M. Bento
APPLICANT: Efstratiadis, Algriris
TITLE OF INVENTION: METHOD FOR CONSTRUCTION OF NORMALIZED
TITLE OF INVENTION: CDNA LIBRARIES
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White, c/o Cooper & Dunham

STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/126.594
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 42840/JPW/AKC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
TELEX: 422523 COOP UT
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-126-594-25

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 4 G 4

RESULT 38
US-08-188-943-1
Sequence 1, Application US/08188943
Patent No. 5635347
GENERAL INFORMATION:
APPLICANT: Link, John R.
APPLICANT: Gudibande, Satyanarayana R.
APPLICANT: Kenten, John H.
TITLE OF INVENTION: Rapid Assays for Amplification
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford
ADDRESS: c/o Barry Evans
STREET: 530 Fifth Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,943
FILING DATE: 28-JAN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/792,602
FILING DATE: 15-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Evans, Barry
REGISTRATION NUMBER: 22,802
REFERENCE/DOCKET NUMBER: 370068-3630
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-0712
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-188-943-1

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 4 G 4

RESULT 38
US-08-188-943-1
Sequence 1, Application US/08188943
Patent No. 5635347
GENERAL INFORMATION:
APPLICANT: Link, John R.
APPLICANT: Gudibande, Satyanarayana R.
APPLICANT: Kenten, John H.
TITLE OF INVENTION: Rapid Assays for Amplification
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford
ADDRESS: c/o Barry Evans
STREET: 530 Fifth Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,943
FILING DATE: 28-JAN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/792,602
FILING DATE: 15-NOV-1991

ATTORNEY/AGENT INFORMATION:
NAME: Evans, Barry
REGISTRATION NUMBER: 22,802
REFERENCE/DOCKET NUMBER: 370068-3630
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-188-943-1

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 3 G 3

RESULT 39
US-08-188-943-1/c
Sequence 1, Application US/08188943
Patent No. 5635347
GENERAL INFORMATION:
APPLICANT: Link, John R.
APPLICANT: Gudibande, Satyanarayana R.
APPLICANT: Kenten, John H.
TITLE OF INVENTION: Rapid Assays for Amplification
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford
ADDRESS: c/o Barry Evans
STREET: 530 Fifth Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,943
FILING DATE: 28-JAN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/792,602
FILING DATE: 15-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Evans, Barry
REGISTRATION NUMBER: 22,802
REFERENCE/DOCKET NUMBER: 370068-3630
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-188-943-1

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1

Db 4 G 4

RESULT 40

US-08-188-943-2
; Sequence 2, Application US/08188943
; Patent No. 5635347
; GENERAL INFORMATION:
; APPLICANT: Link, John R.
; APPLICANT: Gudibande, Satyanarayana R.
; APPLICANT: Kenten, John H.
; TITLE OF INVENTION: Rapid Assays for Amplification
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford
; ADDRESSEE: C/O Barry Evans
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/188,943
; FILING DATE: 28-JAN-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/792,602
; FILING DATE: 15-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Evans, Barry
; REGISTRATION NUMBER: 22,802
; REFERENCE/DOCKET NUMBER: 370068-3630
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-08-188-943-2

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1

Db 1 G 1

RESULT 41

US-08-188-943-2/c
; Sequence 2, Application US/08188943
; Patent No. 5635347
; GENERAL INFORMATION:
; APPLICANT: Link, John R.
; APPLICANT: Gudibande, Satyanarayana R.
; APPLICANT: Kenten, John H.
; TITLE OF INVENTION: Rapid Assays for Amplification
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Curtis, Morris & Safford
; ADDRESSEE: C/O Barry Evans
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/188,943
; FILING DATE: 28-JAN-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/792,602
; FILING DATE: 15-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Evans, Barry
; REGISTRATION NUMBER: 22,802
; REFERENCE/DOCKET NUMBER: 370068-3630
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-188-943-2

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1

Db 2 G 2

RESULT 42

US-08-465-811A-25
; Sequence 25, Application US/08465811A
; Patent No. 5637685
; GENERAL INFORMATION:
; APPLICANT: Soares, M. Bento
; APPLICANT: Efstratiadis, Argiris
; TITLE OF INVENTION: METHOD FOR CONSTRUCTION OF
; TITLE OF INVENTION: NORMALIZED CDNA LIBRARIES
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White, c/o Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,811A
; FILING DATE: June 6, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 42840/JPW/AKC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-465-811A-25

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
|
Db 3 G 3

RESULT 43
US-08-465-811A-25/c
Sequence 25, Application US/08465811A
Patent No. 5637685
GENERAL INFORMATION:
APPLICANT: Soares, M. Bento
APPLICANT: Efstathiadis, Argiris
TITLE OF INVENTION: METHOD FOR CONSTRUCTION OF
TITLE OF INVENTION: NORMALIZED CDNA LIBRARIES
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White, c/o Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,811A
FILING DATE: June 6, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 42840/JPW/AKC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-465-811A-25

Query Match 100.0%; Score 1; DB 1; Length 4;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 g 1
|
Db 4 G 4
RESULT 44
US-08-199-317-2
Sequence 2, Application US/08199317
Patent No. 5670316
GENERAL INFORMATION:
APPLICANT: Sena, Elissa P.
APPLICANT: Calhoun, Cornelia J.
APPLICANT: Zarling, David A.
TITLE OF INVENTION: Diagnostic Applications of Double D-loop
TITLE OF INVENTION: Formation
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/199,317
FILING DATE: 25-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/910,791
FILING DATE: 09-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/755,462
FILING DATE: 04-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/520,321
FILING DATE: 07-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 9150-0004
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-324-0880
TELEFAX: 415-324-0960
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Cleavage site for Dpn I
US-08-199-317-2

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 g 1
|
Db 1 G 1

RESULT 45
US-08-199-317-2/c
; Sequence 2, Application US/08199317
; Patent No. 5670316
; GENERAL INFORMATION:
; APPLICANT: Sena, Elissa P.
; APPLICANT: Calhoun, Cornelia J.
; APPLICANT: Zarling, David A.
; TITLE OF INVENTION: Diagnostic Applications of Double D-loop
; TITLE OF INVENTION: Formation
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Ave., Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/199,317
; FILING DATE: 25-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/910,791
; FILING DATE: 09-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/755,462
; FILING DATE: 04-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/520,321
; FILING DATE: 07-MAY-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 9150-0004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-324-0880
; TELEFAX: 415-324-0960
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Cleavage site for Dpn I
US-08-199-317-2

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 9 1
Db 4 G 4

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 15, 2002, 23:10:11 ; Search time 932.4 Seconds
(without alignments)
1.841 Million cell updates/sec

Title: US-09-375-248-1_COPY_2588_2588

Perfect score: 1
Sequence: 1 g 1

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 1736436 seqs, 858457221 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N_Geneseq_032802.*

- 1: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.*
- 2: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.*
- 3: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.*
- 4: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1983.DAT.*
- 5: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.*
- 6: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1985.DAT.*
- 7: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1986.DAT.*
- 8: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1987.DAT.*
- 9: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1988.DAT.*
- 10: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1989.DAT.*
- 11: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1990.DAT.*
- 12: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1991.DAT.*
- 13: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1992.DAT.*
- 14: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1993.DAT.*
- 15: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1994.DAT.*
- 16: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1995.DAT.*
- 17: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1996.DAT.*
- 18: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1997.DAT.*
- 19: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1998.DAT.*
- 20: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1999.DAT.*
- 21: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.*
- 22: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
- 23: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
- 24: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1	100.0	3	17 AAT33326	CAPL trinucleotide
2	1	100.0	3	17 AAT33326	CAPL trinucleotide
3	1	100.0	3	21 AAA94655	Human TUB gene pro
4	1	100.0	3	22 AAL20244	Human breast cance
5	1	100.0	4	16 AAQ81664	bFGF binding oligo
6	1	100.0	4	16 AAQ81664	bFGF binding oligo
7	1	100.0	4	16 AAQ81665	bFGF binding oligo
8	1	100.0	4	16 AAQ81665	bFGF binding oligo
9	1	100.0	4	18 AAT86385	Probe for target n

c	10	1	100.0	4	18	AAT96385	Probe for target n
	11	1	100.0	4	18	AAT77252	Immunostimulatory
c	12	1	100.0	4	18	AAT77252	Immunostimulatory
c	13	1	100.0	4	22	AAL17191	Human breast cancer
c	14	1	100.0	4	22	AAL17191	Human breast cancer
c	15	1	100.0	4	22	AAL24357	Human breast cancer
c	16	1	100.0	4	22	AAF61450	Cyclin binding ham
c	17	1	100.0	5	10	AAQ93676	Synthetic probe for
c	18	1	100.0	5	15	AAQ68752	CHA255 heavy chain
c	19	1	100.0	5	16	AAQ81667	bFGF binding oligo
c	20	1	100.0	5	17	AAT12043	Cleavable replicab
c	21	1	100.0	5	19	AAV61663	Fusarium sp. 18S r
c	22	1	100.0	5	19	AAV61663	Fusarium sp. 18S r
c	23	1	100.0	5	19	AAT96299	Fungal telomeric n
c	24	1	100.0	5	20	AAZ10695	Oligonucleotide se
c	25	1	100.0	5	20	AAZ10696	Oligonucleotide se
c	26	1	100.0	5	20	AAZ11611	DNA enhancer sequ
c	27	1	100.0	5	20	AAZ11611	DNA enhancer sequ
c	28	1	100.0	5	20	AAV72347	US5908745 primer #
c	29	1	100.0	5	20	AAV72348	US5908745 primer #
c	30	1	100.0	5	20	AAV72348	US5908745 primer #
c	31	1	100.0	5	20	AAV72349	US5908745 primer #
c	32	1	100.0	5	20	AAV72350	US5908745 primer #
c	33	1	100.0	5	20	AAX56964	Ras gene modulat
c	34	1	100.0	5	20	AAX56964	Ras gene modulat
c	35	1	100.0	5	20	AAZ11608	Mutant H-ras spec
c	36	1	100.0	5	20	AAZ11608	Mutant H-ras spec
c	37	1	100.0	5	21	AAA56981	Human colon cancer
c	38	1	100.0	5	21	AAA56981	Human colon cancer
c	39	1	100.0	5	21	AAZ93601	Transcription fact
c	40	1	100.0	5	21	AAZ93601	Transcription fact
c	41	1	100.0	5	21	AAZ93602	Transcription fact
c	42	1	100.0	5	21	AAZ89330	Human UCP3 promote
c	43	1	100.0	5	21	AAZ89331	Human UCP3 promote
c	44	1	100.0	5	21	AAZ89332	Human UCP3 promote
c	45	1	100.0	5	21	AAZ48433	First DNA arm segm

ALIGNMENTS

RESULT 1
AAT33326
ID AAT33326 standard; RNA; 3 BP.
XX
AC AAT33326;
XX
DT 12-NOV-1996 (first entry)
XX
DE CAPL trinucleotide.
XX
KW CAPL; antisense oligonucleotide; ribozyme; cancer; metastasis;
KW osteosarcoma; therapy; ss.
XX
OS Synthetic.
XX
PN WO9625499-A1.
XX
PD 22-AUG-1996.
XX
PF 16-FEB-1996; 96WO-US02108.
XX
PR 17-FEB-1995; 95US-0391375.
XX
(HYBR-) HYBRIDON INC.
PA (NORA-) NORWEGIAN RADIUM HOSPITAL RES FOUND.
XX
PI Agrawal S, Engebraaten O, Fodstad O, Hovig E, Maelandsmo GJ;
PI Von Hofe E;
XX
DR WPI; 1996-393400/39.
XX
PT Synthetic oligo:nucleotide(s) inhibiting CAPL gene expression -

PT useful to inhibit metastatic cancer, partic. osteosarcoma
 XX
 PS Claim 2; Page 56; 70pp; English.
 XX
 CC Novel antisense oligonucleotides capable of inhibiting CAPL gene
 CC expression may include the trinucleotide GUC (AAT33326, given in 5'
 CC to 3' direction) found in codon 14 of CAPL mRNA. These and
 CC other antisense oligonucleotides (AAT33327-36) complementary to
 CC specific regions of the CAPL gene (see also AAT33345), as well as
 CC CAPL-specific ribozymes (AAT33337-40) can be administered to a
 CC patient as a means of inhibiting metastatic cancer.
 XX
 XX Sequence 3 BP; 0 A; 1 C; 1 G; 1 U; 0 other;
 SQ

Query Match 100.0%; Score 1; DB 17; Length 3;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 g 1
 DB 3 g 3

RESULT 2
 AAT33326/c
 ID AAT33326 standard; RNA; 3 BP.
 XX
 AC AAT33326;
 XX
 DT 12-NOV-1996 (first entry)
 XX
 DE CAPL trinucleotide.
 DE
 XX CAPL; antisense oligonucleotide; ribozyme; cancer; metastasis;
 KW osteosarcoma; therapy; ss.
 KW
 XX
 OS Synthetic.
 XX
 XX WO9625499-A1.
 PN
 XX
 PD 22-AUG-1996.
 XX
 PF 16-FEB-1996; 96WO-US02108.
 XX
 XX 17-FEB-1995; 95US-0391375.
 PR
 XX (HYBR-) HYBRIDON INC.
 PA
 PA (NORA-) NORWEGIAN RADIUM HOSPITAL RES FOUND.
 XX
 XX Agrawal S, Engebraaten O, Fodstad O, Hovig E, Maelandsmo GJ;
 PI Von Hofe E;
 PI
 XX WPI; 1996-393400/39.
 DR
 XX Synthetic oligo:nucleotide(s) inhibiting CAPL gene expression -
 PT useful to inhibit metastatic cancer, partic. osteosarcoma
 PT
 XX
 PS Claim 2; Page 56; 70pp; English.
 XX
 XX Novel antisense oligonucleotides capable of inhibiting CAPL gene
 CC expression may include the trinucleotide GUC (AAT33326, given in 5'
 CC to 3' direction) found in codon 14 of CAPL mRNA. These and
 CC other antisense oligonucleotides (AAT33327-36) complementary to
 CC specific regions of the CAPL gene (see also AAT33345), as well as
 CC CAPL-specific ribozymes (AAT33337-40) can be administered to a
 CC patient as a means of inhibiting metastatic cancer.
 CC
 XX Sequence 3 BP; 0 A; 1 C; 1 G; 1 U; 0 other;
 SQ

Query Match 100.0%; Score 1; DB 17; Length 3;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 g 1
 DB 3 g 3

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 g 1
 DB 1 g 1

RESULT 3
 AAA94655
 ID AAA94655 standard; DNA; 3 BP.
 XX
 AC AAA94655;
 XX
 DT 15-JAN-2001 (first entry)
 XX
 DE Human TUB gene probe #2.
 DE
 XX Human; TULP; neurosensory defect; retina; retinal dystrophy; probe;
 KW TUB; ss.
 KW
 XX Homo sapiens.
 OS
 XX US6114502-A.
 PN
 XX 05-SEP-2000.
 PD
 XX 27-FEB-1998; 98US-0032365.
 PF
 XX 22-AUG-1996; 96US-0701380.
 PR
 PR 04-SEP-1996; 96US-0706292.
 PR
 PR 10-APR-1996; 96US-0630592.
 PR
 PR 17-SEP-1996; 96US-0714991.
 PR
 PR 30-APR-1997; 97US-0850218.
 PR
 PR 01-AUG-1997; 97US-0904699.
 PR
 PR 17-SEP-1997; 97US-0932306.
 XX
 XX (AXYS-) AXYS PHARM INC.
 PA
 XX North M, Nishina P, Noben-Trauth K, Naggert J;
 PI
 XX WPI; 2000-586483/55.
 DR
 XX Mammalian proteins expressed in retina and brain, useful for producing
 PT antibodies and for diagnosing neurosensory defects including cochlear
 PT degeneration, peripheral retinal degeneration and cone-rod retinal
 PT dystrophy -
 XX
 PS Disclosure; Columns 81-82; 61pp; English.
 XX
 CC The present invention relates to human and murine cDNAs from a
 CC neurosensory defect associated gene family. The novel cDNAs are mouse
 CC tub form I (see AAA94632), mouse tub form II (see AAA94630), human TUB
 CC form 6 (see AAA94632), human TUB form 1 (see AAA94633), human TULP1 (see
 CC AAA94635), human TULP2 (see AAA94636), human TULP3 (see AAA94637) and
 CC mouse TULP4 (see AAA94638). The novel coding sequences are useful as
 CC immunogens to raise antibodies that specifically identify TUB/TULP
 CC expressing cells and in drug screening assays directed at neurosensory
 CC defects. The novel proteins encoded by the present sequence can be used
 CC for the treatment of neurosensory degenerative conditions e.g. retinal
 CC dystrophies. The present sequence is a probe used to isolate the novel
 CC genes of the present invention.
 XX
 SQ Sequence 3 BP; 0 A; 0 C; 3 G; 0 U; 0 other;
 XX

Query Match 100.0%; Score 1; DB 21; Length 3;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 g 1
 DB 1 g 1

RESULT 4
AAL20244/c
ID AAL20244 standard; cDNA; 3 BP.

XV AAL20244;

XX 07-DEC-2001 (first entry)

XX Human breast cancer expressed polynucleotide 12701.

XX Human; breast cancer; cell marker; cytostatic; ss.

XX Homo sapiens.

XX WO200151628-A2.

XX 19-JUL-2001.

XX 10-JAN-2001; 2001WO-US00798.

XX 14-JAN-2000; 2000US-0176077.

XX 14-MAR-2000; 2000US-0189167.

XX 24-MAR-2000; 2000US-0192099.

XX 29-MAR-2000; 2000US-0193480.

XX 15-MAY-2000; 2000US-0205230.

XX 09-JUN-2000; 2000US-0211315.

XX 25-JUL-2000; 2000US-0220534.

XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX Lillie J, Xu Y, Wang Y, Steinmann K;

XX WPI; 2001-451856/48.

XX New peptide useful as a marker for the diagnosis of breast cancer

XX Claim 1; Page 2245; 3695pp; English.

XX The invention relates to human breast cancer expressed polynucleotides (AAL07544-AAL26789) and methods of assessing whether a patient is afflicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells. The polynucleotides and encoded polypeptides are potential markers for detecting, diagnosing, monitoring, characterising treating and potentially preventing breast cancer. The polynucleotides and encoded polypeptides are also useful for isolating compounds with cytostatic activity.

XX Sequence 3 BP; 1 A; 1 C; 0 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 22; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1

Db 2 G 2

RESULT 5

AAQ81664

XX AAQ81664 standard; RNA; 4 BP.

XX AC AAQ81664;

XX 29-SEP-1995 (first entry)

XX bFGF binding oligomer core sequence #1.

XX Basic; fibroblast growth factor; bFGF; stem-loop structure;

KW bubble structure; pseudoknot; receptor; heparin; competition;

KW inhibition; enhance; neovascularisation; solid tumour; cancer;
KW metastasis; diagnosis; gene therapy; ss.

OS Synthetic.

XX WO9500528-A.

XX 05-JAN-1995.

XX 17-JUN-1994; 94WO-US06884.

XX 18-JUN-1993; 93US-0079677.

XX 07-JAN-1994; 94US-0179491.

XX (PHAR-) PHARMAGENICS INC.

XX Beutel BA, Joesten ME;

XX WPI; 1995-051992/07.

XX New oligo-nucleotide(s) that bind to basic fibroblast growth factor - modulating, esp. inhibiting, its activity, useful in treating cancer, preventing metastasis, and diagnosis.

XX Claim 3; Page 25; 44pp; English.

XX The sequences given in AAQ81642-95 are oligonucleotides which modulate the activity of basic fibroblast growth factor (bFGF) by binding to the bFGF protein. Most esp. the sequences given in AAQ81664-67 represent core sequences of which at least one is present in each of the binding oligos. These oligonucleotides may form a single strand, double strand, a stem-loop structure, a bubble structure, a pseudoknot or a closed, circular structure. bFGF binds to high affinity receptor and low affinity heparin-like molecules on the cell surface. These oligonucleotides bind to bFGF in competition with its receptor and heparin. These oligonucleotides may inhibit or enhance the activity of bFGF. Particularly, they inhibit neovascularisation so they can be used to suppress growth of solid tumours and to reduce the risk of metastasis. They can be used as diagnostic reagents to determine the presence of thrombin, or used in gene therapy.

XX Sequence 4 BP; 0 A; 1 C; 2 G; 1 U; 0 other;

Query Match 100.0%; Score 1; DB 16; Length 4;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1

Db 1 g 1

RESULT 6

AAQ81664/c

XX ID AAQ81664 standard; RNA; 4 BP.

XX AC AAQ81664;

XX 29-SEP-1995 (first entry)

XX bFGF binding oligomer core sequence #1.

XX Basic; fibroblast growth factor; bFGF; stem-loop structure;

KW bubble structure; pseudoknot; receptor; heparin; competition;

KW inhibition; enhance; neovascularisation; solid tumour; cancer;

KW metastasis; diagnosis; gene therapy; ss.

XX Synthetic.

XX WO9500528-A.

```

PD 05-JAN-1995.
XX
PF 17-JUN-1994; 94WO-US06884.
XX
PR 18-JUN-1993; 93US-0079677.
PR 07-JAN-1994; 94US-0179491.
XX
PA (PHAR-) PHARMAGENICS INC.
XX
PI Beutel BA, Joesten ME;
XX
DR WPI; 1995-051992/07.
XX
PT New oligo-nucleotide(s) that bind to basic fibroblast growth
PT factor - modulating, esp. inhibiting, its activity, useful in
PT treating cancer, preventing metastasis, and diagnosis.
XX
PS Claim 3; Page 25; 44pp; English.
XX
CC The sequences given in AAQ81642-95 are oligonucleotides which modulate
CC the activity of basic fibroblast growth factor (bFGF) by binding
CC to the bFGF protein. Most esp. the sequences given in AAQ81664-67
CC represent core sequences of which at least one is present in each of
CC the binding oligos. These oligonucleotides may form a single
CC strand, double strand, a stem-loop structure, a bubble structure, a
CC pseudoknot or a closed, circular structure. bFGF binds to high
CC affinity receptor and low affinity heparin-like molecules on the
CC cell surface. These oligonucleotides bind to bFGF in competition
CC with its receptor and heparin. These oligonucleotides may inhibit
CC or enhance the activity of bFGF. Particularly, they inhibit
CC neovascularisation so they can be used to suppress growth of solid
CC tumours and to reduce the risk of metastasis. They can be used as
CC diagnostic reagents to determine the presence of thrombin, or used in
CC gene therapy.
XX
SQ Sequence 4 BP; 0 A; 1 C; 2 G; 1 U; 0 other;

Query Match 100.0%; Score 1; DB 16; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 g 1
Db 4 G 4

RESULT 7
AAQ81665
ID AAQ81665 standard; RNA; 4 BP.
AC
AC AAQ81665;
XX
DT 29-SEP-1995 (first entry)
XX
DE bFGF binding oligomer core sequence #2.
XX
KW Basic; fibroblast growth factor; bFGF; stem-loop structure;
KW bubble structure; pseudoknot; receptor; heparin; competition;
KW inhibition; enhance; neovascularisation; solid tumour; cancer;
KW metastasis; diagnosis; gene therapy; ss.
XX
OS Synthetic.
XX
PN WO9500528-A.
XX
PD 05-JAN-1995.
XX
PF 17-JUN-1994; 94WO-US06884.
XX
PR 18-JUN-1993; 93US-0079677.
PR 07-JAN-1994; 94US-0179491.
XX
PA (PHAR-) PHARMAGENICS INC.
XX
PI Beutel BA, Joesten ME;
XX
DR WPI; 1995-051992/07.
XX
PT New oligo-nucleotide(s) that bind to basic fibroblast growth

```

PT factor - modulating, esp. inhibiting, its activity, useful in
PT treating cancer, preventing metastasis, and diagnosis.
XX
PS Claim 3; Page 25; 44pp; English.
XX
CC The sequences given in AAQ81642-95 are oligonucleotides which modulate
CC the activity of basic fibroblast growth factor (bFGF) by binding
CC to the bFGF protein. Most esp. the sequences given in AAQ81664-67
CC represent core sequences of which at least one is present in each of
CC the binding oligos. These oligonucleotides may form a single
CC strand, double strand, a stem-loop structure, a bubble structure, a
CC pseudoknot or a closed, circular structure. bFGF binds to high
CC affinity receptor and low affinity heparin-like molecules on the
CC cell surface. These oligonucleotides bind to bFGF in competition
CC with its receptor and heparin. These oligonucleotides may inhibit
CC or enhance the activity of bFGF. Particularly, they inhibit
CC neovascularisation so they can be used to suppress growth of solid
CC tumours and to reduce the risk of metastasis. They can be used as
CC diagnostic reagents to determine the presence of thrombin, or used in
XX gene therapy.
XX
SQ Sequence 4 BP; 0 A; 2 C; 1 G; 1 U; 0 other;

Query Match 100.0%; Score 1; DB 16; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 4 G 4

RESULT 9
AAT86385
ID AAT86385 standard; DNA: 4 BP.
XX
AC AAT86385;
XX
DT 23-APR-1998 (first entry)
XX
DE Probe for target nucleic acid sequence P0.
XX
KW Point mutation detection; nucleic acid sequence analysis; probe;
KW viral disease diagnosis; genetic disease diagnosis; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1 /*tag= a
FT /*note= "C-5'phosphate"
XX
PN WO9738131-A1.
XX
PD 16-OCT-1997.
XX
PF 11-APR-1996; 96WO-RU000087.
XX
PR 11-APR-1996; 96WO-RU000087.
XX
PA (DYMS/) DYMSHITS G M.
PA (IVAN/) IVANOVA E M.
PA (KRIV/) KRIVENKO A A.
PA (KULI/) KULIKOVA V F.
PA (LOKH/) LOKHOV S G.
PA (PYSH/) PYSHNY D V.
XX
PI Dymshits GM, Ivanova EM, Krivenko AA, Kulikova VF;
PI Lokhov SG, Pyshtny DV;
XX
DR WPI; 1997-512737/47.
XX

PT Detection of target nucleic acid sequence - based on ligation of
PT hybridised short probe to flanking target-complementary sequences
XX
PS Example; Page 4; 15pp; Russian.
XX
CC This sequence represents a probe for the target sequence P0 (shown in
CC AAT86376). This sequence was used to test the method of the invention.
CC The method of the invention is for detecting a nucleic acid sequence to
CC be analysed, and comprises hybridisation of an oligonucleotide probe
CC complementary to the sequence to be analysed and bearing a reporter
CC group, the novelty is that detection of a sequence is based on the
CC ligation of a short oligonucleotide (with a length of 4-6 units) with
CC flanking oligonucleotide sequences (or their derivatives bearing
CC polycyclic aromatic groups). The method is especially useful for
CC detecting point mutations. Diagnosis of viral, genetic and other
XX diseases is also mentioned.
XX
SQ Sequence 4 BP; 1 A; 2 C; 1 G; 0 U; 0 other;

Query Match 100.0%; Score 1; DB 18; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 3 g 3

RESULT 10
AAT86385/c
ID AAT86385 standard; DNA: 4 BP.
XX
AC AAT86385;
XX
DT 23-APR-1998 (first entry)
XX
DE Probe for target nucleic acid sequence P0.
XX
KW Point mutation detection; nucleic acid sequence analysis; probe;
KW viral disease diagnosis; genetic disease diagnosis; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1 /*tag= a
FT /*note= "C-5'phosphate"
XX
PN WO9738131-A1.
XX
PD 16-OCT-1997.
XX
PF 11-APR-1996; 96WO-RU000087.
XX
PR 11-APR-1996; 96WO-RU000087.
XX
PA (DYMS/) DYMSHITS G M.
PA (IVAN/) IVANOVA E M.
PA (KRIV/) KRIVENKO A A.
PA (KULI/) KULIKOVA V F.
PA (LOKH/) LOKHOV S G.
PA (PYSH/) PYSHNY D V.
XX
PI Dymshits GM, Ivanova EM, Krivenko AA, Kulikova VF;
PI Lokhov SG, Pyshtny DV;
XX
DR WPI; 1997-512737/47.
XX
PT Detection of target nucleic acid sequence - based on ligation of
PT hybridised short probe to flanking target-complementary sequences
XX
PS Example; Page 4; 15pp; Russian.
XX

XX This sequence represents a probe for the target sequence P0 (shown in
 CC AAT86376). This sequence was used to test the method of the invention.
 CC The method of the invention is for detecting a nucleic acid sequence to
 CC be analysed, and comprises hybridisation of an oligonucleotide probe
 CC complementary to the sequence to be analysed and bearing a reporter
 CC group, the novelty is that detection of a sequence is based on the
 CC ligation of a short oligonucleotide (with a length of 4-6 units) with
 CC flanking oligonucleotide sequences (or their derivatives bearing
 CC polycyclic aromatic groups). The method is especially useful for
 CC detecting point mutations. Diagnosis of viral, genetic and other
 CC diseases is also mentioned.
 XX
 SQ Sequence 4 BP; 1 A; 2 C; 1 G; 0 U; 0 other;

Query Match 100.0%; Score 1; DB 18; Length 4;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
 |
 Db 4 G 4

RESULT 11
 AAT77252
 ID AAT77252 standard; DNA; 4 BP.

XX
 AC AAT77252;

XX 18-MAR-1998 (first entry)

XX Immunostimulatory polynucleotide 11.

XX Immunostimulatory polynucleotide; ISP; palindrome: vaccine;
 KW immune response; antigen; naked gene expression vector; IgE;
 KW antibody; immunotherapy; ss.

OS Synthetic.

XX WO9728259-A1.

XX 07-AUG-1997.

XX 28-JAN-1997; 97WO-US01277.

XX 30-JAN-1996; 96US-0593554.

XX (REGC) UNIV CALIFORNIA.

XX Carson DA, Raz E;

XX WPI; 1997-402613/37.

XX Recombinant vector containing immunostimulatory palindromic
 PT polynucleotide - useful for selectively enhancing the Th1 immune
 PT response in a host, whilst reducing the risk of anaphylaxis

PS Claim 16; Page 15; 102pp; English.

XX This sequence represents a non-coding immunostimulatory polynucleotide
 CC (ISP) comprised of at least one strand of a palindrome, which includes
 CC at least one dinucleotide consisting of adjacent, unmethylated cytosine
 CC and guanine residues. ISP's could be used in vaccination methods
 CC for enhancing the immune response of a host to an antigen. Administration
 CC of naked gene expression vectors which encode antigens or their
 CC immunostimulatory fragments suppresses IgE antibody production
 CC reducing the risk of anaphylaxis posed by conventional immunotherapy.

XX Sequence 4 BP; 1 A; 1 C; 1 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 18; Length 4;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
 |
 Db 3 g 3

RESULT 12
 AAT77252/c
 ID AAT77252 standard; DNA; 4 BP.

XX
 AC AAT77252;

XX 18-MAR-1998 (first entry)

XX Immunostimulatory polynucleotide 11.

XX Immunostimulatory polynucleotide; ISP; palindrome: vaccine;
 KW immune response; antigen; naked gene expression vector; IgE;
 KW antibody; immunotherapy; ss.

OS Synthetic.

XX WO9728259-A1.

XX 07-AUG-1997.

XX 28-JAN-1997; 97WO-US01277.

XX 30-JAN-1996; 96US-0593554.

XX (REGC) UNIV CALIFORNIA.

XX Carson DA, Raz E;

XX WPI; 1997-402613/37.

XX Recombinant vector containing immunostimulatory palindromic
 PT polynucleotide - useful for selectively enhancing the Th1 immune
 PT response in a host, whilst reducing the risk of anaphylaxis

PS Claim 16; Page 15; 102pp; English.

XX This sequence represents a non-coding immunostimulatory polynucleotide
 CC (ISP) comprised of at least one strand of a palindrome, which includes
 CC at least one dinucleotide consisting of adjacent, unmethylated cytosine
 CC and guanine residues. ISP's could be used in vaccination methods
 CC for enhancing the immune response of a host to an antigen. Administration
 CC of naked gene expression vectors which encode antigens or their
 CC immunostimulatory fragments suppresses IgE antibody production
 CC reducing the risk of anaphylaxis posed by conventional immunotherapy.

SQ Sequence 4 BP; 1 A; 1 C; 1 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 18; Length 4;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
 |
 Db 2 G 2

RESULT 13
 AAL17191
 ID AAL17191 standard; cDNA; 4 BP.

XX
 AC AAL17191;

XX 07-DEC-2001 (first entry)

```
XX DE Human breast cancer expressed polynucleotide 9648.
XX KW Human; breast cancer; cell marker; cytostatic; ss.
XX OS Homo sapiens.
XX PN WO200151628-A2.
XX PD 19-JUL-2001.
XX PF 10-JAN-2001; 2001WO-US00798.
XX PR 14-JAN-2000; 2000US-0176077.
XX PR 14-MAR-2000; 2000US-0189167.
XX PR 24-MAR-2000; 2000US-0192099.
XX PR 29-MAR-2000; 2000US-0193480.
XX PR 15-MAY-2000; 2000US-0205230.
XX PR 09-JUN-2000; 2000US-0211315.
XX PR 25-JUL-2000; 2000US-0220534.
XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX PI Lillie J, Xu Y, Wang Y, Steinmann K;
XX WPI; 2001-451856/48.
XX PT New peptide useful as a marker for the diagnosis of breast cancer -
XX PS Claim 1; Page 1720; 3695pp; English.
XX CC The invention relates to human breast cancer expressed polynucleotides
XX CC (AAL07544-AAL26789) and methods of assessing whether a patient is
XX CC afflicted with breast cancer by examining the correlation between the
XX CC expression of certain markers and the cancerous state of breast cells.
XX CC The polynucleotides and encoded polypeptides are potential markers for
XX CC detecting, diagnosing, monitoring, characterising treating and
XX CC potentially preventing breast cancer. The polynucleotides and encoded
XX CC polypeptides are also useful for isolating compounds with cytostatic
XX CC activity.
XX SQ Sequence 4 BP; 1 A; 1 C; 1 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 22; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 1 g 1

RESULT 14
AAL17191/c
ID AAL17191 standard; cDNA; 4 BP.
AC AAL17191;
XX 07-DEC-2001 (first entry)
XX Human breast cancer expressed polynucleotide 9648.
XX DE Human; breast cancer; cell marker; cytostatic; ss.
XX KW Homo sapiens.
XX OS WO200151628-A2.
XX PN 19-JUL-2001.
XX PD 10-JAN-2001; 2001WO-US00798.
XX PF
```

```
PR 14-JAN-2000; 2000US-0176077.
PR 14-MAR-2000; 2000US-0189167.
PR 24-MAR-2000; 2000US-0192099.
PR 29-MAR-2000; 2000US-0193480.
PR 15-MAY-2000; 2000US-0205230.
PR 09-JUN-2000; 2000US-0211315.
PR 25-JUL-2000; 2000US-0220534.
XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX PI Lillie J, Xu Y, Wang Y, Steinmann K;
XX WPI; 2001-451856/48.
XX PT New peptide useful as a marker for the diagnosis of breast cancer -
XX PS Claim 1; Page 1720; 3695pp; English.
XX CC The invention relates to human breast cancer expressed polynucleotides
XX CC (AAL07544-AAL26789) and methods of assessing whether a patient is
XX CC afflicted with breast cancer by examining the correlation between the
XX CC expression of certain markers and the cancerous state of breast cells.
XX CC The polynucleotides and encoded polypeptides are potential markers for
XX CC detecting, diagnosing, monitoring, characterising treating and
XX CC potentially preventing breast cancer. The polynucleotides and encoded
XX CC polypeptides are also useful for isolating compounds with cytostatic
XX CC activity.
XX SQ Sequence 4 BP; 1 A; 1 C; 1 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 22; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 3 G 3

RESULT 15
AAL24357/c
ID AAL24357 standard; cDNA; 4 BP.
XX 07-DEC-2001 (first entry)
XX Human breast cancer expressed polynucleotide 16814.
XX DE Human; breast cancer; cell marker; cytostatic; ss.
XX KW Homo sapiens.
XX OS WO200151628-A2.
XX PN 19-JUL-2001.
XX PD 10-JAN-2001; 2001WO-US00798.
XX PF 14-JAN-2000; 2000US-0176077.
XX PR 14-MAR-2000; 2000US-0189167.
XX PR 24-MAR-2000; 2000US-0192099.
XX PR 29-MAR-2000; 2000US-0193480.
XX PR 15-MAY-2000; 2000US-0205230.
XX PR 09-JUN-2000; 2000US-0211315.
XX PR 25-JUL-2000; 2000US-0220534.
XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX PI Lillie J, Xu Y, Wang Y, Steinmann K;
XX WPI; 2001-451856/48.
XX DR
```

XX New peptide useful as a marker for the diagnosis of breast cancer -
 PT Claim 1: Page 3087; 3695pp; English.
 PS
 XX The invention relates to human breast cancer expressed polynucleotides
 CC (AAL07544-AAL26789) and methods of assessing whether a patient is
 CC afflicted with breast cancer by examining the correlation between the
 CC expression of certain markers and the cancerous state of breast cells.
 CC The polynucleotides and encoded polypeptides are potential markers for
 CC detecting, diagnosing, monitoring, characterising treating and
 CC potentially preventing breast cancer. The polynucleotides and encoded
 CC polypeptides are also useful for isolating compounds with cytostatic
 CC activity.
 XX Sequence 4 BP; 0 A; 1 C; 0 G; 3 T; 0 other;
 SQ

Query Match 100.0%; Score 1; DB 22; Length 4;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
 |
 Db 3 G 3

RESULT 16
 AAF61450
 ID AAF61450 standard; RNA; 4 BP.
 XX AC AAF61450;
 XX
 DT 18-JUN-2001 (first entry)
 XX
 DE Cyclin binding hammerhead ribozyme 3' catalytic fragment SEQ ID 19.
 XX
 KW Hammerhead ribozyme; cyclin E; restenosis; catalytic; angioplasty;
 KW cyclin E2F1; vasotropic; gene therapy; cell cycle arrest; ss.
 XX Synthetic.
 OS
 XX WO200121789-A1.
 XX
 PD 29-MAR-2001.
 XX
 PF 22-SEP-1999; 99WO-EP07049.
 XX
 PR 22-SEP-1999; 99WO-EP07049.
 XX
 XX (UYTU-) UNIV TUEBINGEN EBERHARD-KARLS.
 PA
 XX Grassi G, Kuhn AC, Kandolf R;
 PI
 XX WPI; 2001-257985/26.
 DR
 XX New catalytically acting RNA molecule comprising hammerhead ribozyme
 PT directed against mRNA molecules encoding cyclin E or E2F1, useful for
 PT inhibiting vascular smooth muscle cell proliferation and restenosis -
 XX
 XX Claim 12: Page 28; 40pp; German.
 PS
 CC This invention describes a novel catalytic RNA molecule which is directed
 CC against mRNA molecules (II) which encode the cell-relevant protein cyclin
 CC E or E2F1. The products of the invention have vasotropic activity and can
 CC be used for gene therapy. The use of (I), or a DNA molecule or a plasmid
 CC of the invention is claimed for obtaining a vector for gene therapy and
 CC for inhibiting restenosis of blood vessel after angioplasty; therapeutic
 CC compositions containing these components are also claimed. (I)
 CC efficiently induces cell cycle arrest by combined inactivation of cyclin
 CC E and E2F1.
 XX
 XX Sequence 4 BP; 2 A; 0 C; 1 G; 0 U; 1 other;
 SQ

Query Match 100.0%; Score 1; DB 22; Length 4;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
 |
 Db 2 g 2

RESULT 17
 AAN93676/c
 ID AAN93676 standard; DNA; 5 BP.
 XX AC AAN93676;
 XX
 DT 24-JUN-1990 (first entry)
 XX
 DE Synthetic probe for hop growth retarding viroid (HSV), HSV cucumber
 DE variant (HSV-c) and HSV grape variant (HSV-g).
 XX
 KW Hop growth retarding viroid; cucumber variant; grape variant; probe; ss.
 XX Hop growth retarding viroid.
 OS
 XX JP01040000-A.
 PN
 XX 10-FEB-1989.
 PD
 XX 05-AUG-1987; 87JP-0194377.
 PF
 XX 05-AUG-1987; 87JP-0195377.
 PR
 XX (YUKI) YUKI GOSEI YAKUHIN.
 PA
 XX WPI; 1989-089715/12.
 DR
 XX Fractionating and detecting hop growth retarding viroids -
 PT using synthetic DNA probe contg. specific base sequence
 PT
 XX Disclosure; page 3; 5pp; Japanese.
 PS
 XX The synthetic probes is complementary to the RNA of HSV-g bases 53-59.
 CC HSV, HSV-c and HSV-g are fractionated and detected using the synthetic
 CC probe. The probe is 15-25mer. The probe can be used to diagnose HSV
 CC infections in plants.
 CC
 XX Sequence 5 BP; 1 A; 3 C; 0 G; 1 T; 0 other;
 SQ

Query Match 100.0%; Score 1; DB 10; Length 5;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
 |
 Db 5 G 5

RESULT 18
 AAQ68752
 ID AAQ68752 standard; DNA; 5 BP.
 XX AC AAQ68752;
 XX
 DT 22-FEB-1995 (first entry)
 XX
 DE CHA255 heavy chain CDRI clone 3.3.3. coding sequence.
 XX
 KW Polymerase chain reaction; primer; PCR; amplify; heavy; light;
 KW chain; complementarity determining region; CDR; variable; constant;
 KW region; monoclonal antibody; MAB; binding affinity; EDTA; DOTA;
 KW

KW tumour; cancer; colorectal; breast; metal chelate; hapten; ss.

OS Synthetic.

PN AU9350602-A.

XX 26-MAY-1994.

PF 10-NOV-1993; 93AU-0050602.

XX 12-NOV-1992; 92US-0975230.

PR (HYBR-) HYBRITECH INC.

XX Ahrweiler PM, Moore MD;

XX WPI; 1994-209063/26.

DR P-PSDB; AAR54150.

XX Polypeptide used in imaging and treatment of carcinomas and
PT tumours - comprising substd antibody CDR having binding affinity
PT for metal chelate of EDTA or DETA or analogues

XX Claim 25; Fig 3A; 61pp; English.

XX The sequences given in AAQ86747-57 encode the wild type and mutagenised
CC versions of the complementarity determining region 1 (CDR1) of the
CC antibody designated CHA255. CHA255 is a murine monoclonal antibody
CC (MAB) which is capable of binding complexes. Mutagenesis of these
CC CDRs, causes the production of polypeptides with a particularly
CC high binding affinity for EDTA or DOTA metal complexes. CDR1 and -3
CC of the heavy chain, and CDR2 and -3 of the light chain were targeted
CC for mutagenesis. Five residues of both CDR1 and -3 of the CHA255
CC heavy chain, five of seven residues of light chain CDR and six of
CC nine light chain CDR3 residues were specifically targeted for
CC codon-based mutagenesis. The mutagenised MAB's can be used in
CC compositions for in vivo imaging of malignant tissues or tumours. They
CC are also useful for the treatment of malignant tissues or tumours eg.
CC colorectal or breast cancer. Both methods involve the use of
CC radionuclides which bind to metal chelates or haptens which are
CC specifically delivered to the target site by a targeting molecule. CDR
CC derived peptides may be used to construct bi-functional antibodies
CC having dual specificities, or as donor or recipients of CDR sequences.

XX Sequence 5 BP; 0 A; 0 C; 1 G; 1 T; 3 other;

Query Match 100.0%; Score 1; DB 15; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1

Db 1 g 1

RESULT 19

AAQ81667/C

ID AAQ81667 standard; RNA; 5 BP.

XX AAQ81667;

XX 29-SEP-1995 (first entry)

XX bFGF binding oligomer core sequence #4.

XX Basic: fibroblast growth factor; bFGF; stem-loop structure;
KW bubble structure; pseudoknot; receptor; heparin; competition;
KW inhibition; enhance; neovascularisation; solid tumour; cancer;
KW metastasis; diagnosis; gene therapy; ss.

OS Synthetic.

XX

PN WO9500528-A.

XX 05-JAN-1995.

XX 17-JUN-1994; 94WO-US06884.

XX 18-JUN-1993; 93US-0079677.

PR 07-JAN-1994; 94US-0179491.

XX (PHAR-) PHARMAGENICS INC.

XX Beutel BA, Joesten ME;

XX WPI; 1995-051992/07.

XX New oligo-nucleotide(s) that bind to basic fibroblast growth
PT factor - modulating, esp. inhibiting, its activity, useful in
PT treating cancer, preventing metastasis, and diagnosis.

XX Claim 3; Page 25; 44pp; English.

XX The sequences given in AAQ81642-95 are oligonucleotides which modulate
CC the activity of basic fibroblast growth factor (bFGF) by binding
CC to the bFGF protein. Most esp. the sequences given in AAQ81664-67
CC represent core sequences of which at least one is present in each of
CC the binding oligos. These oligonucleotides may form a single
CC strand, double strand, a stem-loop structure, a bubble structure, a
CC pseudoknot or a closed, circular structure. bFGF binds to high
CC affinity receptor and low affinity heparin-like molecules on the
CC cell surface. These oligonucleotides bind to bFGF in competition
CC with its receptor and heparin. These oligonucleotides may inhibit
CC or enhance the activity of bFGF. Particularly, they inhibit
CC neovascularisation so they can be used to suppress growth of solid
CC tumours and to reduce the risk of metastasis. They can be used as
CC diagnostic reagents to determine the presence of thrombin, or used in
CC gene therapy.

XX Sequence 5 BP; 2 A; 2 C; 0 G; 1 U; 0 other;

Query Match 100.0%; Score 1; DB 16; Length 5;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1

Db 5 G 5

RESULT 20

AAT12043/C

ID AAT12043 standard; RNA; 5 BP.

XX AAT12043;

XX 17-JUL-1996 (first entry)

XX Cleavable replicable-inhibiting sequence.

XX Ribozyme; hairpin; hammerhead; probe; MDV-1; midvariant-1;
KW replication; cleavage; ss.

OS Synthetic.

XX US5472840-A.

XX 05-DEC-1995.

XX 30-SEP-1988; 88US-0252243.

XX 17-DEC-1990; 90US-0630288.

PR 30-SEP-1988; 88US-0252243.

PR 22-JUN-1989; 89US-0370218.

XX (STAD) AMOCO CORP.
XX Stefano JE;
XX WPI; 1996-029807/03.
XX Ribozyme-forming nucleic acid probes - contg. MDV-1 sequence and
XX cleavable replicable-inhibiting sequence.
XX Claim 4; Column 62; 43pp; English.
XX A composition comprises RNA of formula P4-P1-P2-P3 (Ia), a nucleic
XX acid of formula R1-R2 (III), where (Ia) and (III) bind to a target
XX nucleic acid of formula X2-X1-X3 (II) to form a hammerhead ribozyme,
XX where P1 is a MDV-1 sequence capable of autocatalytic replication in
XX the absence of P3; P2 is a sequence (AAT12042 or AAT12044) that binds
XX to (II) and forms a cleavage site between P1 and P3; P3 (AAT12043)
XX is an inhibitory element that binds to X2 and interacts with a
XX region of P1 corresp. to nucleotides 81-126 of MDV-1; P4 contributes
XX nucleotides to form the ribozyme with X1 and P2, or is the terminal
XX nucleotide of P1; X1 is a target region of (II); X2 and X3 are
XX terminal nucleotides or second or third target regions of (II); R1
XX is a ribozyme-forming area of (III); and R2 is a terminal nucleotide
XX of R1 or an area of (III) that binds to (II). X1 and R1 are
XX mutually exclusive and are represented by the sequences of AAT12040 and
XX AAT12041. For hairpin ribozymes, P2 is AAT12045 and R1 is AAT12046.
XX Probes bearing ribozymes are produced in a single step by transcription
XX of DNA of appropriate sequence, thereby reducing costs. The ribozymes
XX produce specific cleavage events, leading to a product RNA with
XX defined replication properties.
XX Sequence 5 BP; 0 A; 1 C; 0 G; 2 U; 2 other;

Query Match 100.0%; Score 1; DB 17; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 5 G 5

RESULT 21
AAV61663
ID AAV61663 standard; DNA; 5 BP.
XX AAV61663;
XX 03-DEC-1998 (first entry)
XX Fusarium sp. 18S rRNA DNA fragment #7.
XX 18S rRNA; detection; identification; fungus; ss.
XX Fusarium sp.
XX JPI0234380-A.
XX 08-SEP-1998.
XX 28-FEB-1997; 97JP-0062104.
XX 28-FEB-1997; 97JP-0062104.
XX (SHIN-) SHINKINRUI KINO KAIHATSU KENKYUSHO KK.
XX WPI; 1998-535034/46.
XX Use of oligo:nucleotide for detecting and identification of fungus
XX of Fusarium genus - as primer or probe to detect or identify
XX microbes rapidly and exactly

Query Match 100.0%; Score 1; DB 19; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 5 G 5

RESULT 23
AAV61663
ID AAT96299 standard; DNA; 5 BP.
XX AAT96299
XX Use of oligo:nucleotide for detecting and identification of fungus
XX of Fusarium genus - as primer or probe to detect or identify
XX microbes rapidly and exactly

XX Claim 1; Page 7; 20pp; Japanese.
XX AAV61657-V61664 are fragments of a Fusarium sp. 18S rRNA gene which are
XX used in a method for the detection and identification of a fungus of
XX Fusarium genus. The process can be used to detect or identify microbes
XX rapidly and exactly.
XX Sequence 5 BP; 1 A; 2 C; 1 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 19; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 4 g 4

RESULT 22
AAV61663/c
ID AAV61663 standard; DNA; 5 BP.
XX AAV61663;
XX 03-DEC-1998 (first entry)
XX Fusarium sp. 18S rRNA DNA fragment #7.
XX 18S rRNA; detection; identification; fungus; ss.
XX Fusarium sp.
XX JPI0234380-A.
XX 08-SEP-1998.
XX 28-FEB-1997; 97JP-0062104.
XX 28-FEB-1997; 97JP-0062104.
XX (SHIN-) SHINKINRUI KINO KAIHATSU KENKYUSHO KK.
XX WPI; 1998-535034/46.
XX Use of oligo:nucleotide for detecting and identification of fungus
XX of Fusarium genus - as primer or probe to detect or identify
XX microbes rapidly and exactly

Query Match 100.0%; Score 1; DB 19; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 5 G 5

RESULT 23
AAV61663
ID AAT96299 standard; DNA; 5 BP.
XX AAT96299
XX Use of oligo:nucleotide for detecting and identification of fungus
XX of Fusarium genus - as primer or probe to detect or identify
XX microbes rapidly and exactly


```

AC AAT96299;
XX
DT 08-APR-1998 (first entry)
XX
DE Fungal telomeric nucleic acid sequence.
XX
KW Detection; eukaryotic pathogen; telomeric nucleic acid sequence;
KW telomerase activity; diagnosis; fungal infection; fungus; fungi;
KW malarial infection; malaria; ss.
XX
OS Saccharomyces cerevisiae.
XX
PN US5695932-A.
XX
PD 09-DEC-1997.
XX
PF 13-MAY-1993; 93US-0060952.
XX
PR 13-MAY-1993; 93US-0060952.
PR 13-MAY-1992; 92US-0882438.
PR 24-MAY-1993; 93US-0038766.
XX
PA (REGC ) UNIV CALIFORNIA.
PA (TEXA ) UNIV TEXAS SYSTEM.
XX
PI Blackburn EH, McEachern MJ, Shay J, West MD, Wright W;
XX WPI; 1998-041292/04.
XX
DR Detection of eukaryotic pathogens, especially fungal or Plasmodium
PT spp. - by detecting telomerase activity
XX
PS Claim 5; Columns 81-82; 82pp; English.
XX
CC The present sequence can be used in a novel method for detecting a
CC eukaryotic pathogen in a patient. The method comprises obtaining a
CC sample of somatic tissue or cells from the patient, determining if
CC telomerase activity is present and correlating this with the
CC presence of the pathogen. The method is useful for diagnosis of
CC fungal infections, especially a fungus of the genus Candida,
CC Kluyveromyces, Saccharomyces, Sporothrix, Coccidioides,
CC Histoplasma, Blastomyces, Paracoccidioides, Cryptococcus,
CC Aspergillus, Mucor or Rhizopus, or malarial infections, especially
CC Plasmodium vivax, P. ovale, P. malariae or P. falciparum.
XX
SQ Sequence 5 BP; 0 A; 0 C; 3 G; 2 T; 0 other;

Query Match 100.0%; Score 1; DB 19; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 g 1
Db 2 g 2

RESULT 24
AAZ10695
ID AAZ10695 standard; DNA; 5 BP.
XX
AC AAZ10695;
XX
DT 23-NOV-1999 (first entry)
XX
DE Oligonucleotide sequence that increases p53 activity in a cell.
XX
KW p53 activity; UV mimetic; UV-irradiation; UV-induced dermatosis;
KW UV-induced hyperproliferative disease; psoriasis; vitiligo;
KW atopic dermatitis; allergic rhinitis; conjunctivitis; photoaging;
KW skin cancer; ss.
XX
OS Synthetic.
XX
PN AAZ10695
XX
PD 13-OCT-1999.
XX
PF 24-MAR-1999; 99GB-0006758.
XX
PR 26-MAR-1998; 98US-0048927.
XX
PA (UYBO-) UNIV BOSTON.
XX
PI Gilchrist BA, Yaar M, Eller M;
XX WPI; 1999-543520/46.
XX
PT DNA fragments useful for increasing p53 activity in a cell and reducing

```

```

XX GB2336157-A.
XX
PN 13-OCT-1999.
XX
PF 24-MAR-1999; 99GB-0006758.
XX
PR 26-MAR-1998; 98US-0048927.
XX
PA (UYBO-) UNIV BOSTON.
XX
PI Gilchrist BA, Yaar M, Eller M;
XX WPI; 1999-543520/46.
XX
PT DNA fragments useful for increasing p53 activity in a cell and reducing
PT susceptibility to UV-induced hyperproliferative diseases -
XX
PS Claim 11; Page 30; 44pp; English.
XX
CC AAZ10692-97 represent DNA fragments that are used for increasing p53
CC activity in a cell. The oligonucleotides are UV mimetics and
CC protect cells against subsequent exposure to UV-irradiation or
CC chemicals. The oligonucleotides are useful for increasing p53 activity
CC in a cell, reducing the susceptibility to UV-induced hyperproliferative
CC diseases, treating psoriasis, vitiligo, atopic dermatitis, allergic
CC rhinitis, conjunctivitis, and UV-induced dermatoses, reducing photoaging
CC and reducing susceptibility to skin cancer.
XX
SQ Sequence 5 BP; 1 A; 0 C; 2 G; 2 T; 0 other;

```

```

Query Match 100.0%; Score 1; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 g 1
Db 1 g 1

RESULT 25
AAZ10696/c
ID AAZ10696 standard; DNA; 5 BP.
XX
AC AAZ10696;
XX
DT 23-NOV-1999 (first entry)
XX
DE Oligonucleotide sequence that increases p53 activity in a cell.
XX
KW p53 activity; UV mimetic; UV-irradiation; UV-induced dermatosis;
KW UV-induced hyperproliferative disease; psoriasis; vitiligo;
KW atopic dermatitis; allergic rhinitis; conjunctivitis; photoaging;
KW skin cancer; ss.
XX
OS Synthetic.
XX
PN GB2336157-A.
XX
PD 13-OCT-1999.
XX
PF 24-MAR-1999; 99GB-0006758.
XX
PR 26-MAR-1998; 98US-0048927.
XX
PA (UYBO-) UNIV BOSTON.
XX
PI Gilchrist BA, Yaar M, Eller M;
XX WPI; 1999-543520/46.
XX
PT DNA fragments useful for increasing p53 activity in a cell and reducing

```

PT susceptibility to UV-induced hyperproliferative diseases -
XX Claim 11; Page 30; 44pp; English.
XX
CC AAZ10692-97 represent DNA fragments that are used for increasing p53
CC activity in a cell. The oligonucleotides are are UV mimetics and
CC protect cells against subsequent exposure to UV-irradiation or
CC chemicals. The oligonucleotides are useful for increasing p53 activity
CC in a cell, reducing the susceptibility to UV-induced hyperproliferative
CC diseases, treating psoriasis, vitiligo, atopic dermatitis, allergic
CC rhinitis, conjunctivitis, and UV-induced dermatoses, reducing photoaging
CC and reducing susceptibility to skin cancer.
XX
SQ Sequence 5 BP; 2 A; 2 C; 0 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 q 1
Db 5 G 5

RESULT 26
AAZ11611
ID AAZ11611 standard; DNA; 5 BP.
XX
AC AAZ11611;
XX
DT 16-NOV-1999 (first entry)
XX
DE DNA enhancer sequence present in an upstream element.
XX
KW Plant promoter; TATA motif; transcription start site; upstream element;
KW gene expression; oxalate oxidase; plant resistance; pathogen; maize;
KW Ubi-1 promoter; Syn II core promoter; ss.
XX
OS Synthetic.
XX
PN WO9943838-A1.
XX
PD 02-SEP-1999.
XX
PF 23-FEB-1999; 99WO-US03863.
XX
PR 24-FEB-1998; 98US-0028819.
XX
PA (PION-) PIONEER HT-BRED INT INC.
XX
PI Bowen BA, Bruce WB, Lu G, Sims LE, Tagliani LA;
XX
DR WPI; 1999-540601/45.
XX
PT New synthetic promoter functional in plants to provide non-tissue
PT specific, constitutive expression, particularly of oxalate oxidase for
PT increased resistance to pathogens -
XX
PS Claim 39; Page 47; 61pp; English.
XX
CC The invention provides a new synthetic plant promoter that comprises a
CC TATA motif; a transcription start site (TSS) and a region between TATA
CC and TSS containing at least 64 percent GC content. The synthetic core
CC promoter, optionally containing additional upstream elements are used to
CC increase expression, provides non-tissue specific, constitutive
CC transcription of heterologous genes in any sort of plant, especially the
CC gene for oxalate oxidase for increasing plant resistance to pathogens.
CC The upstream activating elements can be used to increase transcription
CC from any promoter. A combination of the synthetic core promoter with
CC synthetic upstream elements can induce expression 10 times greater than
CC that provided by the maize Ubi-1 promoter. The present sequence
CC represents a DNA enhancer OSC-like motif present in an upstream element

CC sequence.
XX
SQ Sequence 5 BP; 1 A; 1 C; 2 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 q 1
Db 2 g 2

RESULT 27
AAZ11611/c
ID AAZ11611 standard; DNA; 5 BP.
XX
AC AAZ11611;
XX
DT 16-NOV-1999 (first entry)
XX
DE DNA enhancer sequence present in an upstream element.
XX
KW Plant promoter; TATA motif; transcription start site; upstream element;
KW gene expression; oxalate oxidase; plant resistance; pathogen; maize;
KW Ubi-1 promoter; Syn II core promoter; ss.
XX
OS Synthetic.
XX
PN WO9943838-A1.
XX
PD 02-SEP-1999.
XX
PF 23-FEB-1999; 99WO-US03863.
XX
PR 24-FEB-1998; 98US-0028819.
XX
PA (PION-) PIONEER HT-BRED INT INC.
XX
PI Bowen BA, Bruce WB, Lu G, Sims LE, Tagliani LA;
XX
DR WPI; 1999-540601/45.
XX
PT New synthetic promoter functional in plants to provide non-tissue
PT specific, constitutive expression, particularly of oxalate oxidase for
PT increased resistance to pathogens -
XX
PS Claim 39; Page 47; 61pp; English.
XX
CC The invention provides a new synthetic plant promoter that comprises a
CC TATA motif; a transcription start site (TSS) and a region between TATA
CC and TSS containing at least 64 percent GC content. The synthetic core
CC promoter, optionally containing additional upstream elements are used to
CC increase expression, provides non-tissue specific, constitutive
CC transcription of heterologous genes in any sort of plant, especially the
CC gene for oxalate oxidase for increasing plant resistance to pathogens.
CC The upstream activating elements can be used to increase transcription
CC from any promoter. A combination of the synthetic core promoter with
CC synthetic upstream elements can induce expression 10 times greater than
CC that provided by the maize Ubi-1 promoter. The present sequence
CC represents a DNA enhancer OSC-like motif present in an upstream element
XX
SQ Sequence 5 BP; 1 A; 1 C; 2 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 q 1
Db 1
1

DE	US5908745 primer #5.	
XX	DNA sequencing; disease-associated allele; polyacrylamide matrix;	
KW	continuous/contiguous stacking hybridization technique; detection;	
KW	mutation; diagnosis; primer; ss.	
XX	Synthetic.	
OS		
XX	US5908745-A.	
PN		
XX	01-JUN-1999.	
PD		
XX	16-JAN-1996; 96US-0587332.	
PF		
XX	16-JAN-1996; 96US-0587332.	
PR		
XX	(UYCH-) UNIV CHICAGO.	
PA		
XX	Barski VE, Kirillov EV, Lysov YP, Mirzabekov AD;	
XX	Parinov SV, Yershov GM;	
PI		
XX	WPI: 1999-347002/29.	
DR		
XX	Detecting disease-associated alleles using continuous/contiguous	
PT	stacking hybridization as a diagnostic tool	
PT		
XX	Example 1; Column 9; 16pp; English.	
PS		
XX	This invention describes novel methods for sequencing and analysing DNA	
CC	samples to detect disease-associated alleles, by continuous/contiguous	
CC	stacking hybridization techniques (utilizing universal bases) with	
CC	oligonucleotides immobilized on polyacrylamide matrices. The methods may	
CC	be used to detect multiple DNA base mutations which are specific for	
CC	certain diseases. The methods of the invention provide accurate and	
CC	efficient and sensitive methods for diagnosing disease by detecting	
CC	multiple mutation sequences in patient DNA. The method require the	
CC	minimum number of oligonucleotides and few stacking hybridization steps	
CC	than prior art methods. The methods are also efficient enough to	
CC	discriminate between perfect and imperfect duplexes. The methods also	
CC	obviate the need for the fabrication and array placement of large numbers	
CC	of immobilized oligomers.	
XX	Sequence 5 BP; 2 A; 2 C; 1 G; 0 U; 0 other;	
SQ		
Query Match	100.0%; Score 1; DB 20; Length 5;	
Best Local Similarity	100.0%; Pred. No. 0;	
Matches	1; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
Qy	1 g 1	
Db	2 g 2	
RESULT	30	
AAV72347/c		
ID	AAV72348 standard; DNA; 5 BP.	
XX		
AC	AAV72348;	
XX		
DT	28-JUL-1999 (first entry)	
XX		
DE	US5908745 primer #5.	
XX	DNA sequencing; disease-associated allele; polyacrylamide matrix;	
KW	continuous/contiguous stacking hybridization technique; detection;	
KW	mutation; diagnosis; primer; ss.	
XX	Synthetic.	
OS		
XX	US5908745-A.	
PN		
XX	01-JUN-1999.	
PD		
XX	16-JAN-1996; 96US-0587332.	
PF		
XX	16-JAN-1996; 96US-0587332.	
PR		
XX	(UYCH-) UNIV CHICAGO.	
PA		
XX	Barski VE, Kirillov EV, Lysov YP, Mirzabekov AD;	
XX	Parinov SV, Yershov GM;	
PI		
XX	WPI: 1999-347002/29.	
DR		
XX	Detecting disease-associated alleles using continuous/contiguous	
PT	stacking hybridization as a diagnostic tool	
PT		
XX	Example 1; Column 9; 16pp; English.	
PS		
XX	This invention describes novel methods for sequencing and analysing DNA	
CC	samples to detect disease-associated alleles, by continuous/contiguous	
CC	stacking hybridization techniques (utilizing universal bases) with	
CC	oligonucleotides immobilized on polyacrylamide matrices. The methods may	
CC	be used to detect multiple DNA base mutations which are specific for	
CC	certain diseases. The methods of the invention provide accurate and	
CC	efficient and sensitive methods for diagnosing disease by detecting	
CC	multiple mutation sequences in patient DNA. The method require the	
CC	minimum number of oligonucleotides and few stacking hybridization steps	
CC	than prior art methods. The methods are also efficient enough to	
CC	discriminate between perfect and imperfect duplexes. The methods also	
CC	obviate the need for the fabrication and array placement of large numbers	
CC	of immobilized oligomers.	
XX	Sequence 5 BP; 2 A; 3 C; 0 G; 0 U; 0 other;	
SQ		
Query Match	100.0%; Score 1; DB 20; Length 5;	
Best Local Similarity	100.0%; Pred. No. 0;	
Matches	1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 g 1	
Db	5 G 5	
RESULT	29	
AAV72348		
ID	AAV72348 standard; DNA; 5 BP.	
XX		
AC	AAV72348;	
XX		
DT	28-JUL-1999 (first entry)	
XX		

XX 16-JAN-1996; 96US-0587332.
XX 16-JAN-1996; 96US-0587332.
XX (UYCH-) UNIV CHICAGO.
XX Barski VE, Kirillov EV, Lysov YP, Mirzabekov AD;
XX Parinov SV, Yerшов GM;
XX WPI; 1999-347002/29.
XX Detecting disease-associated alleles using continuous/contiguous
XX stacking hybridization as a diagnostic tool
XX Example 1; Column 9; 16pp; English.
XX This invention describes novel methods for sequencing and analysing DNA
XX samples to detect disease-associated alleles, by continuous/contiguous
XX stacking hybridization techniques (utilizing universal bases) with
XX oligonucleotides immobilized on polyacrylamide matrices. The methods may
XX be used to detect multiple DNA base mutations which are specific for
XX certain diseases. The methods of the invention provide accurate and
XX efficient and sensitive methods for diagnosing disease by detecting
XX multiple mutation sequences in patient DNA. The method require the
XX minimum number of oligonucleotides and few stacking hybridization steps
XX than prior art methods. The methods are also efficient enough to
XX discriminate between perfect and imperfect duplexes. The methods also
XX obviate the need for the fabrication and array placement of large numbers
XX of immobilized oligomers.
XX Sequence 5 BP; 2 A; 2 C; 1 G; 0 U; 0 other;

Query Match 100.0%; Score 1; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 5 G 5

RESULT 31
AAV72349/C
ID AAV72349 standard; DNA; 5 BP.
XX AAV72349;
XX 28-JUL-1999 (first entry)
XX US5908745 primer #6.
XX DNA sequencing; disease-associated allele; polyacrylamide matrix;
XX continuous/contiguous stacking hybridization technique; detection;
XX mutation; diagnosis; primer; ss.
XX Synthetic.
XX US5908745-A.
XX 01-JUN-1999.
XX 16-JAN-1996; 96US-0587332.
XX 16-JAN-1996; 96US-0587332.
XX (UYCH-) UNIV CHICAGO.
XX Barski VE, Kirillov EV, Lysov YP, Mirzabekov AD;
XX Parinov SV, Yerшов GM;
XX WPI; 1999-347002/29.

XX This invention describes novel methods for sequencing and analysing DNA
XX samples to detect disease-associated alleles, by continuous/contiguous
XX stacking hybridization techniques (utilizing universal bases) with
XX oligonucleotides immobilized on polyacrylamide matrices. The methods may
XX be used to detect multiple DNA base mutations which are specific for

XX Detecting disease-associated alleles using continuous/contiguous
XX stacking hybridization as a diagnostic tool
XX Example 1; Column 9; 16pp; English.
XX This invention describes novel methods for sequencing and analysing DNA
XX samples to detect disease-associated alleles, by continuous/contiguous
XX stacking hybridization techniques (utilizing universal bases) with
XX oligonucleotides immobilized on polyacrylamide matrices. The methods may
XX be used to detect multiple DNA base mutations which are specific for
XX certain diseases. The methods of the invention provide accurate and
XX efficient and sensitive methods for diagnosing disease by detecting
XX multiple mutation sequences in patient DNA. The method require the
XX minimum number of oligonucleotides and few stacking hybridization steps
XX than prior art methods. The methods are also efficient enough to
XX discriminate between perfect and imperfect duplexes. The methods also
XX obviate the need for the fabrication and array placement of large numbers
XX of immobilized oligomers.
XX Sequence 5 BP; 2 A; 3 C; 0 G; 0 U; 0 other;

Query Match 100.0%; Score 1; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 5 G 5

RESULT 32
AAV72350/C
ID AAV72350 standard; DNA; 5 BP.
XX AAV72350;
XX 28-JUL-1999 (first entry)
XX US5908745 primer #7.
XX DNA sequencing; disease-associated allele; polyacrylamide matrix;
XX continuous/contiguous stacking hybridization technique; detection;
XX mutation; diagnosis; primer; ss.
XX Synthetic.
XX US5908745-A.
XX 01-JUN-1999.
XX 16-JAN-1996; 96US-0587332.
XX 16-JAN-1996; 96US-0587332.
XX (UYCH-) UNIV CHICAGO.
XX Barski VE, Kirillov EV, Lysov YP, Mirzabekov AD;
XX Parinov SV, Yerшов GM;
XX WPI; 1999-347002/29.
XX Detecting disease-associated alleles using continuous/contiguous
XX stacking hybridization as a diagnostic tool
XX Example 1; Column 9; 16pp; English.
XX This invention describes novel methods for sequencing and analysing DNA
XX samples to detect disease-associated alleles, by continuous/contiguous
XX stacking hybridization techniques (utilizing universal bases) with
XX oligonucleotides immobilized on polyacrylamide matrices. The methods may
XX be used to detect multiple DNA base mutations which are specific for

CC certain diseases. The methods of the invention provide accurate and
CC efficient and sensitive methods for diagnosing disease by detecting
CC multiple mutation sequences in patient DNA. The method requires the
CC minimum number of oligonucleotides and few stacking hybridization steps
CC than prior art methods. The methods are also efficient enough to
CC discriminate between perfect and imperfect duplexes. The methods also
CC obviate the need for the fabrication and array placement of large numbers
CC of immobilized oligomers.

XX
SQ Sequence 5 BP; 3 A; 2 C; 0 G; 0 U; 0 other;

Query Match 100.0%; Score 1; DB 20; Length 5;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1

Db 5 g 5

RESULT 33

AAX56964

ID AAX56964 standard; DNA; 5 BP.

XX AC AAX56964;

XX DT 16-JUL-1999 (first entry)

XX DE Ras gene modulating liposomal entrapped oligonucleotide primer 8.

XX KW Ras gene; modulator; liposome; primer; antisense; anticancer; inhibition;
XX cell growth inhibitor; treatment; cancer; ras protein; ss.
XX OS Synthetic.

XX PN WO9922772-A1.

XX PD 14-MAY-1999.

XX PF 28-OCT-1998; 98WO-US22821.

XX PR 31-OCT-1997; 97US-0961469.

XX PA (ISIS-) ISIS PHARM INC.

XX PI Geary RS, Hardee GE, Howard R, Levin A, Mehta RC;

XX PI Templin MV;

XX DR WPI; 1999-313181/26.

XX PT Liposome-encapsulated oligonucleotides useful for treating or
preventing cancers associated with ras gene activation

XX PS Example 1; Page 107; 120pp; English.

XX CC This invention describes novel compositions comprising oligonucleotides
CC (AAX56957-X57017), entrapped within liposomes, that hybridize
CC specifically to a target DNA or mRNA which encodes a mutant or wild-type
CC ras protein. The products of the invention have anticancer activity and
CC specifically bring about the antisense inhibition of ras genes or mRNA.
CC The products of the invention are used to modulate expression of a ras
CC gene in cells, tissue, organs or organisms, particularly to inhibit cell
CC growth and especially to treat or prevent cancers associated with
CC activation of a ras gene. Encapsulating the oligonucleotide reduces the
CC rate at which it is cleared from the blood when compared with
CC non-encapsulated material, and the oligonucleotides become distributed to
CC practically all parts of the body.

XX SQ Sequence 5 BP; 1 A; 2 C; 2 G; 0 U; 0 other;

Query Match

100.0%; Score 1; DB 20; Length 5;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1

Db 2 g 2

RESULT 34

AAX56964/C

ID AAX56964 standard; DNA; 5 BP.

XX AC AAX56964;

XX DT 16-JUL-1999 (first entry)

XX DE Ras gene modulating liposomal entrapped oligonucleotide primer 8.
XX KW Ras gene; modulator; liposome; primer; antisense; anticancer; inhibition;
XX cell growth inhibitor; treatment; cancer; ras protein; ss.

XX OS Synthetic.

XX PN WO9922772-A1.

XX PD 14-MAY-1999.

XX PF 28-OCT-1998; 98WO-US22821.

XX PR 31-OCT-1997; 97US-0961469.

XX PA (ISIS-) ISIS PHARM INC.

XX PI Geary RS, Hardee GE, Howard R, Levin A, Mehta RC;

XX PI Templin MV;

XX DR WPI; 1999-313181/26.

XX PT Liposome-encapsulated oligonucleotides useful for treating or
preventing cancers associated with ras gene activation

XX PS Example 1; Page 107; 120pp; English.

XX CC This invention describes novel compositions comprising oligonucleotides
CC (AAX56957-X57017), entrapped within liposomes, that hybridize
CC specifically to a target DNA or mRNA which encodes a mutant or wild-type
CC ras protein. The products of the invention have anticancer activity and
CC specifically bring about the antisense inhibition of ras genes or mRNA.
CC The products of the invention are used to modulate expression of a ras
CC gene in cells, tissue, organs or organisms, particularly to inhibit cell
CC growth and especially to treat or prevent cancers associated with
CC activation of a ras gene. Encapsulating the oligonucleotide reduces the
CC rate at which it is cleared from the blood when compared with
CC non-encapsulated material, and the oligonucleotides become distributed to
CC practically all parts of the body.

XX SQ Sequence 5 BP; 1 A; 2 C; 2 G; 0 U; 0 other;

Query Match

100.0%; Score 1; DB 20; Length 5;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1

Db 4 g 4

RESULT 35

AAX21608

ID AAX21608 standard; DNA; 5 BP.

XX AC AAX21608;

```
XX DT 14-MAY-1999 (first entry)
XX DE Mutant H-ras specific antisense oligo ISIS #2563.
XX KW Human; N-ras; inhibition; pharmaceutical; modulation; cancer; oncogene;
XX KW diagnostic; therapeutic; tumour; mutant; H-ras; antisense; ss.
XX OS Synthetic.
XX PN WO9902732-A1.
XX PD 21-JAN-1999.
XX PF 06-JUL-1998; 98WO-US13966.
XX PR 08-JUL-1997; 97US-0889296.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Cowsert LM, Manoharan M, Monia BP;
XX WPI: 1999-120932/10.
XX PT New oligonucleotide targetting human N-ras nucleic acid - is
XX PT capable of inhibiting human N-ras expression, useful for preventing
XX PT or treating conditions arising from the activation of a human N-ras
XX PT oncogene
XX PS Disclosure; Page 22; 97pp; English.
XX CC The invention relates to oligonucleotides, which target a nucleic acid
XX CC encoding human N-ras, and are capable of inhibiting human N-ras
XX CC expression. The antisense oligonucleotides form a pharmaceutical
XX CC composition, which is useful for modulating the expression of human
XX CC N-ras, inhibiting the proliferation of cancer cells, and preventing or
XX CC treating conditions arising from the activation of a human N-ras
XX CC oncogene. The oligonucleotides are also useful in diagnostics,
XX CC therapeutics, and as research reagents and kits. The oligonucleotides
XX CC enable the specific modulation of activated human N-ras expression,
XX CC which is associated with tumour formation. Sequences AAX21601-619
XX CC represent antisense oligonucleotides targeted to mutant H-ras.
XX SQ Sequence 5 BP; 1 A; 2 C; 2 G; 0 U; 0 other;

Query Match 100.0%; Score 1; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 2 g 2

RESULT 36
AAX21608/c
ID AAX21608 standard; DNA; 5 BP.
XX AC AAX21608;
XX DT 14-MAY-1999 (first entry)
XX DE Mutant H-ras specific antisense oligo ISIS #2563.
XX KW Human; N-ras; inhibition; pharmaceutical; modulation; cancer; oncogene;
XX KW diagnostic; therapeutic; tumour; mutant; H-ras; antisense; ss.
XX OS Synthetic.
XX PN WO9902732-A1.
XX PD 21-JAN-1999.

Query Match 100.0%; Score 1; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 2 g 2

RESULT 37
AAA56981
ID AAA56981 standard; cDNA; 5 BP.
XX AC AAA56981;
XX DT 14-NOV-2000 (first entry)
XX DE Human colon cancer cell cDNA sequence #109.
XX KW Human; arbitrary primer; cDNA synthesis; contig sequence construction;
XX KW open reading frame; ORF; low stringency; cDNA sequencing; ss.
XX OS Homo sapiens.
XX PN WO200031299-A2.
XX PD 02-JUN-2000.
XX PF 19-NOV-1999; 99WO-US27430.
XX PR 20-NOV-1998; 98US-0196716.
XX PA (LUDW-) LUDWIG INST CANCER RES.
XX PI Simpson AJG, Dias Neto E, Brentani RR;
XX WPI: 2000-400100/34.

Method for determining open reading frames of the genome of an organism
using primers at low stringency conditions, useful in the construction
```

```
XX PF 06-JUL-1998; 98WO-US13966.
XX PR 08-JUL-1997; 97US-0889296.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Cowsert LM, Manoharan M, Monia BP;
XX WPI: 1999-120932/10.
XX PT New oligonucleotide targetting human N-ras nucleic acid - is
XX PT capable of inhibiting human N-ras expression, useful for preventing
XX PT or treating conditions arising from the activation of a human N-ras
XX PT oncogene
XX PS Disclosure; Page 22; 97pp; English.
XX CC The invention relates to oligonucleotides, which target a nucleic acid
XX CC encoding human N-ras, and are capable of inhibiting human N-ras
XX CC expression. The antisense oligonucleotides form a pharmaceutical
XX CC composition, which is useful for modulating the expression of human
XX CC N-ras, inhibiting the proliferation of cancer cells, and preventing or
XX CC treating conditions arising from the activation of a human N-ras
XX CC oncogene. The oligonucleotides are also useful in diagnostics,
XX CC therapeutics, and as research reagents and kits. The oligonucleotides
XX CC enable the specific modulation of activated human N-ras expression,
XX CC which is associated with tumour formation. Sequences AAX21601-619
XX CC represent antisense oligonucleotides targeted to mutant H-ras.
XX SQ Sequence 5 BP; 1 A; 2 C; 2 G; 0 U; 0 other;

Query Match 100.0%; Score 1; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 4 g 4

RESULT 37
AAA56981
ID AAA56981 standard; cDNA; 5 BP.
XX AC AAA56981;
XX DT 14-NOV-2000 (first entry)
XX DE Human colon cancer cell cDNA sequence #109.
XX KW Human; arbitrary primer; cDNA synthesis; contig sequence construction;
XX KW open reading frame; ORF; low stringency; cDNA sequencing; ss.
XX OS Homo sapiens.
XX PN WO200031299-A2.
XX PD 02-JUN-2000.
XX PF 19-NOV-1999; 99WO-US27430.
XX PR 20-NOV-1998; 98US-0196716.
XX PA (LUDW-) LUDWIG INST CANCER RES.
XX PI Simpson AJG, Dias Neto E, Brentani RR;
XX WPI: 2000-400100/34.

Method for determining open reading frames of the genome of an organism
using primers at low stringency conditions, useful in the construction
```

PT of contigs or constructs of sequenced nucleic acid molecules -
 PS Example 6; Page 47; 113pp; English.

XX The present sequence is a cDNA sequence obtained using a method for
 CC determining open reading frames (ORFs) of the genome of an
 CC organism. An aliquot of mRNA from human colon cancer cells was mixed
 CC with a single, arbitrary primer, Moloney murine leukaemia virus reverse
 CC transcriptase, reverse transcriptase buffer and dNTPs. The mixture was
 CC incubated under low stringency conditions to yield single stranded
 CC cDNA. The same primer was then used to amplify the cDNA by PCR. Rather
 CC than providing nucleotide sequence information from the non-coding
 CC termini of nucleic acid molecules, the method provides information on
 CC the more interesting and relevant internal portions, such as ORFs. The
 CC method also permits the construction of contigs of sequenced nucleic
 CC acid molecules.

XX Sequence 5 BP; 0 A; 3 C; 1 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 21; Length 5;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
 Db 3 g 3

RESULT 38

AAA56981/c
 ID AAA56981 standard; cDNA; 5 BP.

XX
 AC AAA56981;

XX 14-NOV-2000 (first entry)

XX Human colon cancer cell cDNA sequence #109.

XX Human; arbitrary primer; cDNA synthesis; contig sequence construction;
 KW open reading frame; ORF; low stringency; cDNA sequencing; ss.

OS Homo sapiens.

XX WO200031299-A2.

XX 02-JUN-2000.

XX 19-NOV-1999; 99WO-US27430.

XX 20-NOV-1998; 98US-0196716.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Simpson AJG, Dias Neto E, Brentani RR;

XX WPI; 2000-400100/34.

XX Method for determining open reading frames of the genome of an organism
 PT using primers at low stringency conditions, useful in the construction
 PT of contigs or constructs of sequenced nucleic acid molecules -

PS Example 6; Page 47; 113pp; English.

XX The present sequence is a cDNA sequence obtained using a method for
 CC determining open reading frames (ORFs) of the genome of an
 CC organism. An aliquot of mRNA from human colon cancer cells was mixed
 CC with a single, arbitrary primer, Moloney murine leukaemia virus reverse
 CC transcriptase, reverse transcriptase buffer and dNTPs. The mixture was
 CC incubated under low stringency conditions to yield single stranded
 CC cDNA. The same primer was then used to amplify the cDNA by PCR. Rather
 CC than providing nucleotide sequence information from the non-coding
 CC termini of nucleic acid molecules, the method provides information on

CC the more interesting and relevant internal portions, such as ORFs. The
 CC method also permits the construction of contigs of sequenced nucleic
 CC acid molecules.

XX Sequence 5 BP; 0 A; 3 C; 1 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 21; Length 5;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
 Db 5 g 5

RESULT 39

AAZ93601

ID AAZ93601 standard; DNA; 5 BP.

XX
 AC AAZ93601;

XX 24-JUL-2000 (first entry)

XX Transcription factor binding site of tobacco gene promoter sequence.

XX Regulatory sequence; meristem; genetic engineering;
 KW gene expression; crop protection; transgenic plant; resistance;
 KW tobacco; transcription factor; alcohol dehydrogenase-1; Adh1; ss.

XX Synthetic.

OS Nicotiana glauca.

XX WO200012713-A1.

XX 09-MAR-2000.

XX 26-AUG-1999; 99WO-AU000692.

XX 26-AUG-1998; 98AU-0005498.

XX (UYQU) UNIV QUEENSLAND.

XX Mudge SR, Birch RG;

XX WPI; 2000-237875/20.

XX Meristem-expressible nucleic acid sequences, useful for producing
 PT transgenic plants with improved characteristics such as resistance to
 PT pathogens

XX Example 9; Page 51; 102pp; English.

XX Isolated regulatory sequences of plants that are operable in
 CC dividing cells, in particular the meristem cells of plants are useful
 CC in the genetic engineering of plants. The regulatory sequences can
 CC be used to control the expression of foreign genes placed under their
 CC control. Such methods are useful for producing transgenic plants with
 CC altered shape and/or size. The sequences are also useful for
 CC producing transgenic plants capable of rapid regeneration following
 CC harvest or plants having improved resistance to pathogens. This
 CC sequence has been shown to bind a factor involved in the activation
 CC of the maize alcohol dehydrogenase-1 gene (adh1). It occurs three
 CC times in the meristem regulatory sequence of Tobacco described in
 CC GENESEQ record AAZ93567.

XX Sequence 5 BP; 1 A; 3 C; 1 G; 0 U; 0 other;

Query Match 100.0%; Score 1; DB 21; Length 5;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
 |
 Db 5 g 5

RESULT 40
 AA293601/c
 ID AA293601 standard; DNA; 5 BP.
 XX
 AC AA293601;
 XX
 DT 24-JUL-2000 (first entry)
 XX
 DE Transcription factor binding site of tobacco gene promoter sequence.
 XX
 KW Regulatory sequence; meristem; genetic engineering;
 KW gene expression; crop protection; transgenic plant; resistance;
 KW tobacco; transcription factor; alcohol dehydrogenase-1; Adhl; ss.
 XX
 OS Synthetic.
 OS Nicotiana acuminata.
 XX
 PN WO200012713-A1.
 XX
 PD 09-MAR-2000.
 XX
 PF 26-AUG-1999; 99WO-AU00692.
 XX
 PR 26-AUG-1998; 98AU-0005498.
 XX
 PA (UYQU) UNIV QUEENSLAND.
 XX
 PI Mudge SR, Birch RG;
 XX
 DR WPI; 2000-237875/20.
 XX
 PT Meristem-expressible nucleic acid sequences, useful for producing
 PT transgenic plants with improved characteristics such as resistance to
 PT pathogens
 XX
 PS Example 9; Page 51; 102pp; English.
 XX
 CC Isolated regulatory sequences of plants that are operable in
 CC dividing cells, in particular the meristem cells of plants are useful
 CC in the genetic engineering of plants. The regulatory sequences can
 CC be used to control the expression of foreign genes placed under their
 CC control. Such methods are useful for producing transgenic plants with
 CC altered shape and/or size. The sequences are also useful for
 CC producing transgenic plants capable of rapid regeneration following
 CC harvest or plants having improved resistance to pathogens. This
 CC sequence has been shown to bind a factor involved in the activation
 CC of the maize alcohol dehydrogenase-1 gene (adhl). It occurs three
 CC times in the meristem regulatory sequence of Tobacco described in
 CC GENESEQ record AA293567.
 XX
 SQ Sequence 5 BP; 1 A; 3 C; 1 G; 0 U; 0 other;

Query Match 100.0%; Score 1; DB 21; Length 5;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
 |
 Db 4 G 4

RESULT 41
 AA293602/c
 ID AA293602 standard; DNA; 5 BP.
 XX
 AC AA293602;
 XX

DT 24-JUL-2000 (first entry)
 XX
 DE Transcription factor binding site of tobacco gene promoter sequence.
 XX
 KW Regulatory sequence; meristem; genetic engineering;
 KW gene expression; crop protection; transgenic plant; resistance;
 KW tobacco; transcription factor; NIT2; nitrate; ss.
 XX
 OS Synthetic.
 OS Nicotiana acuminata.
 XX
 PN WO200012713-A1.
 XX
 PD 09-MAR-2000.
 XX
 PF 26-AUG-1999; 99WO-AU00692.
 XX
 PR 26-AUG-1998; 98AU-0005498.
 XX
 PA (UYQU) UNIV QUEENSLAND.
 XX
 PI Mudge SR, Birch RG;
 XX
 DR WPI; 2000-237875/20.
 XX
 PT Meristem-expressible nucleic acid sequences, useful for producing
 PT transgenic plants with improved characteristics such as resistance to
 PT pathogens
 XX
 PS Example 9; Page 51; 102pp; English.
 XX
 CC Isolated regulatory sequences of plants that are operable in
 CC dividing cells, in particular the meristem cells of plants are useful
 CC in the genetic engineering of plants. The regulatory sequences can
 CC be used to control the expression of foreign genes placed under their
 CC control. Such methods are useful for producing transgenic plants with
 CC altered shape and/or size. The sequences are also useful for
 CC producing transgenic plants capable of rapid regeneration following
 CC harvest or plants having improved resistance to pathogens. This
 CC sequence has been shown to regulate nitrate metabolism in the
 CC fungus Neurospora crassa. It occurs multiple times in the meristem
 CC regulatory sequence of Tobacco described in GENESEQ record AA293567.
 XX
 SQ Sequence 5 BP; 1 A; 1 C; 0 G; 3 T; 0 other;

Query Match 100.0%; Score 1; DB 21; Length 5;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
 |
 Db 4 G 4

RESULT 42
 AA289330/c
 ID AA289330 standard; DNA; 5 BP.
 XX
 AC AA289330;
 XX
 DT 13-JUN-2000 (first entry)
 XX
 DE Human UCP3 promoter fragment #10.
 XX
 KW UCP3; uncoupling protein 3; human; promoter; fat cell; transcription;
 KW fat metabolism; ss.
 XX
 OS Homo sapiens.
 XX
 PN DE19838837-A1.
 XX
 PD 02-MAR-2000.

XX 27-AUG-1998; 98DE-1038837.
 XX 27-AUG-1998; 98DE-1038837.
 XX (BOEH) BOEHRINGER INGELHEIM INT GMBH.
 PA (NOVO) NOVO-NORDISK AS.
 P. Esterbauer H, Oberkofler H, Patsch W;
 PI WPI; 2000-272214/24.
 XX Recombinant fat and muscle tissue specific uncoupling protein 3
 XX promoters useful for identifying UCP3 modulators -
 PS Claim 25; Page 12; 38pp; German.
 XX This invention describes novel recombinant DNA molecules containing
 CC an uncoupling protein 3 (UCP-3) promoter DNA sequence active in fat
 CC cells but not functional in muscle cells or vice versa. The recombinant
 CC DNA molecules are useful for transcription of genes and, with host cells,
 CC to test for substances that can influence transcription. They can also be
 CC used to identify modulators of UCP3 promoters. UCP3 plays a role in fat
 CC metabolism and control of the promoter is useful in combating diseases
 CC with inappropriate fat tissue metabolism. This sequence represents a
 CC fragment of the human UCP-3 promoter which is used to illustrate the
 CC method of the invention.
 XX Sequence 5 BP; 2 A; 2 C; 0 G; 1 T; 0 other;
 SQ

Query Match 100.0%; Score 1; DB 21; Length 5;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 g 1
 Db 2 G 2

RESULT 43
 AAZ89331
 ID AAZ89331 standard; DNA; 5 BP.
 XX
 AC AAZ89331;
 XX 13-JUN-2000 (first entry)
 DT Human UCP3 promoter fragment #11.
 DE
 XX UCP3; uncoupling protein 3; human; promoter; fat cell; transcription;
 KW fat metabolism; ss.
 XX Homo sapiens.
 OS
 XX DE19838837-A1.
 PN
 XX 02-MAR-2000.
 PD
 XX 27-AUG-1998; 98DE-1038837.
 PF
 XX 27-AUG-1998; 98DE-1038837.
 PR (BOEH) BOEHRINGER INGELHEIM INT GMBH.
 XX (NOVO) NOVO-NORDISK AS.
 PA Esterbauer H, Oberkofler H, Patsch W;
 PI WPI; 2000-272214/24.
 XX Recombinant fat and muscle tissue specific uncoupling protein 3
 XX promoters useful for identifying UCP3 modulators -

PS Claim 28; Page 12; 38pp; German.
 XX This invention describes novel recombinant DNA molecules containing
 CC an uncoupling protein 3 (UCP-3) promoter DNA sequence active in fat
 CC cells but not functional in muscle cells or vice versa. The recombinant
 CC DNA molecules are useful for transcription of genes and, with host cells,
 CC to test for substances that can influence transcription. They can also be
 CC used to identify modulators of UCP3 promoters. UCP3 plays a role in fat
 CC metabolism and control of the promoter is useful in combating diseases
 CC with inappropriate fat tissue metabolism. This sequence represents a
 CC fragment of the human UCP-3 promoter which is used to illustrate the
 CC method of the invention.
 XX Sequence 5 BP; 1 A; 0 C; 2 G; 2 T; 0 other;
 SQ

Query Match 100.0%; Score 1; DB 21; Length 5;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 g 1
 Db 4 g 4

RESULT 44
 AAZ89332
 ID AAZ89332 standard; DNA; 5 BP.
 XX
 AC AAZ89332;
 XX 13-JUN-2000 (first entry)
 DT Human UCP3 promoter fragment #12.
 DE
 XX UCP3; uncoupling protein 3; human; promoter; fat cell; transcription;
 KW fat metabolism; ss.
 XX Homo sapiens.
 OS
 XX DE19838837-A1.
 PN
 XX 02-MAR-2000.
 PD
 XX 27-AUG-1998; 98DE-1038837.
 PF
 XX 27-AUG-1998; 98DE-1038837.
 PR (BOEH) BOEHRINGER INGELHEIM INT GMBH.
 XX (NOVO) NOVO-NORDISK AS.
 PA Esterbauer H, Oberkofler H, Patsch W;
 PI WPI; 2000-272214/24.
 XX Recombinant fat and muscle tissue specific uncoupling protein 3
 XX promoters useful for identifying UCP3 modulators -
 PS Claim 31; Page 12; 38pp; German.
 XX This invention describes novel recombinant DNA molecules containing
 CC an uncoupling protein 3 (UCP-3) promoter DNA sequence active in fat
 CC cells but not functional in muscle cells or vice versa. The recombinant
 CC DNA molecules are useful for transcription of genes and, with host cells,
 CC to test for substances that can influence transcription. They can also be
 CC used to identify modulators of UCP3 promoters. UCP3 plays a role in fat
 CC metabolism and control of the promoter is useful in combating diseases
 CC with inappropriate fat tissue metabolism. This sequence represents a
 CC fragment of the human UCP-3 promoter which is used to illustrate the
 CC method of the invention.
 XX Sequence 5 BP; 1 A; 0 C; 2 G; 2 T; 0 other;
 SQ

Query Match 100.0%; Score 1; DB 21; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
1
Db 4 g 4

RESULT 45
AAZ48433
ID AAZ48433 standard; DNA; 5 BP.
XX
AC AAZ48433;
XX
DT 27-MAR-2000 (first entry)
XX
DE First DNA arm segment.
XX
KW Microorganism; virus; polymerase chain reaction; food; cosmetic;
KW clinical diagnostic; molecular beacon; PCR primer; ss.
XX

OS Synthetic.

XX WO9963112-A2.

XX 09-DEC-1999.

XX 18-MAY-1999; 99WO-US10940.

XX 18-MAY-1998; 98US-0086025.

PR 17-MAY-1999; 99US-0086025.

XX (HUNT-) HUNT WESSON INC.

XX Romick TL, Fraser MS;

PI WPI; 2000-086985/07.

DR Detection of microorganisms and viruses, for use in the food and
PT cosmetic industries and for clinical diagnostics -
XX

PS Claim 51; Page 40; 63pp; English.

XX The invention provides a novel in vitro method for the detection of
CC microorganisms and viruses. The method comprises: (1) forming a
CC polymerase chain reaction (PCR) mixture by combining a predetermined
CC volume of a sample to be tested for the presence of a nucleic acid
CC sequence comprising 5'-TAGAAGC-3', known amounts of a first primer
CC comprising 5'-GCTAAGTCCCAAGT-3', and a second primer comprising
CC 5'-AGAAGCTCTCTACC-3', and PCR reagents; (2) forming a PCR product by
CC cycling the PCR mixture to amplify the nucleic acid sequence, if present,
CC to replicate and attain 0.25-10000mug nucleotide product/mul mixture; (3)
CC adding a probe containing DNA comprising 5'-GGTGGCTGCTTAAGCCACC-3' to
CC the PCR mixture or to the PCR product to cause the DNA to hybridize with
CC the nucleic acid sequence, if present, and change the conformation of the
CC probe; and (4) determining whether or not bacteria are present in the
CC sample by detecting the conformational change of the probe, a
CC conformational change indicating the presence of bacteria in the sample.
CC The methods can be used for the detection of viruses and microorganisms,
CC including bacteria, yeast, molds and protista. They can be used in the
CC food and cosmetic industry and in clinical diagnostics. Using the method
CC it is not necessary to remove non-hybridized probe from the system.

XX Sequence 5 BP; 1 A; 1 C; 2 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 21; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1

Db 1 g 1

Search completed: July 15, 2002, 23:10:11
Job time: 18429 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model
Run on: July 15, 2002, 23:28:08 ; Search time 9532.94 Seconds
(without alignments)
2.195 Million cell updates/sec

Title: US-09-375-248-1_COPY_2588_2588
Perfect score: 1
Sequence: 1 g 1
Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0
Searched: 1797656 seqs, 10463268293 residues
Word size : 0
Total number of hits satisfying chosen parameters: 3595312
Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

GenEmbl:*

- 1: gb_ba:*
- 2: gb_htg:*
- 3: gb_in:*
- 4: gb_om:*
- 5: gb_ov:*
- 6: gb_pat:*
- 7: gb_ph:*
- 8: gb_pl:*
- 9: gb_pr:*
- 10: gb_ro:*
- 11: gb_sts:*
- 12: gb_sy:*
- 13: gb_un:*
- 14: gb_vi:*
- 15: em_ba:*
- 16: em_fun:*
- 17: em_hum:*
- 18: em_in:*
- 19: em_mu:*
- 20: em_om:*
- 21: em_or:*
- 22: em_ov:*
- 23: em_pat:*
- 24: em_ph:*
- 25: em_pl:*
- 26: em_ro:*
- 27: em_sts:*
- 28: em_un:*
- 29: em_vi:*
- 30: em_htg_hum:*
- 31: em_htg_inv:*
- 32: em_htg_other:*
- 33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
------------	-------	-------------	--------	-------	-------------

C	1	1	100.0	6	AX092441	Sequence
C	2	1	100.0	2	AX092442	Sequence
C	3	1	100.0	2	AX092443	Sequence
C	4	1	100.0	2	AX092444	Sequence
C	5	1	100.0	2	AX092445	Sequence
C	6	1	100.0	2	AX092446	Sequence
C	7	1	100.0	2	AX092447	Sequence
C	8	1	100.0	2	AX092448	Sequence
C	9	1	100.0	2	AX092449	Sequence
C	10	1	100.0	2	AX092450	Sequence
C	11	1	100.0	2	AX092451	Sequence
C	12	1	100.0	2	AX092452	Sequence
C	13	1	100.0	2	AX092453	Sequence
C	14	1	100.0	2	AX092454	Sequence
C	15	1	100.0	2	AX092455	Sequence
C	16	1	100.0	2	AX092456	Sequence
C	17	1	100.0	2	AX092457	Sequence
C	18	1	100.0	2	AX092458	Sequence
C	19	1	100.0	2	AX092459	Sequence
C	20	1	100.0	2	AX092460	Sequence
C	21	1	100.0	2	AX092461	Sequence
C	22	1	100.0	2	AX092462	Sequence
C	23	1	100.0	2	AX092463	Sequence
C	24	1	100.0	2	AX092464	Sequence
C	25	1	100.0	2	AX092465	Sequence
C	26	1	100.0	2	AX092466	Sequence
C	27	1	100.0	2	AX092467	Sequence
C	28	1	100.0	2	AX092468	Sequence
C	29	1	100.0	2	AX092469	Sequence
C	30	1	100.0	2	AX092470	Sequence
C	31	1	100.0	2	AX092471	Sequence
C	32	1	100.0	2	AX092472	Sequence
C	33	1	100.0	2	AX092473	Sequence
C	34	1	100.0	2	AX092474	Sequence
C	35	1	100.0	2	AX092475	Sequence
C	36	1	100.0	2	AX092476	Sequence
C	37	1	100.0	2	AX092477	Sequence
C	38	1	100.0	2	AX092478	Sequence
C	39	1	100.0	2	AX092479	Sequence
C	40	1	100.0	2	AX092480	Sequence
C	41	1	100.0	2	AX092481	Sequence
C	42	1	100.0	2	AX092482	Sequence
C	43	1	100.0	2	AX092483	Sequence
C	44	1	100.0	2	AX092484	Sequence
C	45	1	100.0	2	AX092485	Sequence

ALIGNMENTS

RESULT	1	AX092441/c	AX092441	Sequence 2 from Patent WO0116366.	2 bp	DNA	linear	PAT 21-MAR-2001
LOCUS			AX092441					
DEFINITION			AX092441					
ACCESSION			AX092441					
VERSION			AX092441.1	GI:13444536				
KEYWORDS								
SOURCE			unidentified.					
ORGANISM			unidentified.					
REFERENCE			1 (bases 1 to 2)					
AUTHORS			Kless, H.					
TITLE			Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks					
JOURNAL			Patent: WO 0116366-A 2 08-MAR-2001;					
			YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar					
FEATURES			(IL)					
source			Location/Qualifiers					
			1..2					
			/organism="unidentified"					
			/db_xref="taxon:32644"					
			/note="synthetic oligonucleotide;"					
BASE COUNT			1 a	1 c	0 g	0 t		

ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
 Db 2 G 2

RESULT 2

AX092442 LOCUS AX092442 2 bp DNA linear PAT 21-MAR-2001
 DEFINITION Sequence 3 from Patent WO0116366.
 ACCESSION AX092442
 VERSION AX092442.1 GI:13444537
 KEYWORDS .
 SOURCE unidentified.
 ORGANISM unidentified.
 REFERENCE 1 (bases 1 to 2)
 AUTHORS Kless, H.
 TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks
 JOURNAL Patent: WO 0116366-A 3 08-MAR-2001;
 YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

FEATURES
 source Location/Qualifiers
 1..2
 /organism="unidentified"
 /db_xref="taxon:32644"
 /note="synthetic oligonucleotide;"
 1 a 0 c 1 g 0 t

BASE COUNT
 ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
 Db 2 G 2

RESULT 3

AX092444/c LOCUS AX092444 2 bp DNA linear PAT 23-MAR-2001
 DEFINITION Sequence 5 from Patent WO0116366.
 ACCESSION AX092444
 VERSION AX092444.1 GI:13444539
 KEYWORDS .
 SOURCE unidentified.
 ORGANISM unidentified.
 REFERENCE 1 (bases 1 to 2)
 AUTHORS Kless, H.
 TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks
 JOURNAL Patent: WO 0116366-A 5 08-MAR-2001;
 YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

FEATURES
 source Location/Qualifiers
 1..2
 /organism="unidentified"
 /db_xref="taxon:32644"
 /note="synthetic oligonucleotide;"
 1 a 1 c 0 g 0 t

BASE COUNT
 ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
 Db 1 G 1

RESULT 4

AX092445/c LOCUS AX092445 2 bp DNA linear PAT 21-MAR-2001
 DEFINITION Sequence 6 from Patent WO0116366.
 ACCESSION AX092445
 VERSION AX092445.1 GI:13444540
 KEYWORDS .
 SOURCE unidentified.
 ORGANISM unidentified.
 REFERENCE 1 (bases 1 to 2)
 AUTHORS Kless, H.
 TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks
 JOURNAL Patent: WO 0116366-A 6 08-MAR-2001;
 YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

FEATURES
 source Location/Qualifiers
 1..2
 /organism="unidentified"
 /db_xref="taxon:32644"
 /note="synthetic oligonucleotide;"
 0 a 2 c 0 g 0 t

BASE COUNT
 ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
 Db 2 G 2

RESULT 5

AX092446 LOCUS AX092446 2 bp DNA linear PAT 21-MAR-2001
 DEFINITION Sequence 7 from Patent WO0116366.
 ACCESSION AX092446
 VERSION AX092446.1 GI:13444541
 KEYWORDS .
 SOURCE unidentified.
 ORGANISM unidentified.
 REFERENCE 1 (bases 1 to 2)
 AUTHORS Kless, H.
 TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks
 JOURNAL Patent: WO 0116366-A 7 08-MAR-2001;
 YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

FEATURES
 source Location/Qualifiers
 1..2
 /organism="unidentified"
 /db_xref="taxon:32644"
 /note="synthetic oligonucleotide;"
 0 a 1 c 1 g 0 t

BASE COUNT
 ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy 1 g 1
Db 2 G 2

RESULT 6
AX092446/c
LOCUS AX092446 2 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 7 from Patent WO0116366.
ACCESSION AX092446
VERSION AX092446.1 GI:13444541
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Kless,H.
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 7 08-MAR-2001; YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)
FEATURES
source Location/Qualifiers
1..2
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"
BASE COUNT 0 a 1 c 1 g 0 t
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 1 G 1

RESULT 7
AX092447/c
LOCUS AX092447 2 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 8 from Patent WO0116366.
ACCESSION AX092447
VERSION AX092447.1 GI:13444542
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Kless,H.
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 8 08-MAR-2001; YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)
FEATURES
source Location/Qualifiers
1..2
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"
BASE COUNT 0 a 1 c 0 g 1 t
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 1 G 1

RESULT 8
AX092448
LOCUS AX092448 2 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 9 from Patent WO0116366.
ACCESSION AX092448
VERSION AX092448.1 GI:13444543
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Kless,H.
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 9 08-MAR-2001; YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)
FEATURES
source Location/Qualifiers
1..2
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"
BASE COUNT 1 a 0 c 1 g 0 t
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 1 G 1

RESULT 9
AX092449
LOCUS AX092449 2 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 10 from Patent WO0116366.
ACCESSION AX092449
VERSION AX092449.1 GI:13444544
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Kless,H.
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 10 08-MAR-2001; YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)
FEATURES
source Location/Qualifiers
1..2
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"
BASE COUNT 0 a 1 c 1 g 0 t
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 1 G 1

```

RESULT 10
AX092449/c
LOCUS AX092449 2 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 10 from Patent WO0116366.
ACCESSION AX092449
VERSION AX092449.1 GI:13444544
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 2)
AUTHORS Kless, H.
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 10 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)
FEATURES
source Location/Qualifiers
1..2
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"
BASE COUNT 0 a 1 c 1 g 0 t
ORIGIN
Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 g 1
Db 2 G 2
RESULT 11
AX092450
LOCUS AX092450 2 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 11 from Patent WO0116366.
ACCESSION AX092450
VERSION AX092450.1 GI:13444545
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 2)
AUTHORS Kless, H.
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 11 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)
FEATURES
source Location/Qualifiers
1..2
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"
BASE COUNT 0 a 0 c 2 g 0 t
ORIGIN
Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 g 1
Db 1 G 1
RESULT 12
AX092451
LOCUS AX092451 2 bp DNA linear PAT 21-MAR-2001

DEFINITION Sequence 12 from Patent WO0116366.
ACCESSION AX092451
VERSION AX092451.1 GI:13444546
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 2)
AUTHORS Kless, H.
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 12 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)
FEATURES
source Location/Qualifiers
1..2
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"
BASE COUNT 0 a 0 c 1 g 1 t
ORIGIN
Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 g 1
Db 1 G 1
RESULT 13
AX092453/c
LOCUS AX092453 2 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 14 from Patent WO0116366.
ACCESSION AX092453
VERSION AX092453.1 GI:13444548
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 2)
AUTHORS Kless, H.
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 14 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)
FEATURES
source Location/Qualifiers
1..2
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"
BASE COUNT 0 a 1 c 0 g 1 t
ORIGIN
Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 g 1
Db 2 G 2
RESULT 14
AX092454
LOCUS AX092454 2 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 15 from Patent WO0116366.
ACCESSION AX092454
VERSION AX092454.1 GI:13444549

KEYWORDS
SOURCE
ORGANISM
unidentified.
unidentified
unclassified.
REFERENCE
1 (bases 1 to 2)
AUTHORS
Kless,H.
TITLE
Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks
JOURNAL
Patent: WO 0116366-A 15 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)
FEATURES
Source Location/Qualifiers
1..2
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"
BASE COUNT
0 a 0 c 1 g 1 t
ORIGIN
1 t
Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 g 1
Db 2 G 2
RESULT 15
AX092528/c
LOCUS
AX092528
DEFINITION
Sequence 89 from Patent WO0116366.
ACCESSION
AX092528
VERSION
AX092528.1 GI:13444623
KEYWORDS
unidentified.
ORGANISM
unidentified.
REFERENCE
1 (bases 1 to 2)
AUTHORS
Kless,H.
TITLE
Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks
JOURNAL
Patent: WO 0116366-A 89 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)
FEATURES
Source Location/Qualifiers
1..2
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"
BASE COUNT
1 a 1 c 0 g 0 t
ORIGIN
1 a 1 c 0 g 0 t
Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 g 1
Db 1 G 1
RESULT 16
AX092529/c
LOCUS
AX092529
DEFINITION
Sequence 90 from Patent WO0116366.
ACCESSION
AX092529
VERSION
AX092529.1 GI:13444624
KEYWORDS
unidentified.
ORGANISM
unidentified.

unclassified.
REFERENCE
1 (bases 1 to 2)
AUTHORS
Kless,H.
TITLE
Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks
JOURNAL
Patent: WO 0116366-A 90 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)
FEATURES
Source Location/Qualifiers
1..2
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"
BASE COUNT
0 a 2 c 0 g 0 t
ORIGIN
2 c 0 g 0 t
Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 g 1
Db 2 G 2
RESULT 17
AX092530
LOCUS
AX092530
DEFINITION
Sequence 91 from Patent WO0116366.
ACCESSION
AX092530
VERSION
AX092530.1 GI:13444625
KEYWORDS
unidentified.
ORGANISM
unidentified.
REFERENCE
1 (bases 1 to 2)
AUTHORS
Kless,H.
TITLE
Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks
JOURNAL
Patent: WO 0116366-A 91 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)
FEATURES
Source Location/Qualifiers
1..2
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"
BASE COUNT
1 a 0 c 1 g 0 t
ORIGIN
1 a 0 c 1 g 0 t
Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 g 1
Db 2 G 2
RESULT 18
AX092538
LOCUS
AX092538
DEFINITION
Sequence 99 from Patent WO0116366.
ACCESSION
AX092538
VERSION
AX092538.1 GI:13444633
KEYWORDS
unidentified.
ORGANISM
unidentified.
REFERENCE
1 (bases 1 to 2)
AUTHORS
Kless,H.

TITLE Template-dependent nucleic acid polymerization using
oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 99 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL); Kless, Hadar
(IL)

FEATURES Location/Qualifiers
SOURCE 1..2
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"

BASE COUNT 0 a 0 c 1 g 1 t
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
|
Db 1 G 1

RESULT 19

AX175286
LOCUS AX175286 2 bp DNA linear PAT 03-JUL-2001
DEFINITION Sequence 50 from Patent WO0144465.
ACCESSION AX175286
VERSION AX175286.1 GI:14598654

KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 2)
AUTHORS Phillips, N.C. and Fillion, M.C.
TITLE Therapeutically useful synthetic oligonucleotides

JOURNAL Patent: WO 0144465-A 50 21-JUN-2001;
Bioniche Life Sciences Inc. (CA)
FEATURES Location/Qualifiers
SOURCE 1..2
/organism="synthetic construct"
/db_xref="taxon:32630"

BASE COUNT 0 a 0 c 1 g 1 t
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
|
Db 1 G 1

RESULT 20

AX175287
LOCUS AX175287 2 bp DNA linear PAT 03-JUL-2001
DEFINITION Sequence 51 from Patent WO0144465.
ACCESSION AX175287
VERSION AX175287.1 GI:14598655

KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 2)
AUTHORS Phillips, N.C. and Fillion, M.C.

TITLE Therapeutically useful synthetic oligonucleotides
JOURNAL Patent: WO 0144465-A 51 21-JUN-2001;
Bioniche Life Sciences Inc. (CA)
FEATURES Location/Qualifiers
SOURCE 1..2
/organism="synthetic construct"

BASE COUNT 0 a 0 c 1 g 1 t
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
|
Db 2 G 2

RESULT 21
BD009609/c

LOCUS BD009609 2 bp DNA linear PAT 31-JAN-2002
DEFINITION Probes, methods and kits for detection and typing of *Helicobacter pylori*, nucleic acids in biological samples.

ACCESSION BD009609
VERSION BD009609.1 GI:18637982
KEYWORDS JP 2001502536-A/201.
SOURCE unidentified.
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 2)
AUTHORS Quint, W. and Doorn, L.J.V.

TITLE Probes, methods and kits for detection and typing of *Helicobacter pylori*, nucleic acids in biological samples
JOURNAL Patent: JP 2001502536-A 201 27-FEB-2001;
COMMENT INNOGENETICS NV, DDL BV
OS Unidentified
PN JP 2001502536-A/201
PD 27-FEB-2001

PF 10-OCT-1997 JP 1998518004
PR 16-OCT-1996 EP 96870131.8
PI WILHELMUS QUINT, LEENDERT JAN VAN DOORN
PC C12Q1/68, C07K14/205, C12N15/11
CC

KEY Location/Qualifiers
FH source 1..2
FT /organism="unidentified"
FEATURES Location/Qualifiers
SOURCE 1..2
/organism="unidentified"
/db_xref="taxon:32644"

BASE COUNT 0 a 1 c 0 g 0 t 1 others
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
|
Db 2 G 2

RESULT 22

CNS01C99
LOCUS CNS01C99 2 bp mRNA linear PLN 02-SEP-1999
DEFINITION Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation.

ACCESSION AL115237
VERSION AL115237.1 GI:5829856
KEYWORDS cDNA library; nitrogen deprivation.
SOURCE Botryotinia fuckeliana.

ORGANISM Botryotinia fuckeliana
REFERENCE 1 (bases 1 to 2)
AUTHORS Bitton, F., Levis, C., Fortini, D., Pradier, J.M. and Brygoo, Y.

TITLE Direct Submission
JOURNAL Submitted (01-SEP-1999) Phytopathologie, INRA, route de St Cyr,
78026 Versailles, France
REFERENCE 2 (bases 1 to 2)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (01-SEP-1999) Genoscope - Centre National de Sequencage :
CP 5706 91057 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- web : www.genoscope.cns.fr)

COMMENT The cdna library to be analyzed within the framework of this
project was created using a Botrytis cinerea strain which was grown
under conditions of nitrogen deprivation, which is the normal
situation for B. cinerea during its development on its host plant.
The library was produced in an oriented direction, in the pBSII
vector.

FEATURES

source

1. .2 Location/Qualifiers
/organism="Botryotinia fuckelliana"
/strain="T4"
/db_xref="taxon:40559"
/note="Genoscope sequence ID : W04F091"

BASE COUNT 0 a 0 c 1 g 1 t

ORIGIN

Query Match 100.0%; Score 1; DB 8; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1

|

Db 1 G 1

RESULT 23

AC079635

LOCUS AC079635 3 bp DNA linear HTG 14-AUG-2001
DEFINITION Mus musculus clone RP23-152L20, LOW-PASS SEQUENCE SAMPLING.

AC079635

AC079635

AC079635.3 GI:14647267

VERSION HTG: HTGS-PHASE0.

KEYWORDS house mouse.

SOURCE Mus musculus

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

1 (bases 1 to 3)
McCombie,W.R., Baker,J.P., Bahret,A., Yang,C., Ballia,V.,
Dedhia,N.N., de la Bastide,M., Kuit,K., King,L., Kirchoff,K.A.,
Miller,B., Nascimento,L.U., O'Shaughnessy,A.L., Preston,R.R.,
Rodriguez,S., Santos,L., Shah,R.S., Spiegel,L.A., Palmer,L.,
Vil,M.D. and Zukavern,T.
Mouse Genomic Sequence

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Submitted (06-SEP-2000) Lita Annenberg Hazen Genome Sequencing
Center, Cold Spring Harbor Laboratory, 1 Bungtown Road, Cold Spring
Harbor, NY 11724, USA

On Jul 10, 2001 this sequence version replaced gi:14595773.

* NOTE: This record contains 1 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

1 3: contig of 3 bp in length.

This entry has been temporarily removed. An update for RP23-152L20

will be submitted as soon as it becomes available.

FEATURES

source

Location/Qualifiers

1. .3

/organism="Mus musculus"

/db_xref="taxon:10090"

/clone="RP23-152L20"

1 a 0 c 1 g 1 t

BASE COUNT

ORIGIN

Query Match 100.0%; Score 1; DB 2; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1

|

Db 1 G 1

RESULT 24

CHKNCAMC5

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SEGMENT

SOURCE

ORGANISM

CHKNCAMC5

Chicken cardiac neural cell adhesion (NCAM) gene, exon 12D.

M23994 J04140

M23994.1 GI:212442

5 of 6

chicken.

Gallus gallus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

Phasianinae; Gallus.

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

FEATURES

source

Location/Qualifiers

1. .3

/organism="Gallus gallus"

/db_xref="taxon:9031"

/clone="pEC101B"

/tissue_type="cardiac muscle"

/dev_stage="day 10 embryo"

1. .3

/gene="NACM"

/number=12

2 a 0 c 1 g 0 t

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

Matches

Qy 1 g 1

|

Db 3 G 3

RESULT 25

A97991

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

A97991

Sequence 21 from Patent WO9914366.

A97991

A97991.1 GI:6781229

unidentified.

unidentified.

```

REFERENCE 1 (bases 1 to 3)
AUTHORS   Pongers-Willemsse,M.J. and Van,D.J.
TITLE     DETECTION OF MINIMAL RESIDUAL DISEASE IN LYMPHOID MALIGNANCIES
JOURNAL   Patent: WO 9914366-A 21 25-MAR-1999;
          DONGEN JACOBUS JOHANNES MARIA (NL); UNIV ERASMUS (NL)
FEATURES  Location/Qualifiers
          source
            1..3
              /organism="unidentified"
              /db_xref="taxon:32644"
BASE COUNT 0 a 1 c 2 g 0 t
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 2 g 2

RESULT 26
LOCUS      A97991 3 bp DNA linear PAT 26-JAN-2000
DEFINITION Sequence 21 from Patent WO9914366.
ACCESSION  A97991
VERSION     A97991.1 GI:6781229
KEYWORDS   .
SOURCE     .
ORGANISM   unidentified.
           unclassified.
REFERENCE  1 (bases 1 to 3)
AUTHORS   Pongers-Willemsse,M.J. and Van,D.J.
TITLE     DETECTION OF MINIMAL RESIDUAL DISEASE IN LYMPHOID MALIGNANCIES
JOURNAL   Patent: WO 9914366-A 21 25-MAR-1999;
          DONGEN JACOBUS JOHANNES MARIA (NL); UNIV ERASMUS (NL)
FEATURES  Location/Qualifiers
          source
            1..3
              /organism="unidentified"
              /db_xref="taxon:32644"
BASE COUNT 0 a 1 c 2 g 0 t
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 1 g 1

RESULT 27
LOCUS      AX092457/c 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 18 from Patent WO0116366.
ACCESSION  AX092457
VERSION     AX092457.1 GI:13444552
KEYWORDS   .
SOURCE     .
ORGANISM   unidentified.
           unclassified.
REFERENCE  1 (bases 1 to 3)
AUTHORS   Kless,H.
TITLE     Template-dependent nucleic acid polymerization using
          oligonucleotide triphosphates building blocks
JOURNAL   Patent: WO 0116366-A 18 08-MAR-2001;
          YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
          (IL)
FEATURES  Location/Qualifiers
          source
            1..3
              /organism="unidentified"
              /db_xref="taxon:32644"

```

```

source
  1..3
    /organism="unidentified"
    /db_xref="taxon:32644"
    /note="synthetic oligonucleotide:"
BASE COUNT 2 a 1 c 0 g 0 t
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 3 g 3

RESULT 28
LOCUS      AX092458 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 19 from Patent WO0116366.
ACCESSION  AX092458
VERSION     AX092458.1 GI:13444553
KEYWORDS   .
SOURCE     .
ORGANISM   unidentified.
           unclassified.
REFERENCE  1 (bases 1 to 3)
AUTHORS   Kless,H.
TITLE     Template-dependent nucleic acid polymerization using
          oligonucleotide triphosphates building blocks
JOURNAL   Patent: WO 0116366-A 19 08-MAR-2001;
          YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
          (IL)
FEATURES  Location/Qualifiers
          source
            1..3
              /organism="unidentified"
              /db_xref="taxon:32644"
              /note="synthetic oligonucleotide:"
BASE COUNT 2 a 0 c 1 g 0 t
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 3 g 3

RESULT 29
LOCUS      AX092460/c 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 21 from Patent WO0116366.
ACCESSION  AX092460
VERSION     AX092460.1 GI:13444555
KEYWORDS   .
SOURCE     .
ORGANISM   unidentified.
           unclassified.
REFERENCE  1 (bases 1 to 3)
AUTHORS   Kless,H.
TITLE     Template-dependent nucleic acid polymerization using
          oligonucleotide triphosphates building blocks
JOURNAL   Patent: WO 0116366-A 21 08-MAR-2001;
          YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
          (IL)
FEATURES  Location/Qualifiers
          source
            1..3
              /organism="unidentified"
              /db_xref="taxon:32644"

```

BASE COUNT 2 a 1 c 0 g 0 t
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 2 G 2

RESULT 30
AX092461/c
LOCUS AX092461 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 22 from Patent WO0116366.
ACCESSION AX092461
VERSION AX092461.1 GI:13444556
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 3)
AUTHORS Kless, H.
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 22 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

FEATURES
source Location/Qualifiers
1..3
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"

BASE COUNT 1 a 2 c 0 g 0 t
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 3 G 3

RESULT 31
AX092462
LOCUS AX092462 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 23 from Patent WO0116366.
ACCESSION AX092462
VERSION AX092462.1 GI:13444557
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 3)
AUTHORS Kless, H.
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 23 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

FEATURES
source Location/Qualifiers
1..3
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"

BASE COUNT 1 a 1 c 1 g 0 t
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 3 G 3

RESULT 32
AX092462/c
LOCUS AX092462 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 23 from Patent WO0116366.
ACCESSION AX092462
VERSION AX092462.1 GI:13444557
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 3)
AUTHORS Kless, H.
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 23 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

FEATURES
source Location/Qualifiers
1..3
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"

BASE COUNT 1 a 1 c 1 g 0 t
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 2 G 2

RESULT 33
AX092463/c
LOCUS AX092463 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 24 from Patent WO0116366.
ACCESSION AX092463
VERSION AX092463.1 GI:13444558
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 3)
AUTHORS Kless, H.
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 24 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

FEATURES
source Location/Qualifiers
1..3
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"

BASE COUNT 1 a 1 c 0 g 1 t
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;

```

Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
  |
Db 2 G 2

RESULT 34
AX092464 LOCUS AX092464 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 25 from Patent WO0116366.
ACCESSION AX092464
VERSION AX092464.1 GI:13444559
KEYWORDS .
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 3)
AUTHORS Kless,H.
TITLE Template-dependent nucleic acid polymerization using
JOURNAL oligonucleotide triphosphates building blocks
        Patent: WO 0116366-A 25 08-MAR-2001;
        YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
        (IL)
FEATURES
    source      Location/Qualifiers
                1..3
                /organism="unidentified"
                /db_xref="taxon:32644"
                /note="synthetic oligonucleotide;"
BASE COUNT    2 a 0 c 1 g 0 t

Query Match      100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
  |
Db 2 G 2

RESULT 35
AX092465 LOCUS AX092465 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 26 from Patent WO0116366.
ACCESSION AX092465
VERSION AX092465.1 GI:13444560
KEYWORDS .
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 3)
AUTHORS Kless,H.
TITLE Template-dependent nucleic acid polymerization using
JOURNAL oligonucleotide triphosphates building blocks
        Patent: WO 0116366-A 26 08-MAR-2001;
        YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
        (IL)
FEATURES
    source      Location/Qualifiers
                1..3
                /organism="unidentified"
                /db_xref="taxon:32644"
                /note="synthetic oligonucleotide;"
BASE COUNT    1 a 1 c 1 g 0 t

Query Match      100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
  |
Db 2 G 2

RESULT 36
AX092465/c LOCUS AX092465 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 26 from Patent WO0116366.
ACCESSION AX092465
VERSION AX092465.1 GI:13444560
KEYWORDS .
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 3)
AUTHORS Kless,H.
TITLE Template-dependent nucleic acid polymerization using
JOURNAL oligonucleotide triphosphates building blocks
        Patent: WO 0116366-A 26 08-MAR-2001;
        YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
        (IL)
FEATURES
    source      Location/Qualifiers
                1..3
                /organism="unidentified"
                /db_xref="taxon:32644"
                /note="synthetic oligonucleotide;"
BASE COUNT    1 a 1 c 1 g 0 t

Query Match      100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
  |
Db 3 G 3

RESULT 37
AX092466 LOCUS AX092466 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 27 from Patent WO0116366.
ACCESSION AX092466
VERSION AX092466.1 GI:13444561
KEYWORDS .
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 3)
AUTHORS Kless,H.
TITLE Template-dependent nucleic acid polymerization using
JOURNAL oligonucleotide triphosphates building blocks
        Patent: WO 0116366-A 27 08-MAR-2001;
        YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
        (IL)
FEATURES
    source      Location/Qualifiers
                1..3
                /organism="unidentified"
                /db_xref="taxon:32644"
                /note="synthetic oligonucleotide;"
BASE COUNT    1 a 0 c 2 g 0 t

Query Match      100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
  |
Db 2 G 2

RESULT 38
AX092466 LOCUS AX092466 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 27 from Patent WO0116366.
ACCESSION AX092466
VERSION AX092466.1 GI:13444561
KEYWORDS .
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 3)
AUTHORS Kless,H.
TITLE Template-dependent nucleic acid polymerization using
JOURNAL oligonucleotide triphosphates building blocks
        Patent: WO 0116366-A 27 08-MAR-2001;
        YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
        (IL)
FEATURES
    source      Location/Qualifiers
                1..3
                /organism="unidentified"
                /db_xref="taxon:32644"
                /note="synthetic oligonucleotide;"
BASE COUNT    1 a 0 c 2 g 0 t

Query Match      100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
  |
Db 2 G 2

```

RESULT 38
AX092467
LOCUS AX092467 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 28 from Patent WO0116366.
ACCESSION AX092467
VERSION AX092467.1 GI:13444562
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1. .3
Location/Qualifiers
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"
BASE COUNT 1 a 0 c 1 g 1 t
ORIGIN
Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 g 1
Db 2 G 2

RESULT 39
AX092469/c
LOCUS AX092469 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 30 from Patent WO0116366.
ACCESSION AX092469
VERSION AX092469.1 GI:13444564
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1. .3
Location/Qualifiers
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"
BASE COUNT 1 a 1 c 0 g 1 t
ORIGIN
Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 g 1
Db 3 G 3

RESULT 40
AX092473/c
LOCUS AX092473 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 34 from Patent WO0116366.

AX092470
LOCUS AX092470 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 31 from Patent WO0116366.
ACCESSION AX092470
VERSION AX092470.1 GI:13444565
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1. .3
Location/Qualifiers
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"
BASE COUNT 1 a 0 c 1 g 1 t
ORIGIN
Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 g 1
Db 3 G 3

RESULT 41
AX092472/c
LOCUS AX092472 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 33 from Patent WO0116366.
ACCESSION AX092472
VERSION AX092472.1 GI:13444567
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1. .3
Location/Qualifiers
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"
BASE COUNT 2 a 1 c 0 g 0 t
ORIGIN
Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 g 1
Db 1 G 1

RESULT 42
AX092473/c
LOCUS AX092473 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 34 from Patent WO0116366.

ACCESSION AX092473
VERSION AX092473.1 GI:13444568
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 3)
AUTHORS Kless,H.
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 34 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)
FEATURES
source Location/Qualifiers
1..3
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"
BASE COUNT 1 a 2 c 0 g 0 t
ORIGIN
Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 g 1
Db 3 G 3
RESULT 43
AX092474
LOCUS AX092474 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 35 from Patent WO0116366.
ACCESSION AX092474
VERSION AX092474.1 GI:13444569
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 3)
AUTHORS Kless,H.
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 35 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)
FEATURES
source Location/Qualifiers
1..3
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"
BASE COUNT 1 a 1 c 1 g 0 t
ORIGIN
Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 g 1
Db 3 G 3
RESULT 44
AX092474/c
LOCUS AX092474/c 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 35 from Patent WO0116366.
ACCESSION AX092474
VERSION AX092474.1 GI:13444569
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 3)
AUTHORS Kless,H.
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 35 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)
FEATURES
source Location/Qualifiers
1..3
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"
BASE COUNT 1 a 1 c 1 g 0 t
ORIGIN
Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 g 1
Db 3 G 3

SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 3)
AUTHORS Kless,H.
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 35 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)
FEATURES
source Location/Qualifiers
1..3
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"
BASE COUNT 1 a 1 c 1 g 0 t
ORIGIN
Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 g 1
Db 1 G 1
RESULT 45
AX092475/c
LOCUS AX092475 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 36 from Patent WO0116366.
ACCESSION AX092475
VERSION AX092475.1 GI:13444570
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 3)
AUTHORS Kless,H.
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 36 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)
FEATURES
source Location/Qualifiers
1..3
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"
BASE COUNT 1 a 1 c 0 g 1 t
ORIGIN
Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 g 1
Db 1 G 1
Search completed: July 15, 2002, 23:28:08
Job time: 24541 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 15, 2002, 20:07:24 ; Search time 7067.1 seconds
(without alignments)
578.678 Million cell updates/sec

Title: US-09-375-248-1_COPY_2546_2848
Perfect score: 303
Sequence: 1 gagcgctgcacctgggag.....acttcctgcgcgaagcgg 303

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 13736207 seqs, 6748477542 residues

Word size : 0

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

EST:*

- 1: em_estba:*
- 2: em_esthum:*
- 3: em_estin:*
- 4: em_estnu:*
- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_hic:*
- 9: gb_est1:*
- 10: gb_est2:*
- 11: gb_hic:*
- 12: gb_gss:*
- 13: em_gss_hum:*
- 14: em_gss_inv:*
- 15: em_gss_pln:*
- 16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	184	60.7	284	9	AA367842 EST79262
2	32	10.6	448	10	BM285802
3	24	7.9	233	10	R86582
4	24	7.9	270	10	R86469
5	24	7.9	309	10	R86465
6	24	7.9	314	10	R86522
7	24	7.9	1036	10	B1100914
8	23	7.6	441	10	BG384720
9	23	7.6	512	10	BG384715
10	21	6.9	498	10	BF652351
11	21	6.9	498	10	BF652352
12	21	6.9	531	10	BM482403
13	21	6.9	538	9	AV601195
14	21	6.9	544	9	AV601196
15	20	6.6	293	10	W57847
16	20	6.6	434	10	B1182263
17	20	6.6	558	10	BM261245

18	20	6.6	619	12	BH142039
19	20	6.6	810	10	BG709462
20	20	6.6	856	10	BG746729
21	20	6.6	862	10	BG615859
22	20	6.6	864	10	BI763816
23	20	6.6	885	10	BM048480
24	19	6.3	201	10	BF927018
25	19	6.3	208	10	BF925651
26	19	6.3	1257	10	BI524514
27	18	5.9	244	9	AV321924
28	18	5.9	261	10	BM241884
29	18	5.9	271	10	BM409650
30	18	5.9	319	9	AW009058
31	18	5.9	360	12	AQ216651
32	18	5.9	369	9	AI744037
33	18	5.9	470	10	BE460395
34	18	5.9	478	12	BH392477
35	18	5.9	480	10	BI405811
36	18	5.9	498	10	BG767090
37	18	5.9	498	10	BM417681
38	18	5.9	505	10	BM089435
39	18	5.9	509	12	AQ154758
40	18	5.9	512	10	BE435943
41	18	5.9	517	10	BG280611
42	18	5.9	521	10	BF265245
43	18	5.9	524	10	BM410739
44	18	5.9	525	10	BF513456
45	18	5.9	528	10	BJ187298

ALIGNMENTS

RESULT 1	AA367842	284 bp	mRNA	linear	EST 21-APR-1997
LOCUS	EST79262	Placenta I	Homo sapiens	cDNA similar to tyrosine kinase,	
DEFINITION	receptor FLT4, class III, mRNA sequence.				
ACCESSION	AA367842				
VERSION	AA367842.1	GI:2020386			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				

REFERENCE	1 (bases 1 to 284)
-----------	--------------------

AUTHORS	Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitchugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodok,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palanco,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W., Hu,J.-S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillon,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.
---------	--

TITLE	Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
JOURNAL	Nature 377 (6547 Suppl), 3-174 (1995)
MEDLINE	96026280
COMMENT	Other ESTs: THC85507 Contact: Kerlavage, AR Bioinformatics The Institute for Genomic Research 9712 Medical Center Drive, Rockville, MD 20850 USA Tel: 3018699056

Fax: 3018699423

Email: arkerlav@tigr.org

For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/tdb/hgi/hgi.html>)
Seq primer: M13-21.

FEATURES

Location/Qualifiers

1..284
/organism="Homo sapiens"
/db_xref="ATCC (inhost):172752"
/db_xref="taxon:9606"
/clone_lib="Placenta 1"
/tissue_type="placenta"
/dev_stage="fetus"
/note="Organ: placenta; Vector: pBluescript SK-; Site:1:
EcoRI; Site:2: EcoRI"

BASE COUNT 56 a 91 c 91 g 46 t
ORIGIN

Query Match 60.7%; Score 184; DB 9; Length 284;
Best Local Similarity 99.6%; Pred. No. 1.3e-81;
Matches 234; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 gagcgctgcacctgggagagtgctcgctcgacgccttcggagagtggtgaaacc 60
|||||
Db 6 GAGCGGCTGCACCTGGGAGAGTGTCTCGCTACGGCGCTTCGGGAAGGTGGTGAAGCC 65

Qy 61 Lccgcttcgcgcacccacaaagggcagcagctgtgacacgltggcgtgaaatgcctgaaa 120
|||||
Db 66 TCCCGCTTCGGCATCCACGAGGGCAGCAGCTGTGACACCGTGGCGTGCAAAATCGTGAAA 125

Qy 121 gagggcgccagggcagcagcagccgcgcgtgtgtcgaggctcagagatcctcattcac 180
|||||
Db 126 GAGGGCGCCACGGCCAGCCAGCAGCCGCGCTGTGTCTGGAGCTCAAGATCCTCATTTCC 185

Qy 181 atcggcaaccactcaacgtgtgtcaacctcctcgggcgctgcacacaaagccgacg 235
|||||
Db 186 ATCGGCACACCCTCAACGTGTCAACCTCTCGGGCGCTGCACCAAGCCGACG 240

RESULT 2

LOCUS BM285802 448 bp mRNA linear EST 28-DEC-2001
DEFINITION 524533 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BM285802
VERSION BM285802.1 GI:17994828
KEYWORDS EST.
SOURCE cow.

ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 448)
Smith, T.P.L., Grosse, M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett,
G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G.,
Pertes, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
Keefe, J.W.

TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)

JOURNAL 21180013
MEDLINE
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390

Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR Primers

FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCTCAGTCAGCAGC
Plate: 130 row: O column: 20
Seq primer: ATTAGGTGACACTATAG.
Location/Qualifiers

FEATURES

source 1..448
Location/Qualifiers
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 3BOV"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site:1: XbaI; Site:2: XhoI;
Library made from pooled tissue from marrow, alveolar,
macrophage, ovary, fetal semitendinosus muscle, and fetal
longissimus muscle."

BASE COUNT 104 a 134 c 131 g 78 t 1 others
ORIGIN

Query Match 10.6%; Score 32; DB 10; Length 448;
Best Local Similarity 100.0%; Pred. No. 2e-05;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 100 gtggccgtgaaatgctgaaagagggcgccac 131
|||||
Db 42 GTGCCGTGAAATGCTGAAAGAGGGCGCCAC 73

RESULT 3

LOCUS R86582 233 bp mRNA linear EST 17-AUG-1995
DEFINITION RABEST157T Rabbit Osteoclast, Dennis Sakai Oryctolagus cuniculus
cDNA clone pRABOC157 5' similar to c-fms, mRNA sequence.
ACCESSION R86582
VERSION R86582.1 GI:947236
KEYWORDS EST.
SOURCE rabbit.

ORGANISM Oryctolagus cuniculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
1 (bases 1 to 233)
Sakai, D., Tong, H.-S. and Minkin, C.
Osteoclast Molecular Phenotyping by Random cDNA Sequencing
Bone 17 (2), 111-119 (1995)
96021365
Other_ESTs: RABEST035T, RABEST040T, RABEST075T
Contact: Sakai D
Basic Sciences
University of Southern California
USC School of Dentistry, 925 West 34th Street, DEN-4220, Los
Angeles, CA 90089-0641
Tel: 2137405563
Fax: 2137407560
Email: sakai@molbio.usc.edu

Seq primer: T7 promoter.
Location/Qualifiers
1..233
/organism="Oryctolagus cuniculus"
/strain="New Zealand White"
/db_xref="taxon:9986"
/clone="pRABOC157"
/clone_lib="Rabbit Osteoclast, Dennis Sakai"
/lab_host="E. coli DH12S"
/note="Vector: pSPORT1; Site:1: SalI; Site:2: NotI; Poly(A
) + RNA was purified from a 97% pure population of
osteoclasts prepared from the long bones of 10 day old
rabbits. First strand cDNA was synthesized by priming
with an oligo(dT)-NotI anchor-primer and second strand
cDNA was synthesized by replacement synthesis as described
by Gubler and Hoffman (Gene 25:283, 1983). Following the
addition of SalI adapters and NotI digestion, the cDNA was
cloned between the SalI (50) and NotI (30) sites of the
pSPORT1 (BRL) plasmid vector."

FEATURES

source

BASE COUNT 53 a 61 c 79 g 40 t

Query Match 7.9%; Score 24; DB 10; Length 233;
Best Local Similarity 100.0%; Pred. No. 0.18; Mismatches 0; Indels 0; Gaps 0;
Matches 24; Conservative 0

Qy 33 cggcgcccttcgggaagtggtgga 56
|||||
Db 75 CGGCGCCTTCGGGAAGTGGTGA 98

RESULT 4

R86469 270 bp mRNA linear EST 17-AUG-1995
LOCUS RABEST040T Rabbit Osteoclast, Dennis Sakai Oryctolagus cuniculus
DEFINITION cDNA clone PRABOC040 5' similar to c-fms, mRNA sequence.

ACCESSION R86469
VERSION R86469.1 GI:947151
KEYWORDS EST.
SOURCE rabbit.
ORGANISM Oryctolagus cuniculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

REFERENCE 1 (bases 1 to 270)
AUTHORS Sakai,D., Tong,H.-S. and Minkin,C.
TITLE Osteoclast Molecular Phenotyping by Random cDNA Sequencing
JOURNAL Bone 17 (2), 111-119 (1995)
MEDLINE 96021365

COMMENT Other_ESTs: RABEST035T, RABEST075T, RABEST157T
Contact: Sakai D
Basic Sciences
University of Southern California
USC School of Dentistry, 925 West 34th Street, DEN-4220, Los Angeles, CA 90089-0641
Tel: 2137405563
Fax: 2137407560
Email: sakai@molbio.usc.edu
Seq primer: T7 promoter.
Location/Qualifiers
1. .270
/organism="Oryctolagus cuniculus"
/strain="New Zealand White"
/db_xref="taxon:9986"
/clone_lib="Rabbit Osteoclast, Dennis Sakai"
/lab_host="E. coli DH12S"
/note="vector: pSPORT1; Site_1: Sali; Site_2: NotI; Poly(A)+ RNA was purified from a 97% pure population of osteoclasts prepared from the long bones of 10 day old rabbits. First strand cDNA was synthesized by priming with an oligo(dT)-NotI anchor-primer and second strand cDNA was synthesized by replacement synthesis as described by Gubler and Hoffman (Gene 25:283, 1983). Following the addition of Sali adapters and NotI digestion, the cDNA was cloned between the Sali (50) and NotI (30) sites of the pSPORT1 (BRL) plasmid vector."

BASE COUNT 62 a 73 c 89 g 46 t

Query Match 7.9%; Score 24; DB 10; Length 270;
Best Local Similarity 100.0%; Pred. No. 0.18; Mismatches 0; Indels 0; Gaps 0;
Matches 24; Conservative 0

Qy 33 cggcgcccttcgggaagtggtgga 56
|||||
Db 74 CGGCGCCTTCGGGAAGTGGTGA 97

RESULT 5

R86465 314 bp mRNA linear EST 17-AUG-1995
LOCUS RABEST075T Rabbit Osteoclast, Dennis Sakai Oryctolagus cuniculus
DEFINITION cDNA clone PRABOC075 5' similar to c-fms, mRNA sequence.

ACCESSION R86522
VERSION R86522.1 GI:947328
KEYWORDS EST.
SOURCE rabbit.
ORGANISM Oryctolagus cuniculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

REFERENCE 1 (bases 1 to 314)
AUTHORS Sakai,D., Tong,H.-S. and Minkin,C.
TITLE Osteoclast Molecular Phenotyping by Random cDNA Sequencing
JOURNAL Bone 17 (2), 111-119 (1995)
MEDLINE 96021365

R86465 309 bp mRNA linear EST 17-AUG-1995
LOCUS RABEST035T Rabbit Osteoclast, Dennis Sakai Oryctolagus cuniculus
DEFINITION cDNA clone PRABOC035 5' similar to c-fms, mRNA sequence.

ACCESSION R86465
VERSION R86465.1 GI:947147
KEYWORDS EST.
SOURCE rabbit.
ORGANISM Oryctolagus cuniculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

REFERENCE 1 (bases 1 to 309)
AUTHORS Sakai,D., Tong,H.-S. and Minkin,C.
TITLE Osteoclast Molecular Phenotyping by Random cDNA Sequencing
JOURNAL Bone 17 (2), 111-119 (1995)
MEDLINE 96021365

COMMENT Other_ESTs: RABEST040T, RABEST075T, RABEST157T
Contact: Sakai D
Basic Sciences
University of Southern California
USC School of Dentistry, 925 West 34th Street, DEN-4220, Los Angeles, CA 90089-0641
Tel: 2137405563
Fax: 2137407560
Email: sakai@molbio.usc.edu
Seq primer: T7 promoter.
Location/Qualifiers
1. .309
/organism="Oryctolagus cuniculus"
/strain="New Zealand White"
/db_xref="taxon:9986"
/clone_lib="Rabbit Osteoclast, Dennis Sakai"
/lab_host="E. coli DH12S"
/note="vector: pSPORT1; Site_1: Sali; Site_2: NotI; Poly(A)+ RNA was purified from a 97% pure population of osteoclasts prepared from the long bones of 10 day old rabbits. First strand cDNA was synthesized by priming with an oligo(dT)-NotI anchor-primer and second strand cDNA was synthesized by replacement synthesis as described by Gubler and Hoffman (Gene 25:283, 1983). Following the addition of Sali adapters and NotI digestion, the cDNA was cloned between the Sali (50) and NotI (30) sites of the pSPORT1 (BRL) plasmid vector."

BASE COUNT 68 a 81 c 102 g 58 t

Query Match 7.9%; Score 24; DB 10; Length 309;
Best Local Similarity 100.0%; Pred. No. 0.19; Mismatches 0; Indels 0; Gaps 0;
Matches 24; Conservative 0

Qy 33 cggcgcccttcgggaagtggtgga 56
|||||
Db 74 CGGCGCCTTCGGGAAGTGGTGA 97

RESULT 6

R86522 314 bp mRNA linear EST 17-AUG-1995
LOCUS RABEST075T Rabbit Osteoclast, Dennis Sakai Oryctolagus cuniculus
DEFINITION cDNA clone PRABOC075 5' similar to c-fms, mRNA sequence.

ACCESSION R86522
VERSION R86522.1 GI:947328
KEYWORDS EST.
SOURCE rabbit.
ORGANISM Oryctolagus cuniculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

REFERENCE 1 (bases 1 to 314)
AUTHORS Sakai,D., Tong,H.-S. and Minkin,C.
TITLE Osteoclast Molecular Phenotyping by Random cDNA Sequencing
JOURNAL Bone 17 (2), 111-119 (1995)
MEDLINE 96021365

COMMENT Other_ESTS: RABEST035T, RABEST040T, RABEST157T

Contact: Sakai D
Basic Sciences
University of Southern California
USC School of Dentistry, 925 West 34th Street, DEN-4220, Los
Angeles, CA 90089-0641
Tel: 2137405363
Fax: 2137407560
Email: sakai@molbio.usc.edu
Seq primer: T7 promoter.

FEATURES Location/Qualifiers

Source 1..314

/organism="Oryctolagus cuniculus"
/strain="New Zealand White"
/db_xref="taxon:9986"
/clone="pRABOC075"
/lab_host="E. coli DH12S"
/note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; Poly(A)
)+ RNA was purified from a 97% pure population of
osteoclasts prepared from the long bones of 10 day old
rabbits. First strand cDNA was synthesized by priming
with an oligo(dT)-NotI anchor-primer and second strand
cDNA was synthesized by replacement synthesis as described
by Gubler and Hoffman (Gene 25:283, 1983). Following the
addition of SalI adapters and NotI digestion, the cDNA was
cloned between the SalI (50) and NotI (30) sites of the
pSPORT1 (BRL) plasmid vector."

BASE COUNT 71 a 79 c 103 g 60 t 1 others

ORIGIN

Query Match

Best Local Similarity 7.9%; Score 24; DB 10; Length 314;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 33 cggcgccctcggaaggtgggtgga 56

|||||

Db 59 CGCGCCCTTCGGGAAGGTGGTGA 82

RESULT 7

B1100914

LOCUS B1100914 1036 bp mRNA linear EST 26-JUN-2001

DEFINITION 602886236P1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:5041569

5', mRNA sequence.

ACCESSION B1100914

VERSION B1100914.1 GI:14551807

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 1036)

TITLE NIH-MGC <http://mgc.nci.nih.gov/>.

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgaps-r@mail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM1114 row: g column: 10

High quality sequence stop: 308.

Location/Qualifiers

Source 1..1036

/organism="Mus musculus"

/strain="FVB/N"

/db_xref="taxon:10090"

/clone="IMAGE:5041569"

/lab_host="NCI_CGAP_Kid14"

/note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: NotI;

Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.

Average insert size 1.75 kb. Constructed by Life

Technologies. Note: this is a NCI_CGAP Library. }

BASE COUNT 322 a 247 c 298 g 169 t

ORIGIN

Query Match

Best Local Similarity 7.9%; Score 24; DB 10; Length 1036;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 42 cgggaagtggtggaagcctccgc 65

|||||

Db 397 CGGGAAGGTGGTGAAGCCTCCGC 420

RESULT 8

BG384720

LOCUS BG384720 441 bp mRNA linear EST 12-MAR-2001

DEFINITION 303961 MARC lPIG Sus scrofa cDNA 5', mRNA sequence.

ACCESSION BG384720

VERSION BG384720.1 GI:13309192

KEYWORDS EST.

SOURCE pig.

ORGANISM Sus scrofa

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

1 (bases 1 to 441)

AUTHORS Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E.,

Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W.

and Keele, J.W.

Design and use of two pooled tissue normalized cDNA libraries for

EST discovery in swine

Unpublished (2000)

Contact: Smith TPL

PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4366

Fax: 402 762 4390

Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called and alt-trimmed with phred

v0.980904.e. Vector identified by cross_match with the -minscore 18

and -minmatch 12 options.

PCR Primers

FORWARD: AGGAACAGCTATGACCAT

BACKWARD: GTTTCCTCAGTCACGACG

Plate: 92 row: C column: 14

Seq primer: ATTAGGTGACACTATAG.

Location/Qualifiers

Source 1..441

/organism="Sus scrofa"

/db_xref="taxon:9823"

/clone_lib="MARC lPIG"

/tissue_type="pooled"

/lab_host="DH10B"

/note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;

Library made from pooled tissue from day 11, 13, 15, 20,

and 30 embryos."

BASE COUNT 122 a 110 c 120 g 89 t

ORIGIN

Query Match

Best Local Similarity 7.6%; Score 23; DB 10; Length 441;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 109 aaatgctgaaagagggcgccac 131

|||||

Db 218 AAAATGCTGAAGAGGCGCCAC 240

```

RESULT 9
BG384715          512 bp      mRNA      linear      EST 12-MAR-2001
LOCUS
DEFINITION       303951 MARC lPIG Sus scrofa cDNA 5', mRNA sequence.
ACCESSION        BG384715
VERSION          BG384715.1 GI:13309187
KEYWORDS         EST.
SOURCE           pig.
ORGANISM         Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE
AUTHORS          Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E.,
Stone, K.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W.,
and Keele, J.W.
TITLE            Design and use of two pooled tissue normalized cDNA libraries for
EST discovery in swine
JOURNAL
COMMENT          Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@mail.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
Plate: 92 row: A column: 16
Seq primer: ATTTAGTGACACTATAG.
Location/Qualifiers
BASE COUNT      146 a 128 c 144 g 94 t
ORIGIN
1..512
/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC lPIG"
/tissue_type="pooled"
/lab_host="DH10B"
/notice="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled tissue from day 11, 13, 15, 20,
and 30 embryos."
Query Match      7.6%; Score 23; DB 10; Length 512;
Best Local Similarity 100.0%; Pred. No. 0.68;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 aaaaatgctgaaagaggcgccac 131
Dbb 188 AAAATGCTGAAAGAGGGCGCCAC 210

RESULT 10
BF652351          498 bp      mRNA      linear      EST 25-APR-2001
LOCUS
DEFINITION       273882 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION        BF652351
VERSION          BF652351.1 GI:11917481
KEYWORDS         EST.
SOURCE           cow.
ORGANISM         Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
REFERENCE
AUTHORS          Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett
G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-Mckown, C.G.,
Perte, G., Holt, I., Karanycheva, S., Liang, F., Quackenbush, J. and
Keele, J.W.
TITLE            Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
JOURNAL
COMMENT          Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@mail.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred

```

```

Perte, G., Holt, I., Karanycheva, S., Liang, F., Quackenbush, J. and
Keele, J.W.
TITLE            Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
JOURNAL
MEDLINE
COMMENT          Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@mail.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
Plate: 65 row: N column: 7
Seq primer: ATTTAGTGACACTATAG.
Location/Qualifiers
BASE COUNT      108 a 149 c 149 g 92 t
ORIGIN
1..498
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 3BOV"
/tissue_type="pooled"
/lab_host="DH10B"
/notice="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled tissue from marrow, alveolar
macrophage, ovary, fetal semitendinosus muscle, and fetal
longissimus muscle."
Query Match      6.9%; Score 21; DB 10; Length 498;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 cgcgccttcgggaagtggt 53
Dbb 394 CGCGCCCTCGGGAAGGTGGT 414

RESULT 11
BF652352          498 bp      mRNA      linear      EST 25-APR-2001
LOCUS
DEFINITION       275883 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION        BF652352
VERSION          BF652352.1 GI:11917482
KEYWORDS         EST.
SOURCE           cow.
ORGANISM         Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
REFERENCE
AUTHORS          Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett
G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-Mckown, C.G.,
Perte, G., Holt, I., Karanycheva, S., Liang, F., Quackenbush, J. and
Keele, J.W.
TITLE            Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
JOURNAL
MEDLINE
COMMENT          Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@mail.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred

```

v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.

PCR Primers

FORWARD: AGGAACACGCTATGACCAT

BACKWARD: GTTTTCCAGTCAGCAGC

Plate: 65 row: N column: 8

Seq primer: ATTTAGTGACACTATAG.

Location/Qualifiers

1. 498

/organism="Bos taurus"

/db_xref="taxon:9913"

/clone_lib="MARC 3BOV"

/tissue_type="pooled"

/lab_host="DH10B"

/note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;

Library made from pooled tissue from marrow, alveolar

macrophage, ovary, fetal semitendinosus muscle, and fetal

longissimus muscle."

BASE COUNT 108 a 149 c 149 g 92 t

ORIGIN

Query Match 6.9%; Score 21; DB 10; Length 498;

Best Local Similarity 100.0%; Pred. No. 6.8;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 cggcgcccttcgggaaggtggt 53

|||||

Db 394 CGCGCCCTTCGGGAAGGTGCT 414

RESULT 12

BM482403

LOCUS

DEFINITION 531 bp mRNA linear EST 05-FEB-2002

535280 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.

ACCESSION BM482403

VERSION BM482403.1 GI:18532731

KEYWORDS EST.

SOURCE COW.

ORGANISM

Bos taurus

Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

Bovidae; Bovinae; Bos.

1 (bases 1 to 531)

Smith, T. P. L., Grosse, W. M., Freking, B. A., Roberts, A. J., Stone, R. T.,

Casas, E., Wray, J. E., White, J., Cho, J., Fahrenkrug, S. C., Bennett

, G. L., Heaton, M. P., Laegreid, W. W., Rohrer, G. A., Chitko-Mckown, C. G.,

Perle, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J., and

Keele, J. W.

Sequence evaluation of four pooled-tissue normalized bovine cDNA

libraries and construction of a gene index for cattle

Genome Res. 11 (4), 626-630 (2001)

21180013

Contact: Smith TPL

USDA, ARS, US Meat Animal Research Center

PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4366

Fax: 402 762 4390

Email: smith@mail.marc.usda.gov

Single pass sequencing. Bases called and alt_trimmed with phred

v0.980904.e. Vector identified by cross_match with the -minscore 18

and -minmatch 12 options.

PCR Primers

FORWARD: AGGAACACGCTATGACCAT

BACKWARD: GTTTTCCAGTCAGCAGC

Plate: 3 row: I column: 5

Seq primer: ATTTAGTGACACTATAG.

Location/Qualifiers

1. 531

/organism="Bos taurus"

/db_xref="taxon:9913"

/clone_lib="MARC 3BOV"

/tissue_type="pooled"

FEATURES

source

/lab_host="DH10B"

/note="vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;

Library made from pooled tissue from marrow, alveolar

macrophage, ovary, fetal semitendinosus muscle, and fetal

longissimus muscle."

BASE COUNT 91 a 145 c 169 g 125 t

ORIGIN

Query Match 6.9%; Score 21; DB 10; Length 531;

Best Local Similarity 100.0%; Pred. No. 6.9;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 cggcgcccttcgggaaggtggt 53

|||||

Db 82 CGCGCCCTTCGGGAAGGTGCT 102

RESULT 13

AV601195/c

LOCUS

DEFINITION 538 bp mRNA linear EST 27-NOV-2001

3', mRNA sequence.

ACCESSION AV601195

VERSION AV601195.1 GI:9723513

KEYWORDS EST.

SOURCE COW.

ORGANISM

Bos taurus

Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

Bovidae; Bovinae; Bos.

1 (bases 1 to 538)

Takasuga, A., Hirotsune, S., Itoh, R., Jitohzono, A., Suzuki, H., Aso, H.

and Sugimoto, Y.

Establishment of a high throughput EST sequencing system using

poly(A) tail-removed cDNA libraries and determination of 36,000

bovine ESTs

Nucleic Acids Res. 29 (22), E108 (2001)

21570554

Contact: Yoshikazu Sugimoto

Animal Genetics Division

Shirakawa Institute of Animal Genetics

Odakura, Nishigo, Nishi-shirakawa, Fukushima 961-8061, Japan

Tel: 81-248-25-5641

Fax: 81-248-25-5725

Email: kazusugie@ocn.ne.jp

Single pass sequencing.

This clone was obtained from a polyA-deleted cDNA library.

FEATURES

Location/Qualifiers

1. 538

/organism="Bos taurus"

/db_xref="taxon:9913"

/clone="EIKI002H06"

/clone_lib="Bos taurus kidney fetus"

/tissue_type="kidney"

/dev_stage="fetus"

/lab_host="DH10B"

/note="Vector: pZL1; Site_1: SalI; Site_2: NotI; Poly A

was deleted from a NotI site"

BASE COUNT 100 a 158 c 150 g 126 t

ORIGIN

Query Match 6.9%; Score 21; DB 9; Length 538;

Best Local Similarity 100.0%; Pred. No. 6.9;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 cggcgcccttcgggaaggtggt 53

|||||

Db 344 CGCGCCCTTCGGGAAGGTGCT 324

RESULT 14

AV601196
LOCUS
DEFINITION AV601196 Bos taurus kidney fetus Bos taurus cDNA clone EIK1002H06
5', mRNA sequence.
ACCESSION AV601196
VERSION AV601196.1 GI:9723514
KEYWORDS EST.
SOURCE COW.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 544)
AUTHORS Takasuga,A., Hirotsune,S., Itoh,R., Jitohzono,A., Suzuki,H., Aso,H.
and Sugimoto,Y.
TITLE Establishment of a high throughput EST sequencing system using
poly(A) tail-removed cDNA libraries and determination of 36,000
bovine ESTs
JOURNAL Nucleic Acids Res. 29 (22), E108 (2001)
MEDLINE 21570554
COMMENT Contact: Yoshikazu Sugimoto
Animal Genetics Division
Shirakawa Institute of Animal Genetics
Odakura, Nishio, Nishi-shirakawa, Fukushima 961-8061, Japan
Tel: 81-248-25-5641
Fax: 81-248-25-5725
Email: kazusugi@ocn.ocn.ne.jp
Single pass sequencing.
This clone was obtained from a polyA-deleted cDNA library.

FEATURES
source
1..544
Location/Qualifiers
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone="EIK1002H06"
/clone_lib="Bos taurus kidney fetus"
/tissue_type="kidney"
/dev_stage="fetus"
/lab_host="DH10B"
/note="Vector: pZL1; Site_1: SalI; Site_2: NotI; Poly A
was deleted from a NotI site"

BASE COUNT 126 a 152 c 160 g 105 t 1.others
ORIGIN

Query Match 6.9%; Score 21; DB 9; Length 544;
Best Local Similarity 100.0%; Pred. No. 6.9;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 33 cggcgccctcggaagtgggt 53
|||||
Db 195 CGGCGCCCTCGGAAGTGGT 215

RESULT 15
W57847
LOCUS
DEFINITION zdl7h05.r1 Soares_fetal_heart_NBHH19W Homo sapiens cDNA clone
IMAGE:340953 5', mRNA sequence.
ACCESSION W57847
VERSION W57847.1 GI:1364581
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 293)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman
M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J.,
Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston
R., Williamson,A., Wohldmann,P. and Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL : contact the
IMAGE Consortium (info@image.lnl.gov) for further information..
Insert length: 788 Std Error: 0.00
Seq primer: mob.REGA+ET
High quality sequence stop: 278.
Location/Qualifiers
1..293
/organism="Homo sapiens"
/db_xref="CDB:1266328"
/db_xref="taxon:9606"
/clone="IMAGE:340953"
/clone_lib="Soares_fetal_heart_NBHH19W"
/sex="unknown"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: heart; Vector: pT7T3D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTACCAATCTCAAGTGGAGCGCGCATCTTTTCTTTTCTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by
M.Patima Bonaldo. This library was constructed from the
same fetus as the fetal lung library, Soares fetal lung
NBHH19W."

FEATURES
source
1..293
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="CDB:1266328"
/db_xref="taxon:9606"
/clone="IMAGE:340953"
/clone_lib="Soares_fetal_heart_NBHH19W"
/sex="unknown"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: heart; Vector: pT7T3D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTACCAATCTCAAGTGGAGCGCGCATCTTTTCTTTTCTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by
M.Patima Bonaldo. This library was constructed from the
same fetus as the fetal lung library, Soares fetal lung
NBHH19W."

BASE COUNT 71 a 78 c 52 g 89 t 3 others
ORIGIN

Query Match 6.6%; Score 20; DB 10; Length 293;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 101 tggccgtgaaatgctgaaa 120
|||||
Db 231 TGGCCGTGAAATGCTGAAA 250

RESULT 16
B1182263
LOCUS
DEFINITION UNL-P-FN-bf-e-12-0-UNL.s1 UNL-P-FN Sus scrofa cDNA clone
IMAGE:340953 5', mRNA sequence.
ACCESSION B1182263
VERSION B1182263.1 GI:14656672
KEYWORDS EST.
SOURCE pig.

ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
REFERENCE 1 (bases 1 to 434)
AUTHORS Caetano,A.R., Johnson,R.K. and Pomp,D.
TITLE Generation and sequence characterization of a normalized cDNA
library from swine ovarian follicles
JOURNAL Unpublished (2001)
COMMENT Contact: Pomp, D
Department of Animal Science
University of Nebraska, Lincoln
Lincoln, NE 68583-0908, USA
Tel: 402 472 6416
Fax: 402 472 6362
Email: dpomp@unl.edu
Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message.
Seq primer: M13 -29
POLYA=No.

BASE COUNT 71 a 78 c 52 g 89 t 3 others
ORIGIN

Query Match 6.6%; Score 20; DB 10; Length 293;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 101 tggccgtgaaatgctgaaa 120
|||||
Db 231 TGGCCGTGAAATGCTGAAA 250

RESULT 16
B1182263
LOCUS
DEFINITION UNL-P-FN-bf-e-12-0-UNL.s1 UNL-P-FN Sus scrofa cDNA clone
IMAGE:340953 5', mRNA sequence.
ACCESSION B1182263
VERSION B1182263.1 GI:14656672
KEYWORDS EST.
SOURCE pig.

ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
REFERENCE 1 (bases 1 to 434)
AUTHORS Caetano,A.R., Johnson,R.K. and Pomp,D.
TITLE Generation and sequence characterization of a normalized cDNA
library from swine ovarian follicles
JOURNAL Unpublished (2001)
COMMENT Contact: Pomp, D
Department of Animal Science
University of Nebraska, Lincoln
Lincoln, NE 68583-0908, USA
Tel: 402 472 6416
Fax: 402 472 6362
Email: dpomp@unl.edu
Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message.
Seq primer: M13 -29
POLYA=No.

```

FEATURES
Source
Location/Qualifiers
1. .434
/organism="Sus scrofa"
/strain="University of Nebraska, Lincoln Swine Selection
Lines"
/db_xref="taxon:9823"
/clone="UNL-P-FN-bf-e-12-0-UNL"
/clone_lib="UNL-P-FN"
/dev_stage="ADULT"
/lab_host="DH10B (Life Technologies)"
/notes="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UNL-P-FN
library is a normalized library representing porcine
ovarian follicles, ranging between 2.0 to 10.0 mm in
diameter, collected during 7 days of the follicular phase
of the pig estrous cycle. This library was derived from
the library UNL-P-F2. The tag is a string of 5-6
nucleotides present between the Not I site and the
oligo-dT track. The library was constructed as described
by Bonaldo, Lennon and Soares, Genome Research 6: 791-806
, 1996.
TAG_SEQ=None found"
BASE COUNT 103 a 114 c 120 g 97 t
ORIGIN

Query Match 6.6%; Score 20; DB 10; Length 434;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 163 ctcaagalcctcattcacat 182
Db 343 CTCAAGATCCTCATTACAT 362

RESULT 17
BM261245
LOCUS
DEFINITION
da145402.y1 NICHD XGC Sp1 xenopus laevis cDNA clone IMAGE:4964906
5' similar to TR:P79701 P79701 VASCULAR ENDOTHELIAL GROWTH FACTOR
RECEPTOR. ;, mRNA sequence.
ACCESSION
BM261245
VERSION
BM261245.1 GI:17924285
KEYWORDS
EST.
SOURCE
African clawed frog.
ORGANISM
Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
Xenopodinae; Xenopus.
1 (bases 1 to 558)
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
JOURNAL
Contact: Robert Strausberg, Ph.D.
Email: coapbs@email.nih.gov
Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA sequencing by: Washington University Genome Sequencing Center
Clone distribution: Xenopus clones from this library are available
through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov
Seq primer: -48RP from Gibco
High quality sequence stop: 442.
Location/Qualifiers
1. .558
/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="IMAGE:4964906"
/clone_lib="NICHD XGC Sp1"
/dev_stage="adult"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: spleen; Vector: pCMV-SPORT6; Site_1: NotI;

Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.4 kb. Constructed by Life
Technologies."
BASE COUNT 162 a 119 c 149 g 128 t
ORIGIN

Query Match 6.6%; Score 20; DB 10; Length 558;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 106 gtgaaatgctgaaagagg 125
Db 130 GTGAAATGCTGAAAGAGG 149

RESULT 18
BH142039
LOCUS
DEFINITION
TGDDK45TH CTOG Lycopersicon esculentum genomic clone CTOG23G17, DNA
sequence.
ACCESSION
BH142039
VERSION
BH142039.1 GI:15194268
KEYWORDS
GSS.
SOURCE
tomato.
ORGANISM
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
1 (bases 1 to 619)
van der Hoeven,R., Sun,H., Cho,J., Utterback,T., Ronning,C. and
Tanksley,S.
Tomato Demethylated Genomic DNA Sequences
Unpublished (2001)
Contact: CUGI
JOURNAL
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
tomato demethylated genomic DNA
Insert Length: 1270 Std Error: 0.00
Seq primer: M13F-R
Class: shotgun.
Location/Qualifiers
1. .619
/organism="Lycopersicon esculentum"
/cultivar="E6203"
/db_xref="taxon:4081"
/clone="CTOG23G17"
/clone_lib="CTOG"
/tissue_type="young leaves"
/dev_stage="12-14 weeks post harvest"
/lab_host="E.coli JM109"
/notes="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; This library was made from short EcoRI digested
fragments of the genome of Lycopersicon esculentum ligated
into pBS (SK-). The fragments were cloned into the
methylation restrictive E.coli strain JM109 with the
purpose of enriching the library for non-methylated DNA
fragments. This procedure may enrich the pool of cloned
fragments in JM109 cells for sequences representing
expressed genes. Average insert size 1.27 kb."
BASE COUNT 233 a 102 c 121 g 163 t
ORIGIN

Query Match 6.6%; Score 20; DB 12; Length 619;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 106 gtgaaatgctgaaagagg 125
|||||

```


Db 392 GTGAAATGCTGAAAGAGG 411

RESULT 19

LOCUS BG709462

DEFINITION 602674728F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:4797343 5',
mRNA sequence.

ACCESSION BG709462

VERSION BG709462.1 GI:13987822

KEYWORDS EST.

SOURCE human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 810)

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

cDNA Library Preparation: Miklos Palkovits, M.D., Ph.D.

Tissue Procurement: Michael J. Brownstein (NHGRI), Shiraki

Toshiyuki and Piero Carninci (RIKEN)

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LHAM10683 row: g column: 08

High quality sequence stop: 743.

FEATURES

source

1..810

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:4797343"

/clone_lib="NIH_MGC_96"

/tissue_type="hypothalamus"

/lab_host="DH10B"

/note="Organ: brain; Vector: pBluescriptR (modified

pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcag

); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTVN-3',

size-selected for average insert size 2.3 kb and

normalized to ROT 5. This is a primary library enriched

for full-length clones and constructed using the

Cap-trapper method (Carninci, in preparation). Library

constructed by M. Brownstein (NIH/NHGRI, National

Institutes of Health). Note: this is a NIH_MGC Library."

177 a 184 c 203 g 246 t

BASE COUNT

ORIGIN

Query Match

Best Local Similarity 6.6%; Score 20; DB 10; Length 810;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 101 tggccgtgaaaatgctgaaa 120

|||||

Db 784 TGGCCGTGAAATGCTGAAA 803

RESULT 20

LOCUS BG746729

DEFINITION 602704056F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4857469 5',
mRNA sequence.

ACCESSION BG746729

VERSION BG746729.1 GI:14057382

KEYWORDS EST.

SOURCE human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: NIH Intramural Sequencing Center

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LUCM1709 row: p column: 14

High quality sequence stop: 850.

FEATURES

source

1..856

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:4857469"

/clone_lib="NIH_MGC_15"

/tissue_type="adenocarcinoma cell line"

/lab_host="DH10B (phage-resistant)"

/note="Organ: colon; Vector: pOT87; Site_1: XhoI; Site_2:

ECORI; cDNA made by oligo-dT priming. Directionally

cloned into EcoRI/XhoI sites using the following 5'

adaptor: GGCACGAG(G). Size-selected >500bp for average

insert size 1.8kb. Library constructed by Ling Hong in

the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies)"

192 a 198 c 199 g 267 t

BASE COUNT

ORIGIN

Query Match 6.6%; Score 20; DB 10; Length 856;

Best Local Similarity 100.0%; Pred. No. 25;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 101 tggccgtgaaaatgctgaaa 120

|||||

Db 772 TGGCCGTGAAATGCTGAAA 791

RESULT 21

LOCUS BG615859

DEFINITION 602643265F1 NIH_MGC_61 Homo sapiens cDNA clone IMAGE:4774168 5',
mRNA sequence.

ACCESSION BG615859

VERSION BG615859.1 GI:13667230

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 862)

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: CLONETECH Laboratories, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LUCM1647 row: a column: 17

High quality sequence stop: 711.

FEATURES

source

1..862

```
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4774168"
/clone_lib="NIH_MGC_61"
/tissue_type="embryonal carcinoma"
/lab_host="DH10B (T1 phage-resistant)"
/notes="Organ: testis; Vector: pDNR-LIB (Clontech); Site_1:
SfiI (ggccctatggcc); Site_2: SfiI (ggccctatggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CAGGCCATTATGGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGCCGAGCGGCGGCATG-dT(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
Library."
BASE COUNT      198 a 185 c 201 g 278 t
ORIGIN

Query Match      6.6%; Score 20; DB 10; Length 862;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 101 tggccgtgaaaaatgctgaaa 120
      |||||||
Db 726 TGGCCGTGAAAAATGCTGAAA 745

RESULT 22
LOCUS      BI763816      864 bp      mRNA      linear      EST 25-SEP-2001
DEFINITION 603049766P1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5189729 5',
      mRNA sequence.
ACCESSION  BI763816
VERSION    BI763816.1 GI:15755394
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 864)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11474 row: d column: 18
            High quality sequence stop: 862.
            Location/Qualifiers
                1..864
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="IMAGE:5189729"
                /clone_lib="NIH_MGC_116"
                /lab_host="DH10B"
                /note="Organ: pooled colon, kidney, stomach; Vector:
                pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
                source anonymous pool of 3 colons, age 26 yo male, 49 yo
                female, 71 yo male colon; 46 yo male kidney, and pool of 2
                stomachs, 62 yo male and 70 yo female. Library is
                oligo-dT primed and directionally cloned (EcoRV site is
                destroyed upon cloning). Average insert size 1.4 kb,
                insert size range 1-3 kb. Library is normalized and
```

```
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH_MGC Library."
BASE COUNT      195 a 198 c 210 g 260 t
ORIGIN

Query Match      6.6%; Score 20; DB 10; Length 864;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 101 tggccgtgaaaaatgctgaaa 120
      |||||||
Db 791 TGGCCGTGAAAAATGCTGAAA 810

RESULT 23
LOCUS      BM048480      885 bp      mRNA      linear      EST 07-NOV-2001
DEFINITION 603628170F1 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:5456776 5',
      mRNA sequence.
ACCESSION  BM048480
VERSION    BM048480.1 GI:16777747
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 885)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTF
            cDNA Library Preparation: Ling Hong/Rubin Laboratory
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCMI955 row: k column: 17
            High quality sequence stop: 807.
            Location/Qualifiers
                1..885
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="IMAGE:5456776"
                /clone_lib="NIH_MGC_40"
                /tissue_type="carcinoma, cell line"
                /lab_host="DH10B (phage-resistant)"
                /note="Organ: prostate; Vector: pOTB7; Site_1: XhoI;
                Site_2: EcoRI; cDNA made by oligo-dT priming.
                Directionally cloned into EcoRI/XhoI sites using the
                following 5' adaptor: GGCACGAG(G). Library constructed by
                Ling Hong in the laboratory of Gerald M. Rubin (University
                of California, Berkeley) using ZAP-cDNA synthesis kit
                (Stratagene) and Superscript II RT (Life Technologies).
                Note: this is a NIH_MGC Library."
BASE COUNT      195 a 209 c 208 g 273 t
ORIGIN

Query Match      6.6%; Score 20; DB 10; Length 885;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 101 tggccgtgaaaaatgctgaaa 120
      |||||||
Db 770 TGGCCGTGAAAAATGCTGAAA 789

RESULT 24
```

```

BF927018
LOCUS      BF927018      201 bp      mRNA      linear      EST 19-JAN-2001
DEFINITION CM2-NT0192-051200-577-f09 NT0192 Homo sapiens cDNA, mRNA sequence.
ACCESSION  BF927018
VERSION     BF927018.1  GI:12324874
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 201)
AUTHORS     Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
            Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
            Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
            Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
            , M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
            Simpson, A.J.
            Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
JOURNAL     Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE     20202663
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM2&t2=CM2-NT0192-
            051200-577-f09&t3=2000-12-05&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 126
            High quality sequence stop: 201.
            Location/Qualifiers
FEATURES             source
     source           1..201
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="NT0192"
                     /dev_stage="Adult"
                     /note="Organ: nervous_tumor; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 - Ludwig Institute for Cancer Research)
                     profiles into the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
BASE COUNT  58 a 43 c 62 g 38 t
ORIGIN
1
tcacacagggcagcagctg 92
|||||
Db 171 TCACAAAGGGCAGCAGCTG 189

Query Match 6.3%; Score 19; DB 10; Length 201;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 74 tcacacagggcagcagctg 92
|||||
Db 171 TCACAAAGGGCAGCAGCTG 189

RESULT 25
LOCUS      BF925651      208 bp      mRNA      linear      EST 19-JAN-2001
DEFINITION CM2-NT0192-291100-578-e05 NT0192 Homo sapiens cDNA, mRNA sequence.
ACCESSION  BF925651
VERSION     BF925651.1  GI:12322186
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 208)
AUTHORS     Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
            Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
            Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
            Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
            , M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
            Simpson, A.J.
            Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
JOURNAL     Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE     20202663
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM2&t2=CM2-NT0192-
            291100-578-e05&t3=2000-11-29&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 12
            High quality sequence stop: 208.
            Location/Qualifiers
FEATURES             source
     source           1..208
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="NT0192"
                     /dev_stage="Adult"
                     /note="Organ: nervous_tumor; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 - Ludwig Institute for Cancer Research)
                     profiles into the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
BASE COUNT  57 a 44 c 62 g 45 t
ORIGIN
1
tcacacagggcagcagctg 92
|||||
Db 178 TCACAAAGGGCAGCAGCTG 196

Query Match 6.3%; Score 19; DB 10; Length 208;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 74 tcacacagggcagcagctg 92
|||||
Db 178 TCACAAAGGGCAGCAGCTG 196

RESULT 26
LOCUS      BF524514/c 1257 bp      mRNA      linear      EST 29-AUG-2001
DEFINITION 603051580r1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5201514 3',
            mRNA sequence.
ACCESSION  BF524514
VERSION     BF524514.1  GI:15349306
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1257)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

```

```

REFERENCE   1 (bases 1 to 208)
AUTHORS     Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
            Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
            Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
            Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
            , M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
            Simpson, A.J.
            Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
JOURNAL     Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE     20202663
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM2&t2=CM2-NT0192-
            291100-578-e05&t3=2000-11-29&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 12
            High quality sequence stop: 208.
            Location/Qualifiers
FEATURES             source
     source           1..208
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="NT0192"
                     /dev_stage="Adult"
                     /note="Organ: nervous_tumor; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 - Ludwig Institute for Cancer Research)
                     profiles into the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
BASE COUNT  57 a 44 c 62 g 45 t
ORIGIN
1
tcacacagggcagcagctg 92
|||||
Db 178 TCACAAAGGGCAGCAGCTG 196

Query Match 6.3%; Score 19; DB 10; Length 208;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 74 tcacacagggcagcagctg 92
|||||
Db 178 TCACAAAGGGCAGCAGCTG 196

RESULT 26
LOCUS      BF524514/c 1257 bp      mRNA      linear      EST 29-AUG-2001
DEFINITION 603051580r1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5201514 3',
            mRNA sequence.
ACCESSION  BF524514
VERSION     BF524514.1  GI:15349306
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1257)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

```


JOURNAL COMMENT Unpublished (2001)
Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@igsun.grc.nia.nih.gov
Plate: K0624 row: A column: 01
Seq primer: -21M13 Forward
High quality sequence stop: 261
POLYA-Yes.

FEATURES
source Location/Qualifiers
1. .261
/organism="Mus musculus"
/strain="C57BL/6Ncr"
/db_xref="niaEST:K0624A01-3"
/db_xref="taxon:10090"
/clone="K0624A01"
/clone_lib="NIA Mouse Hematopoietic Stem Cell
(Lin-/C-Kit-/Sca-1+) cDNA Library (long)"
/tissue_type="Hematopoietic Stem Cell (Lin-/C-Kit-/Sca-1+)"
/dev_stage="Age approx.10 weeks old"
/lab_host="DH10B"
/note="Vector: pSPORT1 (Invitrogen); Site_1: SalI; Site_2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://igsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were obtained from Drs. Dennis Taub, Dan Longo (National Institute on Aging, USA), Jonathan Keller (National Cancer Institute, USA). Double-stranded cDNAs were synthesized with an oligo(dT) primer [Invitrogen]:
5'-pGACTAGTTCTAGATCGAGCGCGCCCTTTTTTTTTTT-3' from 1.1 ug of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to lone-linker Lu-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pSPORT1 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.2 kb. The library was constructed by Yulan Piao (NIA)."

BASE COUNT 58 a 63 c 57 g 83 t
ORIGIN

Query Match 5.9%; Score 18; DB 10; Length 261;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 82 ggcagcagctgtgacacc 99
|||||

Db 225 GCCAGCAGCTGTGACACC 242

RESULT 29
BM409650/c
LOCUS
EST583977 tomato breaker fruit Lycopersicon esculentum cDNA clone
cLEG49022 5' end, mRNA sequence.

ACCESSION
BM409650
VERSION
KEYWORDS
SOURCE
ORGANISM
tomato.
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgabrs-r@mail.nih.gov
Tissue Procurement: Elias Campo, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arraying: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution Information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/brp/image/image.html
Insert Length: 968 Std Error: 0.00

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Unpublished (2002)
Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
This clone is available through the Clemson University Genomics Institute
Seq primer: T3.
Location/Qualifiers
1. .271
/organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="cLEG49022"
/clone_lib="tomato breaker fruit"
/tissue_type="Pericarp"
/dev_stage="Breaker"
/lab_host="SOLR"
/note="Vector: pBluescriptSKmCudapt; Site_1: EcoRI; Site_2: XhoI; supplier: Boyce Thompson Institute; sequencing: The Institute for Genomic Research. Fruit were harvested at the breaker stage for genomic research. Lycopersene accumulation on the blossom end of fruit). Fruit were cut in half and the seeds and locules were discarded prior to freezing the pericarp."

BASE COUNT 73 a 56 c 60 g 82 t
ORIGIN

Query Match 5.9%; Score 18; DB 10; Length 271;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 71 gcatccacagggcgacga 88
|||||

Db 57 GCATCCACAAGGGCAGCA 40

RESULT 30
AW009058/c
LOCUS
ws75g02.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2503826 3', mRNA sequence.

DEFINITION
AW009058
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens
human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgabrs-r@mail.nih.gov
Tissue Procurement: Elias Campo, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arraying: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution Information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/brp/image/image.html
Insert Length: 968 Std Error: 0.00

Seq primer: -40UP from Gibco
High quality sequence stop: 318.

FEATURES

Location/Qualifiers
1. .319
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="IMAGE:2503826"
/clone_lib="NCI_CGAP_Co3"
/sex="pooled"
/tissue_type="colon"
/lab_host="DH10B"

/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from 12 pooled bulk tumor samples and primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization."
65 a 116 c 117 g 21 t

BASE COUNT

ORIGIN

Query Match 5.9%; Score 18; DB 9; Length 319;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 acggcgcttcgggaagg 49

|||||

Db 55 ACGGCGCCTTCGGGAAGG 38

RESULT 31

AQ216651/c

LOCUS

DEFINITION HS_2139_A2_C03_MR CIT Approved Human Genomic Sperm Library D Homo

sapiens genomic clone Plate=2139 Col=6 Row=E, DNA sequence.

ACCESSION AQ216651

VERSION AQ216651.1

KEYWORDS GSS.

SOURCE AQ216651.1 GI:3631971

ORGANISM human.

REFERENCE Homo sapiens

AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

MAHAIRES, G.G., WALLACE, J.C., SMITH, K., SWARTZELL, S., HOLZMAN, T.,

KELLER, A., SHAKER, R., FURLONG, J., YOUNG, J., ZHAO, S., ADAMS, M.D. and

HOOD, L.

Sequence-tagged connectors: A sequence approach to mapping and

scanning the human genome

Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)

99380589

Contact: Mahalras GG, Wallace JC, Hood L

High Throughput Sequencing Center

University of Washington

401 Queen Anne Avenue North, Seattle, WA 98109, USA

Tel: (206) 616-3618

Fax: (206) 616-3887

Email: jwallace@u.washington.edu

Sequence Tagged Connector

Plate: 2139 row: E column: 6

Class: BAC ends

High quality sequence stop: 360.

Location/Qualifiers

1. .360

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="Plate=2139 Col=6 Row=E"

/clone_lib="CIT Approved Human Genomic Sperm Library D"

/sex="male"

/note="Organ: sperm; Vector: pBelOBAC11; BAC Clones in

E-Coli DH10B"

104 a 63 c 76 g 105 t 12 others

BASE COUNT

ORIGIN

Query Match 5.9%; Score 18; DB 12; Length 360;

Best Local Similarity 100.0%; Pred. No. 2e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 108 gaaaatgctgaagagg 125

|||||

Db 95 GAAATGCTGAAGAGGG 78

RESULT 32

A1744037/c

LOCUS

DEFINITION wc32hl1.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2316933 3',

mRNA sequence.

ACCESSION A1744037

VERSION A1744037.1

KEYWORDS EST.

SOURCE A1744037.1 GI:5112325

ORGANISM human.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 369)

AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

JOURNAL Contact: Robert Strausberg, Ph.D.

COMMENT Email: cgapbs-remail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.

DNA Sequencing by: Greg Lennon, Ph.D.

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 1520 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 329.

Location/Qualifiers

1. .369

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:2316933"

/clone_lib="NCI_CGAP_Kid11"

/lab_host="DH10B"

/note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with

a modified polylinker; Site_1: Not I; Site_2: Eco RI;

Plasmid DNA from the normalized library NCI_CGAP_Kid3 was

prepared, and ss circles were made in vitro. Following RAP

purification, this DNA was used as tracer in a subtractive

hybridization reaction. The driver was PCR-amplified cDNAs

from a pool of 5,000 clones made from the same library

(cloneIDs 1322376-1323911, 1456007-1456775, and

1500552-1502855). Subtraction by Bento Soares and M.

Fatima Bonaldo.

77 a 131 c 131 g 30 t

BASE COUNT

ORIGIN

Query Match

Best Local Similarity 100.0%;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 acggcgcttcgggaagg 49

|||||

Db 55 ACGGCGCCTTCGGGAAGG 38

RESULT 33

```

BE460395/c
LOCUS      BE460395              470 bp      mRNA      linear      EST 18-MAY-2001
DEFINITION clone CLG29A14, tomato breaker fruit, TIGR Lycopersicon esculentum cDNA
ACCESSION BE460395
VERSION    BE460395.1  GI:9504697
KEYWORDS   EST.
SOURCE     tomato.
ORGANISM   Lycopersicon esculentum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
            Lycopersicon.
REFERENCE   1 (bases 1 to 470)
            Alcalá, J., Vrebalov, J., White, R., van der Hoeven, K.S., Holt, I.E.,
            Liang, F., Hansen, T.S., Craven, M.B., Bowman, C.L., Konning, C.M.,
            Nierman, W., Fraser, C.M., Martin, G.B., Giovannoni, J.J. and Tanksley
            , S.D.
            Generation of ESTs from tomato fruit tissue, breaker stage
            Unpublished (2000)
            Contact: CUGI
            Clemson University Genomics Institute
            Clemson University
            100 Jordan Hall, Clemson, SC 29634, USA
            Email: http://www.genome.clemson.edu/orders/index.html
            5 prime sequence.
FEATURES             Location/Qualifiers
     source           1..470
                     /organism="Lycopersicon esculentum"
                     /cultivar="TA496"
                     /db_xref="taxon:4081"
                     /clone="CLG29A14"
                     /clone_lib="tomato breaker fruit, TIGR"
                     /tissue_type="pericarp"
                     /dev_stage="breaker"
                     /lab_host="SOLR"
                     /note="Vector: pBluescriptSMCquadapt; Site_1: EcoRI;
                     Site_2: XhoI; Fruit were harvested at the breaker stage
                     (first sign of lycopene accumulation on the blossom end of
                     the fruit). Fruit were cut in half and the seeds and
                     locules were discarded prior to freezing the pericarp."
BASE COUNT      134 a      81 c      118 g      137 t
ORIGIN
Query Match      5.9%; Score 18; DB 10; Length 470;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 71 gcatccacaaggagcagca 88
      |||||||
Db 422 GCATCCACAGCGCAGCA 405

RESULT 34
BH392477
LOCUS      BH392477              478 bp      DNA      linear      GSS 11-DEC-2001
DEFINITION AG-ND-142N21.TF ND-TAM Anopheles gambiae genomic clone AG-ND-142N21
            , DNA sequence.
ACCESSION BH392477
VERSION    BH392477.1  GI:17338618
KEYWORDS   GSS.
SOURCE     African malaria mosquito.
ORGANISM   Anopheles gambiae
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea
            ; Anopheles.
REFERENCE   1 (bases 1 to 478)
            Shetty, J., Malek, J., Koo, H., Collins, F., Gardner, M. and Loftus, B.J.
            Direct Submission of BAC-end sequences from Anopheles gambiae
            Unpublished (2001)
            Contact: Brendan J Loftus
            Department of Eukaryotic Genomics

```

```

The Institute for Genomic Research
712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Email: bjoftus@tigr.org
This clone is from an A. gambiae BAC library (ND-TAM) provided by
F.H. Collins and sequenced by The Institute for Genomic Research
(TIGR). The BAC library was generated from A. gambiae PEST strain
DNA. All DNA was extracted from newly hatched first instar larvae
to minimize the inclusion of DNA from microorganisms that inhabit
the gut. The DNA is derived from mixed sexes of larvae. The BAC
library was constructed at Texas A&M University BAC Center
University, College Station, Texas 77843-2123, USA using a HindIII
partial digest.
Seq primer: M13 For
Class: BAC ends.
FEATURES             Location/Qualifiers
     source           1..478
                     /organism="Anopheles gambiae"
                     /strain="PEST"
                     /db_xref="taxon:7165"
                     /clone="AG-ND-142N21"
                     /clone_lib="ND-TAM"
                     /note="vector: pECBAC1; Site_1: HindIII"
BASE COUNT      121 a      121 c      131 g      105 t
ORIGIN
Query Match      5.9%; Score 18; DB 12; Length 478;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 139 gagcaaccgcgcgcgatg 156
      |||||||
Db 106 GAGCACCGCGCGCTGATG 123

RESULT 35
BH405811/c
LOCUS      BH405811              480 bp      mRNA      linear      EST 14-AUG-2001
DEFINITION 146C09 Mature tuber lambda ZAP Solanum tuberosum cDNA, mRNA
            sequence.
ACCESSION BH405811
VERSION    BH405811.1  GI:15185225
KEYWORDS   EST.
SOURCE     potato.
ORGANISM   Solanum tuberosum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
REFERENCE   1 (bases 1 to 480)
            Nielsen, K.L., Crookshanks, M., Emmersen, J. and Wellinder, K.G.
            EST-sequencing of mature potato tuber (Var. Kuras)
            Unpublished (2000)
            Contact: Karen G. Wellinder
            Institut for bioteknologi
            Aalborg Universitet
            Sohngaardsholmsvej 49, 9000 Aalborg, Denmark
            Tel: +45 96358467
            Fax: +45 98141808
            Email: kgw@bio.auc.dk
            Sequenced from the 5' end.
            High quality sequence stop: 480
POLYA=No.
FEATURES             Location/Qualifiers
     source           1..480
                     /organism="Solanum tuberosum"
                     /cultivar="Field grown Kuras"
                     /db_xref="taxon:4113"
                     /clone_lib="Mature tuber lambda ZAP"
                     /tissue_type="Tuber"
                     /note="vector: Lambda ZAP"
BASE COUNT      141 a      86 c      114 g      139 t

```



```

Oy 71 gcatccacaaggcgagca 88
    |||||||
Db 372 GCATCCACAAGGCGAGCA 355

RESULT 41
LOCUS BG280611
DEFINITION BG280611 517 bp mRNA linear EST 21-FEB-2001
            c5006np.r1 Neurospora crassa sexual cDNA library, Uni-zap vector
            system Neurospora crassa cDNA clone c5006np 5', mRNA sequence.
ACCESSION BG280611
VERSION   BG280611.1 GI:13079190
KEYWORDS  EST.
SOURCE    Neurospora crassa.
           Neurospora crassa
           Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
           Sordariales; Sordariaceae; Neurospora.
REFERENCE 1 (bases 1 to 517)
AUTHORS   Kupfer,D., Lai,H., Nelson,M. and Roe,B.
TITLE     ESTs from a Neurospora crassa Sexual cDNA Library
JOURNAL   Unpublished (2001)
COMMENT   Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
           Department of Chemistry and Biochemistry
           Advanced Center for Genome Technology, University of Oklahoma
           620 Parrington Oval, Norman, OK 73019, USA
           Tel: 405 325 4912
           Fax: 405 325 7762
           Email: broe@ou.edu
           Contact Dr. Mary Anne Nelson, Department of Biology, University of
           New Mexico, Albuquerque, NM 87131 (e-mail address manelson@unm.edu)
           regarding clone availability
           Seq primer: M13 Universal Reverse Primer
           High quality sequence stop: 426.
           Location/Qualifiers
             1..517
               /organism="Neurospora crassa"
               /strain="wild type"
               /db_xref="taxon:5141"
               /clone="c5006np"
               /clone_lib="Neurospora crassa sexual cDNA library, Uni-zap
               vector system"
               /tissue_type="perithecia (fruiting bodies)"
               /dev_stage="sexual"
               /lab_host="E. coli strain SOLR"
               /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
               XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript
               ; 3' end of cDNA cloned into XhoI site of pBluescript"
BASE COUNT 84 a 177 c 129 g 127 t
ORIGIN
Query Match 5.9%; Score 18; DB 10; Length 517;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 270 cggcaacctctccaactt 287
    |||||||
Db 158 CGGCAACCTCTCCAACCTT 175

RESULT 42
LOCUS BF265245/c
DEFINITION BF265245 521 bp mRNA linear EST 23-OCT-2001
            HV_CEA0011P07f Hordeum vulgare seedling green leaf EST library
            HVCNA0004 (Blumeria challenged) Hordeum vulgare cDNA clone
ACCESSION HV_CEA0011P07f
VERSION   BF265245
KEYWORDS  EST.
SOURCE    barley.
           Hordeum vulgare
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae

```

```

; Triticeae; Hordeum.
1 (bases 1 to 521)
Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Wei,F., Begum,D., Choi
Frisch,D., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi
,D.W., Fenton,R.D., Oates,R. and Main,D.
Development of a genetically and physically anchored EST resource
for barley genomics: Blumeria infected incompatible (Mia13)
seedling leaf cDNA library
Unpublished (2001)
On Nov 17, 2000 this sequence version replaced gi:11196335.
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hg bases = 287
Seq primer: AATTAAACCTCACTAAAGG
High quality sequence stop: 486.
           Location/Qualifiers
             1..521
               /organism="Hordeum vulgare"
               /cultivar="C116155 (Mia13)"
               /db_xref="taxon:4513"
               /clone="HV_CEA0011P07f"
               /clone_lib="Hordeum vulgare seedling green leaf EST
               library HVCNA0004 (Blumeria challenged)"
               /tissue_type="seedling green leaf"
               /lab_host="TJC121"
               /note="Vector: lambdaZAP; Site_1: EcoRI; Site_2: XhoI;
               C.I. 16155 (Mia13) plants were greenhouse grown in the R
               Wise lab at Iowa State University, Ames, IA; 7 day old
               green seedlings were challenged with isolate A27 (AvrMla13
               ) of Blumeria graminis f. sp. hordei, and leaves were
               harvested 20 and 24 hr post-inoculation and snap frozen;
               uninoculated leaves were harvested 20 hr post-inoculation
               (Wei, Wise). In the TJ Close lab at the University of
               California, Riverside, total RNA was prepared from each
               sample pool, equal quantities of all three RNA pools were
               combined, poly(A) RNA was purified from the mixture, one
               cDNA library was made, and 1 million pfu were in vivo
               excised to give pBluescript SK(-) cDNA phagemids (Choi,
               Close). Phagemids were plated and picked at the Clemson
               University Genomics Institute (CUGI) (Begum, Palmer,
               Frisch, Atkins and Wing). Plasmid DNA preparations, DNA
               sequencing and sequence analysis were performed at CUGI
               (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main).
               The sequence has been trimmed to remove vector sequence
               and contains a minimum of 100 bases of phred value 20 or
               above. For more details on library preparation and
               sequence analysis see
               http://www.genome.clemson.edu/projects/barley. To order
               this clone see http://www.genome.clemson.edu/orders Also
               see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
               Genetically and physically anchored EST resources for
               barley genomics. Barley Genetics Newsletter 31:29-30.
               (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)*
BASE COUNT 97 a 198 c 143 g 83 t
ORIGIN
Query Match 5.9%; Score 18; DB 10; Length 521;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 41 tcgggaagtggtggaag 58
    |||||||
Db 388 TCGGGAAGTGGTGGAAG 371

RESULT 43
BM410739/c

```

LOCUS BM410739 524 bp mRNA linear EST 22-JAN-2002
DEFINITION EST585066 tomato breaker fruit Lycopersicon esculentum cDNA clone
CLC54K24 5' end, mRNA sequence.
ACCESSION BM410739
VERSION BM410739.1 GI:18262369
KEYWORDS EST.
SOURCE tomato.
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
1 (bases 1 to 524)
REFERENCE Alcalá, J., Vrebalov, J., White, R., Vision, T., Karamycheva, S.A., Tsai
J., Bougri, O., Kirkness, E., Utterback, T., Van Aken, S., Ronning
C.M., Fraser, C.M., Martin, G.B., Tanksley, S.D. and Giovannoni, J.
Generation of ESTs from tomato fruit tissue, breaker stage (2002)
Unpublished (2002)
COMMENT Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: <http://www.genome.clemson.edu/orders/index.html>
This clone is available through the Clemson University Genomics
Institute
Seq primer: T3.
FEATURES Location/Qualifiers
source 1..524
/organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="CLEG54K24"
/clone_lib="tomato breaker fruit"
/tissue_type="Pericarp"
/dev_stage="breaker"
/lab_host="SOUR"
/note="Vector: pBluescriptSKmCvadapt; Site_1: EcoRI;
Site_2: XhoI; supplier: Boyce Thompson Institute;
sequencing: The Institute for Genomic Research. Fruit
were harvested at the breaker stage (first sign of
lycopene accumulation on the blossom end of fruit). Fruit
were cut in half and the seeds and locules were discarded
prior to freezing the pericarp."
BASE COUNT 153 a 98 c 125 g 148 t
ORIGIN
Query Match 5.9%; Score 18; DB 10; Length 524;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 71 qcaccacaaagggcagca 88
Db 372 GCATCCACAAGGGCAGCA 355
RESULT 44
BF513456/c
LOCUS BF513456 525 bp mRNA linear EST 07-DEC-2000
DEFINITION UI-H-BMI-ams-e-03-0-UI-s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone
IMAGE:3070948 3', mRNA sequence.
ACCESSION BF513456
VERSION BF513456.1 GI:11598635
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 525)
REFERENCE NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Oligo-dT track not found, Not 1 site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: NCI-CGAP clone distribution
Information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward
POLYA-No. Location/Qualifiers
source 1..525
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3070948"
/clone_lib="NCI_CGAP_Sub7"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; NCI_CGAP_Sub7
is a subcloned library derived from NCI_CGAP_Sub6. The
NCI_CGAP_Sub7 library had 12 million recombinants. A
single-stranded DNA preparation of NCI_CGAP_Sub6 was used
as a tracer in a subtractive hybridization with a driver
comprising: the IMAGE pool (NCI_CGAP_Kid3 pool 1 LLAM
3334-3337, 3682-3683, 3798-3803 (IMAGE Clones)
1322376-1323911, 1456008-1456775, 1500552-1502855);
NCI_CGAP_Kid3 pool 1 LLAM 3338-3342, 3722-3725, 3776-3778
(IMAGE Clones) 1323912-1325831, 1471368-1472803,
1492104-1493255); NCI_CGAP_Lus pool 1 LLAM 3575-3582,
3851-3854 (IMAGE Clones) 1414920-1417991, 1520904-1522439
); NCI_CGAP_GC4 pool 1 LLAM 3164-3167, 3716-3720,
3733-3735 (IMAGE Clones) 1257096-1258631, 1469064-1470983
1475592-1476743); NCI_CGAP_Pr22 pool 1 LLAM 2457-2459,
2758-2759, 3062-3068 (IMAGE Clones) 985608-986759,
1101152-1101959, 1217928-1220615); NCI_CGAP_Colo pool 1
LLAM 2644-2653, 2871-2872 (IMAGE Clones) 1037416-1061255
1144584-1145351). (6% of the driver population), plus a
pool of 3,840 arrayed clones from NCI_CGAP_Sub1 (IMAGE
Clones) 2708616-2710535) and NCI_CGAP_Sub2 (IMAGE
Clones) 2710536-2712455) (4% of the driver population
), plus a pool of 11,136 clones from NCI_CGAP_Sub3 (IMAGE
Clones) 2712456-2723591) (10% of the driver population),
plus a pool of 5,472 clones from NCI_CGAP_Sub4 (IMAGE
Clones) 2723592-2729326) (40% of the driver population),
plus a pool of 4032 clones from NCI_CGAP_Sub6 (IMAGE
Clones) 2728969-2733190) (40% of the driver population).
Subtraction was performed as previously described [Bonaldi
, Lennon & Soares (1996)]: Normalization and Subtraction:
Two Approaches to Facilitate Gene Discovery. Genome
Research 6, 791-806.
TAG_SEQ=None found".
BASE COUNT 94 a 195 c 179 g 57 t
ORIGIN
Query Match 5.9%; Score 18; DB 10; Length 525;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 32 acggcgcttcgggaagg 49
Db 97 ACGGCGCTTCGGGAAGG 80
RESULT 45
BJ187298/c
LOCUS BJ187298 528 bp mRNA linear EST 24-JAN-2002
DEFINITION BJ187298 normalized full length cDNA library, chloronema,
caulonema and malformed buds Physcomitrella patens subsp. patens
cDNA clone phb40108 5', mRNA sequence.
ACCESSION BJ187298
VERSION BJ187298.1 GI:18355239
KEYWORDS EST.
SOURCE Physcomitrella patens subsp. patens.

ORGANISM Physcomitrella patens subsp. patens
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
 Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella;
 1 (bases 1 to 528)
 REFERENCE Fujita,T., Shin-i,T., Seki,M., Kamiya,A., Uchiyama,I., Nishiyama,T.
 AUTHORS , Carninci,P., Hayashizaki,Y., Shinozaki,K., Kohara,Y. and Hasebe
 ,M.
 TITLE Comparison of the moss Physcomitrella patens genome with flowering
 plants genome
 JOURNAL Unpublished (2002)
 COMMENT Contact: Tadasu Shin-i
 Center For Genetic Resource Information
 National Institute of Genetics
 1111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tshini@genes.nig.ac.jp
 A backbone of the vector is pBluescript II, that was in vivo
 excised from a modified lps phage vector (Mo bi Tec, Germany). XhoI
 digested-5' end of cDNA is ligated to SalI site of the vector, and
 the BamHI digested-3' end including poly-A tail is ligated to BamHI
 site of the vector. cDNA insert could be amplified with
 conventional T7 and T3 primers. This normalized full-length cDNA
 library was generated basically according to the method described
 in Genome Research 10, 1617-1630 (2000). Carninci, P. et al.
 Protonemata were blended by the POLYTRON, and then cultivated on
 the BCD medium containing 0.5uM BA (benzylaminopurine) for 8 to 13
 days under the continuous light.
 FEATURES Location/Qualifiers
 source
 1..528
 /organism="Physcomitrella patens subsp. patens"
 /db_xref="taxon:145481"
 /clone="ppb40108"
 /clone_lib="normalized full length cDNA library,
 chloronemata, caulonemata and malformed buds"
 /tissue_type="mixture of chloronemata, caulonemata and
 malformed buds"
 BASE COUNT 124 a 114 c 166 g 124 t
 ORIGIN

Query Match 5.9%; Score 18; DB 10; Length 528;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 71 gcatccacaaggccagca 88
 ||||||||||||||||
 Db 92 GCATCCACAGGCGAGCA 75

Search completed: July 15, 2002, 20:07:28
 Job time: 14486 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 16, 2002, 02:56:38 ; Search time 808.35 Seconds
(without alignments)
637.960 Million cell updates/sec

Title: US-09-375-248-1_COPY_2546_2848

Perfect score: 303
Sequence: 1 gagcggctgcacctggggag.....acttctgcgcgccaaagcgg 303

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 1163369 seqs, 850982142 r

Word size :

Total number of hits satisfying chosen parameters: 2326738

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Pending_Patents_NA_New: *

```

1: /cgn2_6/prodata/2/pna/pct_NEW_OMB.seq.*
2: /cgn2_6/prodata/2/pna/us07_NEW_OMB.seq.*
3: /cgn2_6/prodata/2/pna/us08_NEW_OMB.seq.*
4: /cgn2_6/prodata/2/pna/us09_NEW_OMB.seq.*
5: /cgn2_6/prodata/2/pna/us10_NEW_OMB.seq.*
6: /cgn2_6/prodata/2/pna/us16_NEW_OMB.seq.*
7: /cgn2_6/prodata/2/pna/us20_NEW_OMB.seq.*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Query			ID	Description
			Length	DB			
1	303	100.0	4416	5	US-09-053-375B-132	Sequence 132, Appl	
2	303	100.0	4416	5	US-09-042-384B-447	Sequence 447, Appl	
3	23	7.6	23	5	US-09-704-167A-7	Sequence 7, Appl	
4	20	6.6	7680	6	US-10-172-118-711	Sequence 711, Appl	
5	18	5.9	992	6	US-10-027-632-10882	Sequence 10882, A	
6	18	5.9	992	6	US-10-027-632-10883	Sequence 10883, A	
7	18	5.9	2329	6	US-10-172-118-116	Sequence 116, Appl	
8	17	5.6	17	6	US-10-138-674-1913	Sequence 1913, Ap	
9	17	5.6	17	6	US-10-138-674-4731	Sequence 4731, Ap	
10	17	5.6	17	6	US-10-138-674-7615	Sequence 7615, Appl	
11	17	5.6	345	5	US-09-721-544-11540	Sequence 11540, A	
12	17	5.6	439	5	US-09-918-995-28414	Sequence 28414, A	
13	17	5.6	583	6	US-10-027-632-125688	Sequence 125688,	
14	17	5.6	1080	7	US-60-360-039-40648	Sequence 40648, A	
15	17	5.6	1101	5	US-09-663-870A-5	Sequence 5, Appl	
16	17	5.6	1289	6	US-10-153-881-36848	Sequence 36848, A	
17	17	5.6	1406	5	US-09-980-285A-19	Sequence 19, Appl	
18	17	5.6	1557	6	US-10-153-881-17149	Sequence 17149, A	
19	17	5.6	1683	6	US-10-153-881-17151	Sequence 17151, A	
20	17	5.6	1901	6	US-10-103-299-8613	Sequence 8613, Ap	
21	17	5.6	1901	6	US-10-103-299-8616	Sequence 8616, Ap	
22	17	5.6	1901	6	US-10-103-299-9023	Sequence 9023, Ap	
23	17	5.6	4071	6	US-10-022-939-1	Sequence 1, Appl	
24	17	5.6	4230	5	US-09-053-375B-136	Sequence 136, Appl	
25	17	5.6	5885	6	US-10-141-260-7	Sequence 7, Appl	
26	17	5.6	5730	6	US-10-141-260-11	Sequence 11, Appl	

Db 2726 atcggaacacacctcaacgtggtcaacctctcgtggggtgacacaaagccgcagggcccc 2785
Qy 241 ctcattggtgacgtggagttctcaagtcacgcaacctctcctcaacttctctgctgcgcgaag 300
|||||
Db 2786 ctcattggtgacgtggagttctcaagtcacgcaacctctcctcaacttctctgctgcgcgaag 2845
Qy 301 cgg 303
|||
Db 2846 cgg 2848
|||
RESULT 2
US-09-442-384B-447
; Sequence 447, Application US/09442384B
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Lukashov, Matvey
; TITLE OF INVENTION: Hematology/Immunology Array
; FILE REFERENCE: CLON-006CIP15
; CURRENT APPLICATION NUMBER: US/09/442,384B
; CURRENT FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 09/053,375
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 830
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 447
; LENGTH: 4416
; TYPE: DNA
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 4243
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 4243
; OTHER INFORMATION: n = A,T,C or G
US-09-442-384B-447

Query Match 100.0%; Score 303; DB 5; Length 4416;
Best Local Similarity 100.0%; Pred. No. 4.6e-152;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gacggctcacctgggagagtcgtcgctacgctcgcccttcgggaagtggtgaaagcc 60
|||||
Db 2546 gacggctcacctgggagagtcgtcgctacgctcgcccttcgggaagtggtgaaagcc 2605
|||||
Qy 61 tccgcttctcgatccacaaaggcagcagctgtgacacgtggtgaaatgctgaaa 120
|||||
Db 2606 tccgcttctcgatccacaaaggcagcagctgtgacacgtggtgaaatgctgaaa 2665
|||||
Qy 121 gggggccacggccagcagcagcgcgctgctgctggagctcaagatctctattcac 180
|||||
Db 2666 gggggccacggccagcagcagcgcgctgctgctggagctcaagatctctattcac 2725
|||||
Qy 181 atcggaacacacctaactggttgcaacctctctcgtggggtgacacaaagccgcagggcccc 240
|||||
Db 2726 atcggaacacacctaactggttgcaacctctctcgtggggtgacacaaagccgcagggcccc 2785
|||||
Qy 241 ctcattggtgacgtggagttctcaagtcacgcaacctctcctcaacttctctgctgcgcgaag 300
|||||
Db 2786 ctcattggtgacgtggagttctcaagtcacgcaacctctcctcaacttctctgctgcgcgaag 2845
Qy 301 cgg 303
|||
Db 2846 cgg 2848
|||

RESULT 3
US-09-704-167A-7
; Sequence 7, Application US/09704167A
; GENERAL INFORMATION:

; APPLICANT: Havemann, Klaus
; TITLE OF INVENTION: Production and Use of Endothelial-like Cells
; FILE REFERENCE: BPD-100
; CURRENT APPLICATION NUMBER: US/09/704,167A
; CURRENT FILING DATE: 2000-11-01
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: VEGFR-3 5'-primer for RT-PCR, VEGFR-3 GenBank accession no. U009704.1
; OTHER INFORMATION: 020
US-09-704-167A-7

Query Match 7.6%; Score 23; DB 5; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 249 gatcgtggagttctgcaagtacg 271
|||||
Db 1 gatcgtggagttctgcaagtacg 23
|||||

RESULT 4
US-10-172-118-711
; Sequence 711, Application US/10172118
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 711
; LENGTH: 7680
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NM_002019
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-711

Query Match 6.6%; Score 20; DB 6; Length 7680;
Best Local Similarity 100.0%; Pred. No. 0.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 106 gtgaaaaatgctgaagaggg 125
|||||
Db 2827 gtgaaaaatgctgaagaggg 2846
|||||

RESULT 5
US-10-027-632-10882
; Sequence 10882, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129

; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10882
; LENGTH: 992
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-10882

Query Match 5.9%; Score 18; DB 6; Length 992;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 cacctggggagagtgctc 27
|||||

Db 928 cacctggggagagtgctc 945

RESULT 6
US-10-027-632-10883
; Sequence 10883, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10883
; LENGTH: 992
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-10883

Query Match 5.9%; Score 18; DB 6; Length 992;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 cacctggggagagtgctc 27
|||||

Db 928 cacctggggagagtgctc 945

RESULT 7
US-10-172-118-116
; Sequence 116, Application US/10172118
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172.118
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380.770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 116
; LENGTH: 2329
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AF049460
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-116

Query Match 5.9%; Score 18; DB 6; Length 2329;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 acggcgcttcgggaagg 49
|||||

Db 324 acggcgcttcgggaagg 341

RESULT 8
US-10-138-674-1913
; Sequence 1913, Application US/10138674
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138.674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1913
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-1913

Query Match 5.6%; Score 17; DB 6; Length 17;
Best Local Similarity 70.6%; Pred. No. 46;
Matches 12; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 163 ctcaagatctcatcca 179
|:|:|:|:|:|:|:|:|:|

Db 1 cucaagaucuccauuca 17

```
RESULT 9
US-10-138-674-4731
; Sequence 4731, Application US/10138674
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4731
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-4731

Query Match      5.6%; Score 17; DB 6; Length 17;
Best Local Similarity 88.2%; Pred. NO. 46;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 108 gaaatgctgaaagagg 124
      |||||..||..|||||||
Db 1 gaaaaugcugaaagagg 17

RESULT 10
US-10-138-674-7615
; Sequence 7615, Application US/10138674
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7615
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-7615

Query Match      5.6%; Score 17; DB 6; Length 17;
Best Local Similarity 82.4%; Pred. NO. 46;
Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 106 gtgaaaatgctgaaaga 122
      |||||..||..|||||||
Db 1 gugaaaaaugcugaaaga 17

RESULT 11
US-09-721-544-11540/C
; Sequence 11540, Application US/09721544
; GENERAL INFORMATION:
; APPLICANT: Arterburn, Matthew
; APPLICANT: Asghari, Vida
; APPLICANT: Damavandi, Simin
; APPLICANT: Dickson, Mark
; APPLICANT: Drake, Jim
```

```
; APPLICANT: Drmanac, Radoje
; APPLICANT: Engleman, Carrie
; APPLICANT: Faulkner, Brandy
; APPLICANT: Garcia, Veronica
; APPLICANT: Giedt, Gretchen
; APPLICANT: Hunter, Kelly
; APPLICANT: Jessen, Aaron
; APPLICANT: Jones, Lee
; APPLICANT: Kita, David
; APPLICANT: Labat, Ivan
; APPLICANT: Laroya, Mimi
; APPLICANT: Lomelli, Michelle
; APPLICANT: Nguyen, Phuong
; APPLICANT: Nogra, Margie
; APPLICANT: Palencia, Servando
; APPLICANT: Raisi, Fariba
; APPLICANT: Smith, Benjamin
; APPLICANT: Tkach, Joe
; APPLICANT: Tran, Lien
; APPLICANT: Verna, Ron
; APPLICANT: Yang, Fel
; APPLICANT: Yim, Kenneth
; TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
; FILE REFERENCE: 728CIP
; CURRENT APPLICATION NUMBER: US/09/721,544
; CURRENT FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: 09/515,128
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 09/034,341
; PRIOR FILING DATE: 1998-02-13
; NUMBER OF SEQ ID NOS: 24489
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11540
; LENGTH: 345
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-721-544-11540

Query Match      5.6%; Score 17; DB 5; Length 345;
Best Local Similarity 100.0%; Pred. NO. 41;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 95 acaccgtgcccgtgaaa 111
      |||||..||..|||||||
Db 139 ACACCGTGGCGGTGAAA 123

RESULT 12
US-09-918-995-28414
; Sequence 28414, Application US/09918995
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28414
; LENGTH: 439
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)-(439)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-28414
```


Query Match 5.6%; Score 17; DB 5; Length 439;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 17; Conservative 0; Mismatches 0; Indels

Qy 197 acgtgggtcaacctctc 213
|||||
pb 117 acgtgggtcaacctctc 133

Query Match 5.6%; Score 17; DB 6; Length 583;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 93 tgacaccgtggccgtga 109
 |||||
 Db 495 tgacaccgtggccgtga 511

Query Match 5.6%; Score 17; DB 7; Length 1080;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 17; Conservative 0; Mismatches 0; Indels

Qy 281 ccaacttctctgcgcgcc 297
 |||
 Db 179 ccaacttctctgcgcgcc 195

Query Match 5.6%; Score 17; DB 5; Length 1101;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 17; Conservative 0; Mismatches 0; Indels

Qy 197 acgtgggtcaacctctc 213
 |||
 pb 311 acgtgggtcaacctctc 327

Query Match 5.6%; Score 17; DB 6; Length 1269;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

us-09-375-248-1_copy_2546_2848.oli.rnnpn

Tue Jul 16 09:39:23 2002

```
QY 54 ggaagcctccgcttctcg 70
    |||||
Db 671 ggaagcctccgcttctcg 687

RESULT 17
US-09-980-285A-19
; Sequence 19, Application US/09980285A
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: HODGSON, David M.
; APPLICANT: LINCOLN, Stephen E.
; APPLICANT: RUSSO, Frank D.
; APPLICANT: SPIRO, Peter A.
; APPLICANT: BANVILLE, Steve C.
; APPLICANT: BRATCHER, Shawn R.
; APPLICANT: DUFOR, Gerard E.
; APPLICANT: COHEN, Howard J.
; APPLICANT: ROSEN, Bruce
; APPLICANT: CHALUP, Michael S.
; APPLICANT: HILLMAN, Jennifer L.
; APPLICANT: JONES, Annisa L.
; APPLICANT: GREENAWALT, Lila B.
; APPLICANT: PANZER, Scott R.
; APPLICANT: ROSEBERRY, Ann M.
; APPLICANT: WRIGHT, Rachel J.
; APPLICANT: DANIELS, Susan E.
; TITLE OF INVENTION: MOLECULES FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: PT-1022 PCT
; CURRENT FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: 60/137,109; 60/137,337; 60/137,258; 60/137,250; 60/137,113;
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: 60/137,396; 60/137,173; 60/137,411;
; 60/137,417; 60/137,259; 60/137,377; 60/147,520; 60/147,536;
; 60/147,436; 60/147,549; 60/147,377; 60/147,527; 60/147,520; 60/147,536;
; 60/147,530; 60/147,547; 60/147,824; 60/147,541; 60/147,542; 60/147,500
; PRIOR FILING DATE: 1999-06-02; 1999-06-03; 1999-06-02; 1999-06-02; 1999-06-03;
; 1999-06-03; 1999-06-02; 1999-06-03; 1999-06-02; 1999-06-03;
; 1999-08-04; 1999-08-05; 1999-08-04; 1999-08-05; 1999-08-05;
; 1999-08-05; 1999-08-05; 1999-08-05; 1999-08-05; 1999-08-05
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PERL Program
; SEQ ID NO 19
; LENGTH: 1406
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 366739.2
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 311
; OTHER INFORMATION: a, t, c, g, or other
US-09-980-285A-19

Query Match 5.6%; Score 17; DB 5; Length 1406;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 276 ccttccaaacttctgc 292
    |||||
Db 227 ccttccaaacttctgc 243

RESULT 18
US-10-155-881-17149
; Sequence 17149, Application US/10155881
; GENERAL INFORMATION:
; APPLICANT: Dotson, Stanton B.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong

Query Match 5.6%; Score 17; DB 6; Length 1557;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 ggaagcctccgcttctcg 70
    |||||
Db 705 ggaagcctccgcttctcg 721

RESULT 19
US-10-155-881-17151
; Sequence 17151, Application US/10155881
; GENERAL INFORMATION:
; APPLICANT: Dotson, Stanton B.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; APPLICANT: Lutfiyya, Linda L.
; APPLICANT: McIninch, James
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; FILE REFERENCE: 38-21(15300)J
; CURRENT APPLICATION NUMBER: US/10/155,881
; CURRENT FILING DATE: 2002-05-22
; NUMBER OF SEQ ID NOS: 37595
; SEQ ID NO 17151
; LENGTH: 1683
; TYPE: DNA
; ORGANISM: Glycine max
US-10-155-881-17151

Query Match 5.6%; Score 17; DB 6; Length 1683;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 ggaagcctccgcttctcg 70
    |||||
Db 895 ggaagcctccgcttctcg 911

RESULT 20
US-10-105-299-8613
; Sequence 8613, Application US/10105299
; GENERAL INFORMATION:
; APPLICANT: Rosen, et. al
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS950
; CURRENT APPLICATION NUMBER: US/10/105,299
; CURRENT FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 15197
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8613
; LENGTH: 1901
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-105-299-8613
```

Query Match 5.6%; Score 17; DB 6; Length 1901;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 276 cctctccaactctctgc 292
|||||
Db 620 cctctccaactctctgc 636

RESULT 21
US-10-105-299-8616
; Sequence 8616, Application US/10105299
; GENERAL INFORMATION:
; APPLICANT: Rosen, et. al
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS950
; CURRENT APPLICATION NUMBER: US/10/105,299
; CURRENT FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 15197
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8616
; LENGTH: 1901
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-105-299-8616

Query Match 5.6%; Score 17; DB 6; Length 1901;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 276 cctctccaactctctgc 292
|||||
Db 620 cctctccaactctctgc 636

RESULT 22
US-10-105-299-9023/c
; Sequence 9023, Application US/10105299
; GENERAL INFORMATION:
; APPLICANT: Rosen, et. al
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS950
; CURRENT APPLICATION NUMBER: US/10/105,299
; CURRENT FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 15197
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9023
; LENGTH: 1901
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-105-299-9023

Query Match 5.6%; Score 17; DB 6; Length 1901;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 276 cctctccaactctctgc 292
|||||
Db 1282 CCTCTCCAACCTCTCTGC 1266

RESULT 23
US-10-022-939-1
; Sequence 1, Application US/10022939
; GENERAL INFORMATION:
; APPLICANT: Kendall, Richard L.
; APPLICANT: Thomas, Kenneth A.
; APPLICANT: Mao, Xianzhi

; APPLICANT: Tebben, Andrew
; TITLE OF INVENTION: HUMAN RECEPTOR TYROSINE KINASE, KDR
; FILE REFERENCE: 19963YDB
; CURRENT APPLICATION NUMBER: US/10/022,939
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: 09/483,539
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 09/098,707
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/050,962
; PRIOR FILING DATE: 1997-06-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4071
; TYPE: DNA
; ORGANISM: Human
US-10-022-939-1

Query Match 5.6%; Score 17; DB 6; Length 4071;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 163 ctcaagatctctcttca 179
|||||
Db 2656 ctcaagatctctcttca 2672

RESULT 24
US-09-053-375B-136
; Sequence 136, Application US/09053375B
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Bibilashvili, Robert
; TITLE OF INVENTION: Nucleic Acid Arrays
; FILE REFERENCE: CLON-006
; CURRENT APPLICATION NUMBER: US/09/053,375B
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 1543
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 136
; LENGTH: 4230
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-053-375B-136

Query Match 5.6%; Score 17; DB 5; Length 4230;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 163 ctcaagatctctcttca 179
|||||
Db 2650 ctcaagatctctcttca 2666

RESULT 25
US-10-141-260-7
; Sequence 7, Application US/10141260
; GENERAL INFORMATION:
; APPLICANT: Yu, Xuanchuan
; APPLICANT: Miranda, Maricar
; APPLICANT: Wilganowski, Nathaniel L.
; TITLE OF INVENTION: Novel Human Semaphorin Receptors and Polynucleotides Encoding
; FILE REFERENCE: LEX-0341-USA
; CURRENT APPLICATION NUMBER: US/10/141,260
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US 60/289,424
; PRIOR FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 7
; LENGTH: 5685
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-141-260-7

Query Match 5.6%; Score 17; DB 6; Length 5685;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 catccacaaggcgagca 88
|||||
Db 5280 catccacaaggcgagca 5296

RESULT 26
US-10-141-260-11
; Sequence 11, Application US/10141260
; GENERAL INFORMATION:
; APPLICANT: Yu, Xuanchuan
; APPLICANT: Miranda, Maricar
; APPLICANT: Wilganowski, Nathaniel L.
; TITLE OF INVENTION: Novel Human Semaphorin Receptors and Polynucleotides Encoding the
; FILE OF INVENTION: Same
; FILE REFERENCE: LEX-0341-USA
; CURRENT APPLICATION NUMBER: US/10/141,260
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US 60/289,424
; PRIOR FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 5730
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-141-260-11

Query Match 5.6%; Score 17; DB 6; Length 5730;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 catccacaaggcgagca 88
|||||
Db 5325 catccacaaggcgagca 5341

RESULT 27
US-10-116-802-18
; Sequence 18, Application US/10116802
; GENERAL INFORMATION:
; APPLICANT: Amy Lasek
; TITLE OF INVENTION: GENES EXPRESSED IN LUNG CANCER
; FILE REFERENCE: PA-0045 US
; CURRENT APPLICATION NUMBER: US/10/116,802
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 60/281,593
; PRIOR FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 519
; SOFTWARE: PERL Program
; SEQ ID NO 18
; LENGTH: 5832
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 247817.4
US-10-116-802-18

Query Match 5.6%; Score 17; DB 6; Length 5832;
Best Local Similarity 100.0%; Pred. No. 37;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 163 ctcaagatctctattca 179
|||||
Db 2959 ctcaagatctctattca 2975

RESULT 28
US-10-133-013-269
; Sequence 269, Application US/10133013
; GENERAL INFORMATION:
; APPLICANT: Astromoff, Anna
; APPLICANT: Bandman, Olga
; APPLICANT: Cocks, Benjamin G.
; TITLE OF INVENTION: GENES ASSOCIATED WITH VASCULAR DISEASE
; FILE REFERENCE: PA-0049 US
; CURRENT APPLICATION NUMBER: US/10/133,013
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: 60/287,067
; PRIOR FILING DATE: 2001-04-27
; NUMBER OF SEQ ID NOS: 271
; SOFTWARE: PERL Program
; SEQ ID NO 269
; LENGTH: 5841
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 247817.4
US-10-133-013-269

Query Match 5.6%; Score 17; DB 6; Length 5841;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 163 ctcaagatctctattca 179
|||||
Db 2959 ctcaagatctctattca 2975

RESULT 29
US-10-141-260-3
; Sequence 3, Application US/10141260
; GENERAL INFORMATION:
; APPLICANT: Yu, Xuanchuan
; APPLICANT: Miranda, Maricar
; APPLICANT: Wilganowski, Nathaniel L.
; TITLE OF INVENTION: Novel Human Semaphorin Receptors and Polynucleotides Encoding
; FILE OF INVENTION: Same
; FILE REFERENCE: LEX-0341-USA
; CURRENT APPLICATION NUMBER: US/10/141,260
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US 60/289,424
; PRIOR FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 5847
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-141-260-3

Query Match 5.6%; Score 17; DB 6; Length 5847;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 catccacaaggcgagca 88
|||||
Db 5442 catccacaaggcgagca 5458

```
RESULT 30
US-10-141-260-5
; Sequence 5, Application US/10141260
; GENERAL INFORMATION:
; APPLICANT: Yu, Xuanchuan
; APPLICANT: Miranda, Maricar
; APPLICANT: Wilganowski, Nathaniel L.
; TITLE OF INVENTION: Novel Human Semaphorin Receptors and Polynucleotides Encoding the
; FILE REFERENCE: Same
; FILE REFERENCE: LEX-0341-USA
; CURRENT APPLICATION NUMBER: US/10/141,260
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US 60/289,424
; PRIOR FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 5880
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-141-260-5

Query Match          5.6%; Score 17; DB 6; Length 5880;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 72 catccacaaggcgagca 88
Db 5475 catccacaaggcgagca 5491
|||||

RESULT 31
US-10-141-260-9
; Sequence 9, Application US/10141260
; GENERAL INFORMATION:
; APPLICANT: Yu, Xuanchuan
; APPLICANT: Miranda, Maricar
; APPLICANT: Wilganowski, Nathaniel L.
; TITLE OF INVENTION: Novel Human Semaphorin Receptors and Polynucleotides Encoding the
; FILE REFERENCE: Same
; FILE REFERENCE: LEX-0341-USA
; CURRENT APPLICATION NUMBER: US/10/141,260
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US 60/289,424
; PRIOR FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 5925
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-141-260-9

Query Match          5.6%; Score 17; DB 6; Length 5925;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 72 catccacaaggcgagca 88
Db 5520 catccacaaggcgagca 5536
|||||

RESULT 32
US-10-141-260-1
; Sequence 1, Application US/10141260
; GENERAL INFORMATION:
; APPLICANT: Yu, Xuanchuan
; APPLICANT: Miranda, Maricar
; APPLICANT: Wilganowski, Nathaniel L.
; TITLE OF INVENTION: Novel Human Semaphorin Receptors and Polynucleotides Encoding the
; FILE REFERENCE: Same
```

```
; FILE REFERENCE: LEX-0341-USA
; CURRENT APPLICATION NUMBER: US/10/141,260
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US 60/289,424
; PRIOR FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 6042
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-141-260-1

Query Match          5.6%; Score 17; DB 6; Length 6042;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 72 catccacaaggcgagca 88
Db 5637 catccacaaggcgagca 5653
|||||

RESULT 33
PCT-US02-09944-259
; Sequence 259, Application PC/TUS0209944
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: DAFPO, Abel
; APPLICANT: JONES, Anissa L.
; APPLICANT: TRAN, Alanna-Phung B.
; APPLICANT: DAHL, Christopher R.
; APPLICANT: GIETZEN, Barryl
; APPLICANT: CHINN, Joyce
; APPLICANT: DUFOUR, Gerard E.
; APPLICANT: HILLMAN, Jennifer L.
; APPLICANT: YU, Jimmy Y.
; APPLICANT: TUASON, Olivia
; APPLICANT: YAP, Pierre E.
; APPLICANT: AMSHEY, Stefan R.
; APPLICANT: DAUGHERTY, Sean C.
; APPLICANT: LIU, Tommy F.
; APPLICANT: NGUYEN, Duy-Viet An
; APPLICANT: KLESEFELD, Yael
; APPLICANT: GERSTIN, JR., Edward H.
; APPLICANT: PERALTA, Careyana H.
; APPLICANT: DAVID, Marie H.
; APPLICANT: LEWIS, Samantha A.
; APPLICANT: CHEN, Alice J.
; APPLICANT: PANZER, Scott R.
; APPLICANT: HARRIS, Bernard
; APPLICANT: FLORES, Vincent
; APPLICANT: MARWAHA, Rakesh
; APPLICANT: LO, Audrey
; APPLICANT: LAN, Ruth Y.
; APPLICANT: URASHKA, Michael E.
; TITLE OF INVENTION: MOLECULES FOR DISEASE DETECTION AND TREATMENT
; FILE REFERENCE: PT-1231 PCT
; CURRENT APPLICATION NUMBER: PCT/US02/09944
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: 60/280,067; 60/279,619; 60/280,068; 60/291,280; 60/291,8
; 60/291,829; 60/299,428; 60/300,001; 60/299,776
; PRIOR FILING DATE: 2001-03-29; 2001-03-28; 2001-03-29; 2001-05-16; 2001-05-17;
; 2001-05-17; 2001-06-19; 2001-06-20; 2001-06-20
; NUMBER OF SEQ ID NOS: 792
; SOFTWARE: PERL Program
; SEQ ID NO 259
; LENGTH: 7136
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
```

; OTHER INFORMATION: Incyte ID NO: LI:355693.18:2001WAY17
PCT-US02-09944-259

Query Match 5.6%; Score 17; DB 1; Length 7136;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 72 catccacaaggcgagca 88
|||||
Db 5985 catccacaaggcgagca 6001

RESULT 34

US-10-172-118-988/c
; Sequence 988, Application US/10172118
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linslev, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 988
; LENGTH: 7515
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NM_004104
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-988

Query Match 5.6%; Score 17; DB 5; Length 7515;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 83 gcacgacgtgtgacacc 99
|||||
Db 1612 GCAGCAGCTGTGACACC 1596

RESULT 35

US-10-138-674-5819
; Sequence 5819, Application US/10138674
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBH800-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5819
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-5819

Query Match 5.3%; Score 16; DB 6; Length 16;
Best Local Similarity 81.2%; Pred. No. 1.6e+02;
Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 107 tgaaaatgctgaaaga 122
:||||:|:|||||
Db 1 ugaaaavgcugaaaga 16

RESULT 36

US-10-138-674-6641
; Sequence 6641, Application US/10138674
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Condition
; FILE REFERENCE: MBH800-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6641
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-6641

Query Match 5.3%; Score 16; DB 6; Length 17;
Best Local Similarity 68.8%; Pred. No. 1.6e+02;
Matches 11; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 164 tcaagatctctcatcca 179
:||||:|:|||||
Db 1 ucaagaucuccauca 16

RESULT 37

US-09-539-800C-4548/c
; Sequence 4548, Application US/09539800C
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Delegeane, Angelo M.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Mullahy, Sara J.
; APPLICANT: Naughton, Rebecca E.
; TITLE OF INVENTION: POLYNUCLEOTIDES OF CONNECTIVE TISSUE
; FILE REFERENCE: PD-1023 CIP
; CURRENT APPLICATION NUMBER: US/09/539,800C
; CURRENT FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: 08/521,383
; PRIOR FILING DATE: August 16, 1995
; PRIOR APPLICATION NUMBER: 08/271,217
; PRIOR FILING DATE: June 27, 1994
; PRIOR APPLICATION NUMBER: 08/334,881
; PRIOR FILING DATE: November 4, 1994
; PRIOR APPLICATION NUMBER: 08/943,978
; PRIOR FILING DATE: October 3, 1997
; PRIOR APPLICATION NUMBER: 60/028,732
; PRIOR FILING DATE: October 4, 1996
; PRIOR APPLICATION NUMBER: 08/943,979
; PRIOR FILING DATE: October 4, 1997
; PRIOR APPLICATION NUMBER: 60/027,782
; PRIOR FILING DATE: October 4, 1996
; PRIOR APPLICATION NUMBER: 08/993,774
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/034,975

; PRIOR FILING DATE: December 20, 1996
; PRIOR APPLICATION NUMBER: 09/250,003
; PRIOR FILING DATE: February 10, 1999
; PRIOR APPLICATION NUMBER: 60/074,364
; PRIOR FILING DATE: February 12, 1998
; PRIOR APPLICATION NUMBER: 09/452,747
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: 60/111,910
; PRIOR FILING DATE: December 10, 1998
; NUMBER OF SEQ ID NOS: 19698
; SOFTWARE: PERL Program
; SEQ ID NO 4548
; LENGTH: 198
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No: hu00608208
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 54, 66-67, 85
; OTHER INFORMATION: a, t, c, g, or other
US-09-539-800C-4548

Query Match 5.3%; Score 16; DB 5; Length 198;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 81 gggcagcagctgtgac 96
|||||
Db 163 GGCACGACGCTGTGAC 148

RESULT 38

US-09-540-210B-7506/c
; Sequence 7506, Application US/09540210B
; GENERAL INFORMATION:
; APPLICANT: Selihamer, Jeffrey J.
; APPLICANT: Delegeane, Angelo M.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Mullahy, Sara J.
; APPLICANT: Naughton, Rebecca E.
; TITLE OF INVENTION: POLYNUCLEOTIDES OF URINARY TRACT TISSUE
; FILE REFERENCE: PD-1037 CIP
; CURRENT APPLICATION NUMBER: US/09/540,210B
; CURRENT FILING DATE: 2002-04-03
; PRIOR FILING DATE: November 18, 1997
; PRIOR APPLICATION NUMBER: 08/972,899
; PRIOR FILING DATE: February 27, 1995
; PRIOR APPLICATION NUMBER: 08/395,244
; PRIOR FILING DATE: September 27, 1996
; PRIOR APPLICATION NUMBER: 08/722,922
; PRIOR FILING DATE: September 29, 1995
; PRIOR APPLICATION NUMBER: 60/005,526
; PRIOR FILING DATE: March 25, 1997
; PRIOR APPLICATION NUMBER: 08/824,029
; PRIOR FILING DATE: March 25, 1996
; PRIOR APPLICATION NUMBER: 08/826,847
; PRIOR FILING DATE: April 10, 1997
; PRIOR APPLICATION NUMBER: 60/015,533
; PRIOR FILING DATE: April 10, 1996
; PRIOR APPLICATION NUMBER: 08/903,555
; PRIOR FILING DATE: July 31, 1997
; PRIOR APPLICATION NUMBER: 60/023,308
; PRIOR FILING DATE: July 31, 1996
; PRIOR APPLICATION NUMBER: 08/862,178
; PRIOR FILING DATE: May 22, 1997
; PRIOR APPLICATION NUMBER: 60/018,217
; PRIOR FILING DATE: May 23, 1996
; PRIOR APPLICATION NUMBER: 08/881,589
; PRIOR FILING DATE: June 24, 1997
; PRIOR APPLICATION NUMBER: 60/021,275
; PRIOR FILING DATE: June 25, 1996
; PRIOR APPLICATION NUMBER: 08/903,802
; PRIOR FILING DATE: July 31, 1997
; PRIOR APPLICATION NUMBER: 60/023,308
; PRIOR FILING DATE: July 31, 1996
; PRIOR APPLICATION NUMBER: 08/905,881
; PRIOR FILING DATE: August 1, 1997
; PRIOR APPLICATION NUMBER: 60/025,204
; PRIOR FILING DATE: August 1, 1996
; PRIOR APPLICATION NUMBER: 08/903,471
; PRIOR FILING DATE: July 30, 1997
; PRIOR APPLICATION NUMBER: 60/025,478
; PRIOR FILING DATE: July 31, 1996
; PRIOR APPLICATION NUMBER: 08/903,556
; PRIOR FILING DATE: July 31, 1997
; PRIOR APPLICATION NUMBER: 60/025,217
; PRIOR FILING DATE: August 22, 1996
; PRIOR APPLICATION NUMBER: 08/937,142
; PRIOR FILING DATE: September 23, 1997
; PRIOR APPLICATION NUMBER: 60/026,598
; PRIOR FILING DATE: September 24, 1996
; PRIOR APPLICATION NUMBER: 08/960,746
; PRIOR FILING DATE: October 29, 1997
; PRIOR APPLICATION NUMBER: 60/030,144
; PRIOR FILING DATE: October 30, 1996
; PRIOR APPLICATION NUMBER: 08/826,847
; PRIOR FILING DATE: April 10, 1997
; PRIOR APPLICATION NUMBER: 60/015,533
; PRIOR FILING DATE: April 10, 1996
; PRIOR APPLICATION NUMBER: 08/755,524
; PRIOR FILING DATE: November 22, 1996
; PRIOR APPLICATION NUMBER: 60/007,495
; PRIOR FILING DATE: November 22, 1995
; PRIOR APPLICATION NUMBER: 09/021,031
; PRIOR FILING DATE: February 10, 1998
; PRIOR APPLICATION NUMBER: 60/039,325
; PRIOR FILING DATE: February 13, 1997
; PRIOR APPLICATION NUMBER: 09/035,172
; PRIOR FILING DATE: March 4, 1998
; PRIOR APPLICATION NUMBER: 60/040,431
; PRIOR FILING DATE: March 5, 1997
; PRIOR APPLICATION NUMBER: 09/041,894
; PRIOR FILING DATE: March 12, 1998
; PRIOR APPLICATION NUMBER: 60/040,199
; PRIOR FILING DATE: March 14, 1997
; PRIOR APPLICATION NUMBER: 09/050,817
; PRIOR FILING DATE: March 30, 1998
; PRIOR APPLICATION NUMBER: 60/043,792
; PRIOR FILING DATE: April 11, 1997
; PRIOR APPLICATION NUMBER: 09/074,999
; PRIOR FILING DATE: May 8, 1998
; PRIOR APPLICATION NUMBER: 60/048,431
; PRIOR FILING DATE: May 29, 1997
; PRIOR APPLICATION NUMBER: 09/107,592
; PRIOR FILING DATE: June 30, 1998
; PRIOR APPLICATION NUMBER: 60/052,751
; PRIOR FILING DATE: July 1, 1997
; PRIOR APPLICATION NUMBER: 09/094,079
; PRIOR FILING DATE: June 9, 1998
; PRIOR APPLICATION NUMBER: 60/049,975
; PRIOR FILING DATE: June 13, 1997
; NUMBER OF SEQ ID NOS: 35654
; SOFTWARE: PERL Program
; SEQ ID NO 7506
; LENGTH: 213
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No: hu00129794
US-09-540-210B-7506

Query Match 5.3%; Score 16; DB 5; Length 213;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 gggcagcagctgtgac 96
|||||
DB 195 GGCAGCAGCTGTGAC 180

RESULT 39

US-09-539-331D-26866/c
; Sequence 26866, Application US/09539331D
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Deleageane, Angelo M.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Mullahy, Sara J.
; APPLICANT: Naughton, Rebecca E.
; TITLE OF INVENTION: POLYNUCLEOTIDES OF CARDIOVASCULAR SYSTEM TISSUE
; FILE REFERENCE: PD-1022 CIP
; CURRENT APPLICATION NUMBER: US/09/539,331D
; CURRENT FILING DATE: 2000-03-30
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 40961
; SOFTWARE: PERL Program
; SEQ ID NO 26866
; LENGTH: 349
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: hu00486369
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 26, 37, 75, 79, 128, 207, 250, 285, 288, 291, 308, 339
; OTHER INFORMATION: a, t, c, g, or other
US-09-539-331D-26866

Query Match 5.3%; Score 16; DB 5; Length 349;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 gggcagcagctgtgac 96
|||||
DB 171 GGCAGCAGCTGTGAC 156

RESULT 40

US-10-027-632-186248
; Sequence 186248, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28

; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 186248
; LENGTH: 468
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-186248

Query Match 5.3%; Score 16; DB 6; Length 468;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 163 ctcaagatctctcattc 178
|||||
DB 129 ctcaagatctctcattc 144

RESULT 41

US-09-918-995-37903
; Sequence 37903, Application US/09918995
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 37903
; LENGTH: 494
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(494)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-37903

Query Match 5.3%; Score 16; DB 5; Length 494;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 gggcagcagctgtgac 96
|||||
DB 82 gggcagcagctgtgac 97

RESULT 42

US-60-377-240-10518
; Sequence 10518, Application US/60377240
; GENERAL INFORMATION:
; APPLICANT: Diggans, James C.
; APPLICANT: Porter, Mark
; APPLICANT: Wei, Tao
; TITLE OF INVENTION: Canine Gene Microarrays for Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5115-PR
; CURRENT APPLICATION NUMBER: US/60/377,240
; CURRENT FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 11109
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10518
; LENGTH: 533
; TYPE: DNA
; ORGANISM: Canis familiaris


```
; FEATURE:
; OTHER INFORMATION:
; NAME/KEY: misc_feature
; LOCATION: (1)...(533)
; OTHER INFORMATION: n = a or c or g or t
US-60-377-240-10518
```

Query Match 5.3%; Score 16; DB 7; Length 533;

Best Local Similarity 100.0%; Pred. No. 1.4e+02;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Oy 227 agccgcagggccccct 242
Db 280 agccgcagggccccct 295
|||||
```

RESULT 43

US-10-027-632-278270/c

; Sequence 278270, Application US/10027632

; GENERAL INFORMATION:

; APPLICANT: Wang, David G.

; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

; FILE REFERENCE: 108827.129

; CURRENT APPLICATION NUMBER: US/10/027,632

; CURRENT FILING DATE: 2002-04-30

; PRIOR APPLICATION NUMBER: US 60/218,006

; PRIOR FILING DATE: 2000-07-12

; PRIOR APPLICATION NUMBER: US 60/198,676

; PRIOR FILING DATE: 2000-04-20

; PRIOR APPLICATION NUMBER: US 60/193,483

; PRIOR FILING DATE: 2000-03-29

; PRIOR APPLICATION NUMBER: US 60/185,218

; PRIOR FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: US 60/167,363

; PRIOR FILING DATE: 1999-11-23

; PRIOR APPLICATION NUMBER: US 60/156,358

; PRIOR FILING DATE: 1999-09-28

; PRIOR APPLICATION NUMBER: US 60/146,002

; PRIOR FILING DATE: 1999-08-09

; NUMBER OF SEQ ID NOS: 325720

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 278270

; LENGTH: 543

; TYPE: DNA

; ORGANISM: Human

US-10-027-632-278270

Query Match 5.3%; Score 16; DB 6; Length 543;

Best Local Similarity 100.0%; Pred. No. 1.4e+02;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Oy 106 gtgaaatgctgaaag 121
Db 23 GTGAAATGCTGAAAG 8
|||||
```

RESULT 44

US-10-027-632-89410

; Sequence 89410, Application US/10027632

; GENERAL INFORMATION:

; APPLICANT: Wang, David G.

; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

; FILE REFERENCE: 108827.129

; CURRENT APPLICATION NUMBER: US/10/027,632

; CURRENT FILING DATE: 2002-04-30

; PRIOR APPLICATION NUMBER: US 60/218,006

; PRIOR FILING DATE: 2000-07-12

; PRIOR APPLICATION NUMBER: US 60/198,676

```
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 89410
; LENGTH: 568
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(568)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-89410
```

Query Match 5.3%; Score 16; DB 6; Length 568;

Best Local Similarity 100.0%; Pred. No. 1.4e+02;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Oy 74 tcacaaagggcagcag 89
Db 439 tcacaaagggcagcag 454
|||||
```

RESULT 45

US-10-027-632-303937

; Sequence 303937, Application US/10027632

; GENERAL INFORMATION:

; APPLICANT: Wang, David G.

; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

; FILE REFERENCE: 108827.129

; CURRENT APPLICATION NUMBER: US/10/027,632

; CURRENT FILING DATE: 2002-04-30

; PRIOR APPLICATION NUMBER: US 60/218,006

; PRIOR FILING DATE: 2000-07-12

; PRIOR APPLICATION NUMBER: US 60/198,676

; PRIOR FILING DATE: 2000-04-20

; PRIOR APPLICATION NUMBER: US 60/193,483

; PRIOR FILING DATE: 2000-03-29

; PRIOR APPLICATION NUMBER: US 60/185,218

; PRIOR FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: US 60/167,363

; PRIOR FILING DATE: 1999-11-23

; PRIOR APPLICATION NUMBER: US 60/156,358

; PRIOR FILING DATE: 1999-09-28

; PRIOR APPLICATION NUMBER: US 60/146,002

; PRIOR FILING DATE: 1999-08-09

; NUMBER OF SEQ ID NOS: 325720

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 303937

; LENGTH: 568

; TYPE: DNA

; ORGANISM: Human

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (1)...(568)

; OTHER INFORMATION: n = A,T,C or G

US-10-027-632-303937

Query Match 5.3%; Score 16; DB 6; Length 568;

Best Local Similarity 100.0%; Pred. No. 1.4e+02;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 74 tccacaagggcagcag 89
|||||
Db 439 tccacaagggcagcag 454

Search completed: July 16, 2002, 02:56:48
Job time: 24546 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 16, 2002, 02:49:40 ; Search time 12941.8 Seconds
(without alignments)
506.528 Million cell updates/sec

Title: us-09-375-248-1_copy_2546_2848

Perfect score: 303

Sequence: 1 gagcgctcacctggggag.....acttctgcgcgaagcgg 303

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 21979536 seqs, 10817449327 residues

Word size : 0

Total number of hits satisfying chosen parameters: 43959072

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Pending_Patents_NA_Main.*

- 1: /cgn2_6/ptodata/2/pna/PCTUS_COMB.seq.*
- 2: /cgn2_6/ptodata/2/pna/US06_COMB.seq.*
- 3: /cgn2_6/ptodata/2/pna/US07_COMB.seq.*
- 4: /cgn2_6/ptodata/2/pna/US080_COMB.seq.*
- 5: /cgn2_6/ptodata/2/pna/US081_COMB.seq.*
- 6: /cgn2_6/ptodata/2/pna/US082_COMB.seq.*
- 7: /cgn2_6/ptodata/2/pna/US083_COMB.seq.*
- 8: /cgn2_6/ptodata/2/pna/US084_COMB.seq.*
- 9: /cgn2_6/ptodata/2/pna/US085_COMB.seq.*
- 10: /cgn2_6/ptodata/2/pna/US086_COMB.seq.*
- 11: /cgn2_6/ptodata/2/pna/US087_COMB.seq.*
- 12: /cgn2_6/ptodata/2/pna/US088_COMB.seq.*
- 13: /cgn2_6/ptodata/2/pna/US089_COMB.seq.*
- 14: /cgn2_6/ptodata/2/pna/US090_COMB.seq.*
- 15: /cgn2_6/ptodata/2/pna/US091_COMB.seq.*
- 16: /cgn2_6/ptodata/2/pna/US092_COMB.seq.*
- 17: /cgn2_6/ptodata/2/pna/US093_COMB.seq.*
- 18: /cgn2_6/ptodata/2/pna/US094_COMB.seq.*
- 19: /cgn2_6/ptodata/2/pna/US095A_COMB.seq.*
- 20: /cgn2_6/ptodata/2/pna/US095B_COMB.seq.*
- 21: /cgn2_6/ptodata/2/pna/US095C_COMB.seq.*
- 22: /cgn2_6/ptodata/2/pna/US095D_COMB.seq.*
- 23: /cgn2_6/ptodata/2/pna/US096A_COMB.seq.*
- 24: /cgn2_6/ptodata/2/pna/US096B_COMB.seq.*
- 25: /cgn2_6/ptodata/2/pna/US096C_COMB.seq.*
- 26: /cgn2_6/ptodata/2/pna/US096D_COMB.seq.*
- 27: /cgn2_6/ptodata/2/pna/US096E_COMB.seq.*
- 28: /cgn2_6/ptodata/2/pna/US097A_COMB.seq.*
- 29: /cgn2_6/ptodata/2/pna/US097B_COMB.seq.*
- 30: /cgn2_6/ptodata/2/pna/US097C_COMB.seq.*
- 31: /cgn2_6/ptodata/2/pna/US098A_COMB.seq.*
- 32: /cgn2_6/ptodata/2/pna/US098B_COMB.seq.*
- 33: /cgn2_6/ptodata/2/pna/US098C_COMB.seq.*
- 34: /cgn2_6/ptodata/2/pna/US099A_COMB.seq.*
- 35: /cgn2_6/ptodata/2/pna/US099B_COMB.seq.*
- 36: /cgn2_6/ptodata/2/pna/US099C_COMB.seq.*
- 37: /cgn2_6/ptodata/2/pna/US100_COMB.seq.*
- 38: /cgn2_6/ptodata/2/pna/US101_COMB.seq.*
- 39: /cgn2_6/ptodata/2/pna/US6000_COMB.seq.*
- 40: /cgn2_6/ptodata/2/pna/US6001_COMB.seq.*
- 41: /cgn2_6/ptodata/2/pna/US6002_COMB.seq.*
- 42: /cgn2_6/ptodata/2/pna/US6003_COMB.seq.*
- 43: /cgn2_6/ptodata/2/pna/US6004_COMB.seq.*

- 44: /cgn2_6/ptodata/2/pna/US6005_COMB.seq.*
- 45: /cgn2_6/ptodata/2/pna/US6006_COMB.seq.*
- 46: /cgn2_6/ptodata/2/pna/US6007_COMB.seq.*
- 47: /cgn2_6/ptodata/2/pna/US6008_COMB.seq.*
- 48: /cgn2_6/ptodata/2/pna/US6009_COMB.seq.*
- 49: /cgn2_6/ptodata/2/pna/US6010_COMB.seq.*
- 50: /cgn2_6/ptodata/2/pna/US6011_COMB.seq.*
- 51: /cgn2_6/ptodata/2/pna/US6012_COMB.seq.*
- 52: /cgn2_6/ptodata/2/pna/US6013_COMB.seq.*
- 53: /cgn2_6/ptodata/2/pna/US6014_COMB.seq.*
- 54: /cgn2_6/ptodata/2/pna/US6015_COMB.seq.*
- 55: /cgn2_6/ptodata/2/pna/US6016_COMB.seq.*
- 56: /cgn2_6/ptodata/2/pna/US6017_COMB.seq.*
- 57: /cgn2_6/ptodata/2/pna/US6018_COMB.seq.*
- 58: /cgn2_6/ptodata/2/pna/US6019_COMB.seq.*
- 59: /cgn2_6/ptodata/2/pna/US6020_COMB.seq.*
- 60: /cgn2_6/ptodata/2/pna/US6021_COMB.seq.*
- 61: /cgn2_6/ptodata/2/pna/US6022_COMB.seq.*
- 62: /cgn2_6/ptodata/2/pna/US6023_COMB.seq.*
- 63: /cgn2_6/ptodata/2/pna/US6024_COMB.seq.*
- 64: /cgn2_6/ptodata/2/pna/US6025_COMB.seq.*
- 65: /cgn2_6/ptodata/2/pna/US6026_COMB.seq.*
- 66: /cgn2_6/ptodata/2/pna/US6027_COMB.seq.*
- 67: /cgn2_6/ptodata/2/pna/US6028_COMB.seq.*
- 68: /cgn2_6/ptodata/2/pna/US6029_COMB.seq.*
- 69: /cgn2_6/ptodata/2/pna/US6030_COMB.seq.*
- 70: /cgn2_6/ptodata/2/pna/US6031_COMB.seq.*
- 71: /cgn2_6/ptodata/2/pna/US6032_COMB.seq.*
- 72: /cgn2_6/ptodata/2/pna/US6033_COMB.seq.*
- 73: /cgn2_6/ptodata/2/pna/US6034_COMB.seq.*
- 74: /cgn2_6/ptodata/2/pna/US6035_COMB.seq.*
- 75: /cgn2_6/ptodata/2/pna/US6036_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	303	100.0	4111	1	PCT-US99-06133-1
2	303	100.0	4111	17	US-09-375-248-1
3	303	100.0	4195	3	US-07-959-951A-1
4	303	100.0	4195	6	US-08-257-754-1
5	303	100.0	4195	15	US-09-169-079-1
6	303	100.0	4416	10	US-08-601-132-36
7	303	100.0	4416	10	US-08-671-573A-36
8	303	100.0	4416	10	US-08-671-573B-36
9	303	100.0	4416	17	US-09-355-700-1
10	303	100.0	4416	18	US-09-440-302A-1035
11	303	100.0	4416	18	US-09-442-384A-447
12	303	100.0	4416	18	US-09-442-589B-636
13	303	100.0	4416	20	US-09-534-376A-1
14	303	100.0	4416	24	US-09-631-092-36
15	303	100.0	4425	8	US-08-446-648-31
16	303	100.0	4425	11	US-08-770-449-31
17	303	100.0	4425	14	US-09-023-655-889
18	303	100.0	4425	36	US-09-982-610-31
19	303	100.0	4795	3	US-07-959-951A-3
20	303	100.0	4795	6	US-08-257-754-3
21	303	100.0	4795	15	US-09-169-079-3
22	303	100.0	9108	8	US-08-446-648-45
23	303	100.0	9108	36	US-09-982-610-45
24	252	83.2	4113	37	US-10-081-126-1
25	252	83.2	4450	1	PCT-US99-08079-1
26	252	83.2	4450	37	US-10-012-214-1
27	252	83.2	4459	71	US-60-324-185-4274
28	238	78.5	4461	55	US-60-167-943-103
29	191	63.0	3277	59	US-60-209-009-455
30	191	63.0	3277	60	US-60-213-360-951
31	191	63.0	3277	71	US-60-324-185-4300

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/671.573A
FILING DATE:
CLASSIFICATION: 435
PRIORITY APPLICATION NUMBER: 08/601.132
FILING DATE: 14-FEB-1996
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/585.895
FILING DATE: 77-JAN-1996
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/510.133
FILING DATE: 01-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 28113/33348
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 4416 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
US-08-671-573A-36

Query Match 100.0%; Score 303; DB 10; Length 4416;
Best Local Similarity 100.0%; Pred. No. 3.9e-147;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gagcggtcacctggggagagtgctcggtctacggcgcttcgggaagtggtggaagcc 60
DB 2546 GAGCGGCTGCACCTGGGGAGAGTGTCTGGCTACGGCGCTTCGGGAAGTGTGGAAGCC 2605
QY 61 tcggtttcggcatccacaaggagcagcgcgtgagtcgagctcaagatctctattcac 180
DB 2606 TCGGCTTTTCGGCATCCACAAGGGCAGCAGCTGTGACACCGTGGCGGTGAAAAATGCTGAAA 2665
QY 121 gagggcgccacgccaagcagcagcgcgtgagtcgagctcaagatctctattcac 180
DB 2666 GAGGGCGCCACGCCACGACGACCGCGCGTGTGATGTCGGAGCTCAAGATCTCTATTAC 2725
QY 181 atcggcaaccactcaactcagtgatcaactctctcggggcggtgcaccaagcgcgagggccc 240
DB 2726 ATCGGCAACACCTCAACCTGTTCAACCTCCCTCGGGCGGTGCACCAAGCGCAGGGCCCC 2785
QY 241 ctcattgtatcgtgagttctgcaagtacggcaacctctcaactctcgcgcgccaag 300
DB 2786 CTCATGGTGATCGTGAGTTCTGCAAGTACGGCAACCTCTCCAACTTCTCGCGGCCCAAG 2845
QY 301 cgg 303
DB 2846 CGG 2848

RESULT 8
US-08-671-573B-36
Sequence 36, Application US/08671573B
GENERAL INFORMATION:
APPLICANT: Alitalo, Kari
APPLICANT: Joukov, Vladimir
TITLE OF INVENTION: Receptor Ligand
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/671.573B
FILING DATE: 28-JUN-1996
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/601.132
FILING DATE: 14-FEB-1996
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/585.895
FILING DATE: 12-JAN-1996
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/510.133
FILING DATE: 01-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 28967/33348
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 4416 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
US-08-671-573B-36

Query Match 100.0%; Score 303; DB 10; Length 4416;
Best Local Similarity 100.0%; Pred. No. 3.9e-147;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gagcggtcgacctggggagagtgctcggtctacggcgcttcgggaagtggtggaagcc 60
DB 2546 GAGCGGCTGCACCTGGGGAGAGTGTCTGGCTACGGCGCTTCGGGAAGTGTGGAAGCC 2605
QY 61 tcggtttcggcatccacaaggagcagcgcgtgagtcgagctcaagatctctattcac 120
DB 2606 TCGGCTTTTCGGCATCCACAAGGGCAGCAGCTGTGACACCGTGGCGGTGAAAAATGCTGAAA 2665
QY 121 gagggcgccacgccaagcagcagcgcgtgagtcgagctcaagatctctattcac 180
DB 2666 GAGGGCGCCACGCCACGACGACCGCGCGTGTGATGTCGGAGCTCAAGATCTCTATTAC 2725
QY 181 atcggcaaccactcaactcagtgatcaactctctcggggcggtgcaccaagcgcgagggccc 240
DB 2726 ATCGGCAACACCTCAACCTGTTCAACCTCCCTCGGGCGGTGCACCAAGCGCAGGGCCCC 2785
QY 241 ctcattgtatcgtgagttctgcaagtacggcaacctctcaactctcgcgcgccaag 300
DB 2786 CTCATGGTGATCGTGAGTTCTGCAAGTACGGCAACCTCTCCAACTTCTCGCGGCCCAAG 2845
QY 301 cgg 303
DB 2846 CGG 2848

RESULT 9
US-09-355-700-1
Sequence 1, Application US/09355700
GENERAL INFORMATION:


```

: TITLE OF INVENTION: Hematology/Immunology Array
:
: FILE REFERENCE: CLON-006CIP15
:
: CURRENT APPLICATION NUMBER: US/09/442,384A
:
: CURRENT FILING DATE: 1999-11-17
:
: PRIOR APPLICATION NUMBER: 09/053,375
:
: PRIOR FILING DATE: 1998-03-31
:
: NUMBER OF SEQ ID NOS: 830
:
: SOFTWARE: FastSEQ for Windows Version 4.0
:
: SEQ ID NO 447
:
: LENGTH: 4416
:
: TYPE: DNA
:
: ORGANISM: homo sapiens
:
: FEATURE:
:
: NAME/KEY: misc_feature
:
: LOCATION: 4243
:
: OTHER INFORMATION: n = A,T,C or G
:
: NAME/KEY: misc_feature
:
: LOCATION: 4243
:
: OTHER INFORMATION: n = A,T,C or G
:
: US-09-442-384A-447

```

Query Match	100.0%	Score	303;	DB	18;	Length	4416;
Best Local Similarity	100.0%;	Pred.	No. 3..9e-147;				
Matches	303;	Conservative	0;	Mismatches	0;	Indels	0; Gaps
O	0;						
Qy	1	gagcgctgcacctggaggagtgtctcggctcacggcgcttcggaagtggttggaaagcc	60				
Dd	2546	gagcgctgcacctggaggagtgtctcggcttacggcgcttcggaagtggttggaaagcc	2605				
Qy	61	tccgctttcggcatccacaaggcagcagcttgtgacaccgtggcgtgaaaatgctgaaa	120				
Dd	2606	tccgctttcggcatccacaaggcagcagcttgtgacaccgtggcgtgaaaatgctgaaa	2665				
Qy	121	gagggcgccacggccagcgacgcgcgctgatgtcgaggctcaagaatctctattcac	180				
Dd	2656	gagggcgccacggccagcgacgcgcgctgatgtcgaggctcaagaatctctattcac	2725				
Qy	181	atcggcaaccacctcaacgtgttaacctctcggggcgtgcaccaagcccgaggcccc	240				
Dd	2726	atcggcaaccacctcaacgtgttaacctctcggggcgtgcaccaagcccgaggcccc	2785				
Qy	241	ctcatggttgatcgtggagttcttgcaagtacggccaacctctccaacttctctgcgcccaag	300				
Dd	2786	ctcatggttgatcgtggagttcttgcaagtacggccaacctctccaacttctctgcgcccaag	2845				
Qy	301	cgg	303				
Dd	2846	cug	2848				

```

RESULT 12
US-09-442-589B-636
: Sequence 636, Application US/09442589B
: GENERAL INFORMATION:
: APPLICANT: Chenchik, Alex
: APPLICANT: Lukashev, Matvey
: TITLE OF INVENTION: Human Cardiovascular Array
: FILE REFERENCE: CLON-006CIP10
: CURRENT APPLICATION NUMBER: US/09/442,589B
: CURRENT FILING DATE: 1999-11-17
: PRIOR APPLICATION NUMBER: 09/053,375
: PRIOR FILING DATE: 1998-03-31
: NUMBER OF SEQ ID NOS: 1194
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 636
: LENGTH: 4416
: TYPE: DNA
: ORGANISM: homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 4243
: OTHER INFORMATION: n = A,T,C or G

```

```

; NAME/KEY: misc_feature
; LOCATION: 4243
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc_feature
; LOCATION: 4243
; OTHER INFORMATION: n = A,T,C or G
US-09-442-589B-636

Query Match      100.0%; Score 303; DB 18; Length 4416;
Best Local Similarity 100.0%; Pred. No. 3.9e-147;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gacgcgtgcacctgggagagtgctcgctacgcgccttcggaagtggtggaagcc 60
|||||
Db 2546 gagcgctgcacctgggagagtgctcgctacgcgccttcggaagtggtggaagcc 2605
|||||

Qy 61 tccgctttcggcatccacaagggcagcagctgtgacacacgtggccgtgaaatgctgaaa 120
|||||
Db 2606 tccgctttcggcatccacaagggcagcagctgtgacacacgtggccgtgaaatgctgaaa 2665
|||||

Qy 121 gagggcgccacgcgcagcagcacgcgcctgtgatgtcggaagctcaagatctcttcac 180
|||||
Db 2666 gagggcgccacgcgcagcagcacgcgcctgtgatgtcggaagctcaagatctcttcac 2725
|||||

Qy 181 atcggcaaccacctcaacgctgtgtaacacctctctcgggcgctgaccacagccgcagggccccc 240
|||||
Db 2726 atcggcaaccacctcaacgctgtgtaacacctctctcgggcgctgaccacagccgcagggccccc 2785
|||||

Qy 241 ctcatgtgtagctgtgagttctgcaagtaaggcaacctctcaacttctctcgcgcccaag 300
|||||
Db 2786 ctcatgtgtagctgtgagttctgcaagtaaggcaacctctcaacttctctcgcgcccaag 2845
|||||

Qy 301 cgg 303
Db 2846 cgg 2848

RESULT 13
US-09-534-376A-1
; Sequence 1, Application US/09534376A
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Karl
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR C (VEGF-C) PROTEIN
; TITLE OF INVENTION: AND GENE, MUTANTS THEREOF, AND USES THEREOF
; FILE REFERENCE: 28967/34140A
; CURRENT APPLICATION NUMBER: US/09/534,376A
; CURRENT FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 09/355,700
; PRIOR FILING DATE: 1999-11-05
; PRIOR APPLICATION NUMBER: PCT/US98/01973
; PRIOR FILING DATE: 1998-02-02
; PRIOR APPLICATION NUMBER: 08/795,430
; PRIOR FILING DATE: 1997-02-05
; PRIOR APPLICATION NUMBER: PCT/FI96/00427
; PRIOR FILING DATE: 1996-08-01
; PRIOR APPLICATION NUMBER: 08/671,573
; PRIOR FILING DATE: 1996-06-28
; PRIOR APPLICATION NUMBER: 08/601,132
; PRIOR FILING DATE: 1996-02-14
; PRIOR APPLICATION NUMBER: 08/585,895
; PRIOR FILING DATE: 1996-01-12
; PRIOR APPLICATION NUMBER: 08/510,133
; PRIOR FILING DATE: 1995-08-01
; PRIOR APPLICATION NUMBER: 08/340,011
; PRIOR FILING DATE: 1994-11-14
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4416
; TYPE: DNA
; ORGANISM: Homo sapiens

```

```

;
; FEATURE:
; OTHER INFORMATION: Human F1L4 cDNA (short form)
; OTHER INFORMATION: At position 4243, n=A,T,G or C
US-09-534-376A-1

Query Match      100.0%; Score 303; DB 20; Length 4416;
Best Local Similarity 100.0%; Pred. No. 3.9e-147;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gaggcgtcaccctgggagagctcgcgtacgcgcctcgcggagagtggtgaaagcc 60
Db 2546 gaggcgtcaccctgggagagctcgcgtacgcgcctcgcggagagtggtgaaagcc 2605
Qy 61 tccgcttttcggcatccacaaggcagcagctgtgacacccgtggccgtgaaatgctgaaa 120
Db 2606 tccgcttttcggcatccacaaggcagcagctgtgacacccgtggccgtgaaatgctgaaa 2665
Qy 121 gaggcgcacacgcagcagcagcagcgcgcgtgagtcggagctcaagatctctatccac 180
Db 2666 gaggcgcacacgcagcagcagcagcgcgcgtgagtcggagctcaagatctctatccac 2725
Qy 181 atcgcaaacaccctcaacgtgtcaacctctcgcggcgctgcaccaagccgcagggccccc 240
Db 2726 atcgcaaacaccctcaacgtgtcaacctctcgcggcgctgcaccaagccgcagggccccc 2785
Qy 241 ctcatggtgatcgtggagttctgcaagtacggcaacctctccaaacttctgcgcgcccaag 300
Db 2786 ctcatggtgatcgtggagttctgcaagtacggcaacctctccaaacttctgcgcgcccaag 2845
Qy 301 cgg 303
Db 2846 cgg 2848

RESULT 14
US-09-631-092-36
; Sequence 36, Application US/09631092
; GENERAL INFORMATION:
; APPLICANT: Joukov, Vladimir
; TITLE OF INVENTION: Receptor Ligand
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/631,092
; FILING DATE: 02-Aug-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/601,132
; FILING DATE: 14-FEB-1996
; APPLICATION NUMBER: 08/585,895
; FILING DATE: 12-JAN-1996
; APPLICATION NUMBER: 08/510,133
; FILING DATE: 01-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Gass, David A.
; REGISTRATION NUMBER: 38,153
; REFERENCE/DOCKET NUMBER: 28967/33348
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448

```

```

;
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4416 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-09-631-092-36

Query Match      100.0%; Score 303; DB 24; Length 4416;
Best Local Similarity 100.0%; Pred. No. 3.9e-147;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gaggcgtcaccctgggagagctcgcgtacgcgcctcgcggagagtggtgaaagcc 60
Db 2546 gaggcgtcaccctgggagagctcgcgtacgcgcctcgcggagagtggtgaaagcc 2605
Qy 61 tccgcttttcggcatccacaaggcagcagctgtgacacccgtggccgtgaaatgctgaaa 120
Db 2606 tccgcttttcggcatccacaaggcagcagctgtgacacccgtggccgtgaaatgctgaaa 2665
Qy 121 gaggcgcacacgcagcagcagcagcgcgcgtgagtcggagctcaagatctctatccac 180
Db 2666 gaggcgcacacgcagcagcagcagcgcgcgtgagtcggagctcaagatctctatccac 2725
Qy 181 atcgcaaacaccctcaacgtgtcaacctctcgcggcgctgcaccaagccgcagggccccc 240
Db 2726 atcgcaaacaccctcaacgtgtcaacctctcgcggcgctgcaccaagccgcagggccccc 2785
Qy 241 ctcatggtgatcgtggagttctgcaagtacggcaacctctccaaacttctgcgcgcccaag 300
Db 2786 ctcatggtgatcgtggagttctgcaagtacggcaacctctccaaacttctgcgcgcccaag 2845
Qy 301 cgg 303
Db 2846 cgg 2848

RESULT 15
US-08-446-648-31
; Sequence 31, Application US/08446648
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Bennett, Brian D.
; APPLICANT: Goeddel, David
; APPLICANT: Lee, James M.
; APPLICANT: Matthews, William
; APPLICANT: Tsai, Siao Ping
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,648
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/222616
; FILING DATE: 04-APR-1994

```


APPLICANT: Alitalo, Kari, et al.
TITLE OF INVENTION: FLT4, A NOVEL RECEPTOR TYROSIN KINASE
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/959,951A
FILING DATE: 19921009
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gruber, Lewis S.
REGISTRATION NUMBER: 30,060
REFERENCE/DOCKET NUMBER: 28113/31104
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 4795 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 20..4111
US-07-959-951A-3

Query Match 100.0%; Score 303; DB 3; Length 4795;
Best Local Similarity 100.0%; Pred. No. 3.9e-147;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gagcggtgcacctggggagagtgctgcgctacgagcgttcgggaaagtgtgaaagcc 60
Db 2546 GAGCGGCTGCACCTGGGGAGAGTGCTCGCTACGGCGCTTCGGGAAGGTGGTGAAGCC 2605
Qy 61 tcggtttcggcatccacaaggagcagctgtgacaccgtggccgtgaaaaatgctgaaa 120
Db 2606 TCCGCTTTTCGGCATCCACAAGGCGAGCAGCTGTGACACCGTGGCGCGTGAAATGCTGAAA 2665
Qy 121 gagggcgccacgcgagcagcgcgctgatgctcgagctcaagatcctcatcacc 180
Db 2666 GAGGGCGCCACGGCCAGCAGCAGCGCGCTGATGTGCGGAGCTCAAGATCCTCATTCAC 2725
Qy 181 atcggaaccacctcaacgttggtcaacctcctcggggtgacacaaagcgcagggccccc 240
Db 2726 ATCGGCAACCACTCAACGTGGTCAACCTCCTCGGGCGGTGCACCAAGCGCGCGGCC 2785
Qy 241 ctcatgtgatcgtggagttctgcaagtaagcgaacctctccaaactcctgcgcgcaag 300
Db 2786 CTCATGTGATCGTGGAGTTCTGCAAGTACGGCAACCTTCCCAACTTCTCGCGCGCAAG 2845
Qy 301 cgg 303
Db 2846 CGG 2848

RESULT 20
US-08-257-754-3
; Sequence 3, Application US/08257754
; GENERAL INFORMATION:

APPLICANT: Alitalo, Kari
APPLICANT: Kaipainen, Arja
APPLICANT: Korhonen, Jaana
APPLICANT: Mustonen, Tuija
APPLICANT: Pajusola, Kari
APPLICANT: Matikainen, Marja-Terttu
APPLICANT: Kannani, Paivi
TITLE OF INVENTION: FLT4 RECEPTOR TYROSINE KINASE AND ITS USE IN
TITLE OF INVENTION: DIAGNOSIS AND THERAPY
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/257,754
FILING DATE: 09-JUN-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/959,951
FILING DATE: 09-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 28344/32133
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 4795 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 20..4111
US-08-257-754-3

Query Match 100.0%; Score 303; DB 6; Length 4795;
Best Local Similarity 100.0%; Pred. No. 3.9e-147;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gagcggtgcacctggggagagtgctgcgctacgagcgttcgggaaagtgtgaaagcc 60
Db 2546 GAGCGGCTGCACCTGGGGAGAGTGCTCGCTACGGCGCTTCGGGAAGGTGGTGAAGCC 2605
Qy 61 tcggtttcggcatccacaaggagcagctgtgacaccgtggccgtgaaaaatgctgaaa 120
Db 2606 TCCGCTTTTCGGCATCCACAAGGCGAGCAGCTGTGACACCGTGGCGCGTGAAATGCTGAAA 2665
Qy 121 gagggcgccacgcgagcagcgcgctgatgctcgagctcaagatcctcatcacc 180
Db 2666 GAGGGCGCCACGGCCAGCAGCAGCGCGCTGATGTGCGGAGCTCAAGATCCTCATTCAC 2725
Qy 181 atcggaaccacctcaacgttggtcaacctcctcggggtgacacaaagcgcagggccccc 240
Db 2726 ATCGGCAACCACTCAACGTGGTCAACCTCCTCGGGCGGTGCACCAAGCGCGCGGCC 2785
Qy 241 ctcatgtgatcgtggagttctgcaagtaagcgaacctctccaaactcctgcgcgcaag 300
Db 2786 CTCATGTGATCGTGGAGTTCTGCAAGTACGGCAACCTTCCCAACTTCTCGCGCGCAAG 2845


```
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (22)..(3915)
PCT-US99-08079-1

Query Match      83.2%; Score 252; DB 1; Length 4450;
Best Local Similarity 99.7%; Pred. No. 1.6e-120;
Matches 302; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 gagcggtgcacctggggagagtgctcggtacggtcgcccttcgggaagtggtggaagcc 60
    |||||
Db 2548 gagcggtgcacctggggagagtgctcggtacggtcgcccttcgggaagtggtggaagcc 2607

QY 61 lccgcttcggcatccacaaggagcagcagctgtgacaccgtgcccgtgaaatgctgaaa 120
    |||||
Db 2608 lccgcttcggcatccacaaggagcagcagctgtgacaccgtgcccgtgaaatgctgaaa 2667

QY 121 gagggcgccacgaccgagcagcagcgcgtgagtcgagctcgaagtcacatctcattcac 180
    |||||
Db 2668 gagggcgccacgaccgagcagcagcgcgtgagtcgagctcgaagtcacatctcattcac 2727

QY 181 atcggaaccacacacacgagtggttcaacctcttcggggcggtgacccaagcgcagggcccc 240
    |||||
Db 2728 atcggaaccacacacacgagtggttcaacctcttcggggcggtgacccaagcgcagggcccc 2787

QY 241 ctcatggtgacgtgagtgctgcaagtagcggcaacctctccaactctctgcgcgccaag 300
    |||||
Db 2788 ctcatggtgacgtgagtgctgcaagtagcggcaacctctccaactctctgcgcgccaag 2847

QY 301 cgg 303
    |||
Db 2848 cgg 2850

RESULT 26
US-10-012-214-1
; Sequence 1, Application US/10012214
; GENERAL INFORMATION:
; APPLICANT: Sai L. Su
; TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS AND TREATMENT OF METASTATIC
; PROSTATE TUMORS
; FILE REFERENCE: 20093-001000US
; CURRENT APPLICATION NUMBER: US/10/012,214
; PRIOR FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: PCT/US99/08079
; PRIOR FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4450
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (22)..(3915)
US-10-012-214-1

Query Match      83.2%; Score 252; DB 37; Length 4450;
Best Local Similarity 99.7%; Pred. No. 1.6e-120;
Matches 302; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 gagcggtgcacctggggagagtgctcggtacggtcgcccttcgggaagtggtggaagcc 60
    |||||
Db 2548 gagcggtgcacctggggagagtgctcggtacggtcgcccttcgggaagtggtggaagcc 2607

QY 61 lccgcttcggcatccacaaggagcagcagctgtgacaccgtgcccgtgaaatgctgaaa 120
    |||||
Db 2608 lccgcttcggcatccacaaggagcagcagctgtgacaccgtgcccgtgaaatgctgaaa 2667

QY 121 gagggcgccacgaccgagcagcagcgcgtgagtcgagctcgaagtcacatctcattcac 180
```

```
Db 2668 gagggcgccacgaccgagcagcagcgcgtgagtcggaagtcacaatctctcattcac 2727

QY 181 atcggaaccacacacacgagtggttcaacctcttcggggcggtgacccaagcgcagggcccc 240
    |||||
Db 2728 atcggaaccacacacacgagtggttcaacctcttcggggcggtgacccaagcgcagggcccc 2787

QY 241 ctcatggtgacgtgagtgctgcaagtagcggcaacctctccaactctctgcgcgccaag 300
    |||||
Db 2788 ctcatggtgacgtgagtgctgcaagtagcggcaacctctccaactctctgcgcgccaag 2847

QY 301 cgg 303
    |||
Db 2848 cgg 2850

RESULT 27
US-60-324-185-4274
; Sequence 4274, Application US/60324185
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preeti
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING
; POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE
; TITLE OF INVENTION: POLYMORPHISMS IDENTIFIED THEREBY
; FILE REFERENCE: GX-0019-1 P
; CURRENT APPLICATION NUMBER: US/60/324,185
; CURRENT FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 35862
; SOFTWARE: PERL Program
; SEQ ID NO 4274
; LENGTH: 4459
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No: 1082992.1
; NAME/KEY: unsure
; LOCATION: 2402-2421
; OTHER INFORMATION: a, t, c, g, or other
US-60-324-185-4274

Query Match      83.2%; Score 252; DB 71; Length 4459;
Best Local Similarity 99.7%; Pred. No. 1.6e-120;
Matches 302; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 gagcggtgcacctggggagagtgctcggtacggtcgcccttcgggaagtggtggaagcc 60
    |||||
Db 2557 gagcggtgcacctggggagagtgctcggtacggtcgcccttcgggaagtggtggaagcc 2616

QY 61 lccgcttcggcatccacaaggagcagcagctgtgacaccgtgcccgtgaaatgctgaaa 120
    |||||
Db 2617 lccgcttcggcatccacaaggagcagcagctgtgacaccgtgcccgtgaaatgctgaaa 2676

QY 121 gagggcgccacgaccgagcagcagcgcgtgagtcggaagtcacatctcattcac 180
    |||||
Db 2677 gagggcgccacgaccgagcagcagcgcgtgagtcggaagtcacatctcattcac 2736

QY 181 atcggaaccacacacacgagtggttcaacctcttcggggcggtgacccaagcgcagggcccc 240
    |||||
Db 2737 atcggaaccacacacacgagtggttcaacctcttcggggcggtgacccaagcgcagggcccc 2796

QY 241 ctcatggtgacgtgagtgctgcaagtagcggcaacctctccaactctctgcgcgccaag 300
    |||||
Db 2797 ctcatggtgacgtgagtgctgcaagtagcggcaacctctccaactctctgcgcgccaag 2856

QY 301 cgg 303
    |||
Db 2857 cgg 2859
```


Db 205 atcggcaaccactcaacgtgtgtaacctctctcgggcggtgcaccaagccgagggcccc 264
Qy 241 ct 242
Db 265 ct 266

RESULT 31
US-60-324-185-4300
; Sequence 4300, Application US/60324185
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preeti
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE
; TITLE OF INVENTION: POLYMORPHISMS IDENTIFIED THEREBY
; FILE REFERENCE: GX-0019-1 P
; CURRENT APPLICATION NUMBER: US/60/324,185
; NUMBER OF SEQ ID NOS: 2001-09-21
; SOFTWARE: PERL Program
; SEQ ID NO 4300
; LENGTH: 3277
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No: 1084493.6
US-60-324-185-4300

Query Match 63.0%; Score 191; DB 71; Length 3277;
Best Local Similarity 99.6%; Pred. No. 1.le-88;
Matches 241; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 gacgcgtcgacctgggagagtgctcgctacgcgccttcggagcgtggaagtggtggaagcc 60
Db 25 gacgcgtcgacctgggagagtgctcgctacgcgccttcggagcgtggaagtggtggaagcc 84
Qy 61 tcgcgtttcggcatcccaaggcagcagctgtgacacccgtgcccgtgaaaaatgctgaaa 120
Db 85 tcgcgtttcggcatcccaaggcagcagctgtgacacccgtgcccgtgaaaaatgctgaaa 144
Qy 121 aagggcgccagcgcagcagcagcgcgcgtgctgagcgtgagcgtcgaagatcctcattcac 180
Db 145 gaggcgccagcgcagcagcagcgcgcgtgctgagcgtgagcgtcgaagatcctcattcac 204
Qy 181 atcggcaaccactcaacgtgtgtaacctctctcgggcggtgcaccaagccgagggcccc 240
Db 205 atcggcaaccactcaacgtgtgtaacctctctcgggcggtgcaccaagccgagggcccc 264
Qy 241 ct 242
Db 265 ct 266

RESULT 32
US-60-172-373-15763
; Sequence 15763, Application US/60172373
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preeti
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
; TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide Polymor
; FILE REFERENCE: GX-0006 P
; CURRENT APPLICATION NUMBER: US/60/172,373
; CURRENT FILING DATE: 1999-12-16
; NUMBER OF SEQ ID NOS: 25,772
; SOFTWARE: PERL Program
; SEQ ID NO 15763

; LENGTH: 4462
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No: 902563.2
; NAME/KEY: unsure
; LOCATION: 2402-2421, 2907, 3602
; OTHER INFORMATION: a, t, c, g, or other
US-60-172-373-15763

Query Match 63.0%; Score 191; DB 56; Length 4462;
Best Local Similarity 99.6%; Pred. No. 1.le-88;
Matches 241; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 gacgcgtcgacctgggagagtgctcgctacgcgccttcggagcgtggaagtggtggaagcc 60
Db 2557 gacgcgtcgacctgggagagtgctcgctacgcgccttcggagcgtggaagtggtggaagcc 2616
Qy 61 tcgcgtttcggcatcccaaggcagcagctgtgacacccgtggcgtgaaaaatgctgaaa 120
Db 2617 tcgcgtttcggcatcccaaggcagcagctgtgacacccgtggcgtgaaaaatgctgaaa 2676
Qy 121 gaggcgccagcgcagcagcagcgcgcgtgctgagcgtcgaagatcctcattcac 180
Db 2677 gaggcgccagcgcagcagcagcgcgcgtgctgagcgtcgaagatcctcattcac 2736
Qy 181 atcggcaaccactcaacgtgtgtaacctctctcgggcggtgcaccaagccgagggcccc 240
Db 2737 atcggcaaccactcaacgtgtgtaacctctctcgggcggtgcaccaagccgagggcccc 2796
Qy 241 ct 242
Db 2797 ct 2798

RESULT 33
US-60-164-285-7458
; Sequence 7458, Application US/60164285
; GENERAL INFORMATION:
; APPLICANT: Ma, Xiao-Jun
; TITLE OF INVENTION: Tumor Associated Molecules (TAMs): Targets for diagnosis, trea
; FILE REFERENCE: 3214
; CURRENT APPLICATION NUMBER: US/60/164,285
; CURRENT FILING DATE: 1999-11-05
; NUMBER OF SEQ ID NOS: 8259
; SEQ ID NO 7458
; LENGTH: 244
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-164-285-7458

Query Match 57.1%; Score 173; DB 55; Length 244;
Best Local Similarity 100.0%; Pred. No. 2.9e-79;
Matches 173; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 120 agaggcgccagcgcagcagcgcgcgtgctgagcgtcgaagatcctcattca 179
Db 72 agaggcgccagcgcagcagcgcgcgtgctgagcgtcgaagatcctcattca 131
Qy 180 catcgcaaccactcaacgtgtgtaacctctctcgggcggtgcaccaagccgagggcccc 239
Db 132 catcgcaaccactcaacgtgtgtaacctctctcgggcggtgcaccaagccgagggcccc 191
Qy 240 cctcatggtgctgctgagcttctgcaagtagtcgcgaacctctccaacttctctgc 292
Db 192 cctcatggtgctgctgagcttctgcaagtagtcgcgaacctctccaacttctctgc 244
RESULT 34

; NUMBER OF SEQ ID NOS: 7494
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2866
; LENGTH: 609
; TYPE: DNA
; ORGANISM: HUMAN
US-60-196-718-2866

Query Match 24.1%; Score 73; DB 58; Length 609;
Best Local Similarity 100.0%; Pred. No. 4.3e-27;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ggaagagtcgctcagctacagcccttcggaaagggtgtaagacctccgcttcggcattc 75
|||||

Db 138 GGAGAGTCTCGCTACCGGCCCTTCGGGAAGGTGGTGAAGCCCTCCGCTTCGGCATC 79
|||||

QY 76 cacaagggcagca 88
|||||

Db 78 CACAAGGCGCAGCA 66
|||||

RESULT 39

US-60-196-711-279

; Sequence 279, Application US/60196711

; GENERAL INFORMATION:

; APPLICANT: Bonazzi, Vivien

; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS OF THE

; TITLE OF INVENTION: SER/THR AND TYR FAMILY OF KINASES, NUCLEIC ACID MOLECULES

; FILE REFERENCE: CL000452

; CURRENT APPLICATION NUMBER: US/60/196,711

; CURRENT FILING DATE: 2000-04-13

; NUMBER OF SEQ ID NOS: 2378

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 279

; LENGTH: 492

; TYPE: DNA

; ORGANISM: HUMAN

US-60-196-711-279

Query Match

Best Local Similarity 100.0%; Score 53; DB 58; Length 492;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 66 ttctggcatccacaagggcagcagctgtgacacccgtggccgtgaaaatgctga 118
|||||

Db 440 ttctggcatccacaagggcagcagctgtgacacccgtggccgtgaaaatgctga 492
|||||

RESULT 40

US-60-196-712-469

; Sequence 469, Application US/60196712

; GENERAL INFORMATION:

; APPLICANT: Bonazzi, Vivien

; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,

; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,

; FILE REFERENCE: CL000451

; CURRENT APPLICATION NUMBER: US/60/196,712

; CURRENT FILING DATE: 2000-04-13

; NUMBER OF SEQ ID NOS: 3846

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 469

; LENGTH: 492

; TYPE: DNA

; ORGANISM: HUMAN

US-60-196-712-469

Query Match

Best Local Similarity 100.0%; Score 53; DB 58; Length 492;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 66 ttctggcatccacaagggcagcagctgtgacacccgtggccgtgaaaatgctga 118
|||||

Db 440 ttctggcatccacaagggcagcagctgtgacacccgtggccgtgaaaatgctga 492
|||||

RESULT 41

US-60-172-373-15764

; Sequence 15764, Application US/60172373

; GENERAL INFORMATION:

; APPLICANT: Morris, MacDonald

; APPLICANT: Lal, Preeti

; APPLICANT: Diep, Dinh

; TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using

; TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide Poly

; FILE REFERENCE: GX-0006 P

; CURRENT APPLICATION NUMBER: US/60/172,373

; CURRENT FILING DATE: 1999-12-16

; NUMBER OF SEQ ID NOS: 25,772

; SOFTWARE: PERL Program

; SEQ ID NO 15764

; LENGTH: 51

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc_feature

; OTHER INFORMATION: Incyte ID No: SNP00023212

; FEATURE:

; NAME/KEY: snp

; LOCATION: 26

; OTHER INFORMATION: 902563.2, 2700, G->C

US-60-172-373-15764

Query Match

Best Local Similarity 100.0%; Score 51; DB 56; Length 51;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 119 aagaggcgccacggccagcagcagccgcgcgtgatctcgagagctcaaga 169
|||||

Db 1 aagaggcgccacggccagcagcagccgcgcgtgatctcgagagctcaaga 51
|||||

RESULT 42

US-08-472-801-1194/c

; Sequence 1194, Application US/08472801

; GENERAL INFORMATION:

; APPLICANT: Hesel 2

; APPLICANT: Smith, Larry J.

; TITLE OF INVENTION: Method and Compositions for Cellular

; TITLE OF INVENTION: Reprogramming

; FILE REFERENCE: Hesel 2

; CURRENT APPLICATION NUMBER: US/08/472,801

; CURRENT FILING DATE: 1995-06-07

; NUMBER OF SEQ ID NOS: 3601

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 1194

; LENGTH: 30

; TYPE: DNA

; ORGANISM: Homo sapiens

US-08-472-801-1194

Query Match

Best Local Similarity 100.0%; Score 30; DB 8; Length 30;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 105 cgtgaaaatgctgaaagagggcgccacggc 134
|||||

Db 30 COTGAAATGCTGAAAGAGGGCGCCACGGC 1
|||||

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 15, 2002, 22:53:39 ; Search time 223.79 Seconds
(without alignments)
332.575 Million cell updates/sec

Title: US-09-375-248-1_COPY_2546_2848

Perfect score: 303

Sequence: 1 gagcggctgcacctggggag.....acttctgcgcgaagcgg 303

Scoring table:

OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 383533 seqs, 122816752 residues

Word size : 0

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents.NA.*

- 1: /cgn2_6/ptodata/2/ina/5A_COMB.seq.*
- 2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*
- 3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*
- 4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*
- 5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq.*
- 6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	303	100.0	4195	1	US-08-340-011-1
2	303	100.0	4195	3	US-08-901-710-1
3	303	100.0	4416	3	US-08-795-430-1
4	303	100.0	4425	1	US-08-222-616-31
5	303	100.0	4425	5	PCT-US95-04228-31
6	303	100.0	4795	1	US-08-340-011-3
7	303	100.0	4795	3	US-08-901-710-3
8	303	100.0	9108	5	PCT-US95-04228-45
9	17	5.6	17	4	US-08-584-040-4146
10	17	5.6	3120	1	US-08-456-647B-19
11	17	5.6	3120	2	US-08-237-401A-19
12	17	5.6	4071	4	US-09-098-707A-1
13	17	5.6	4071	4	US-09-483-539-1
14	17	5.6	4236	1	US-08-810-116-7
15	17	5.6	4236	2	US-07-930-548A-7
16	17	5.6	8460	1	US-08-469-005A-9
17	17	5.6	8519	4	US-09-261-907-1
18	17	5.6	4403765	4	US-09-103-840A-2
19	17	5.6	4411529	4	US-09-103-840A-1
20	16	5.3	78	6	5457037-7
21	16	5.3	850	4	US-08-998-416-314
22	16	5.3	1065	4	US-09-330-611-15
23	16	5.3	1320	1	US-07-681-704A-1
24	16	5.3	1522	3	US-08-993-359-25
25	16	5.3	2185	3	US-08-173-508-3
26	16	5.3	2185	2	US-08-265-310-3
27	16	5.3	2185	3	US-08-951-742-3

28	16	5.3	2514	4	US-09-144-914-3	Sequence 3, Appli
c 29	16	5.3	2625	6	5457037-4	Patent No. 5457037
c 30	16	5.3	3336	6	5457037-1	Patent No. 5457037
c 31	16	5.3	6122	1	US-08-403-545-1	Sequence 1, Appli
c 32	16	5.3	6122	4	US-08-404-381-1	Sequence 1, Appli
c 33	16	5.3	28958	1	US-08-258-261B-6	Sequence 6, Appli
c 34	16	5.3	28958	1	US-08-456-837-6	Sequence 6, Appli
c 35	16	5.3	28958	1	US-08-457-342-6	Sequence 6, Appli
c 36	16	5.3	28958	1	US-08-457-646A-6	Sequence 6, Appli
c 37	16	5.3	28958	1	US-08-458-076A-6	Sequence 6, Appli
c 38	16	5.3	28958	1	US-08-764-233A-4	Sequence 6, Appli
c 39	16	5.3	28958	1	US-08-457-335A-6	Sequence 6, Appli
c 40	16	5.3	28958	1	US-08-729-214-6	Sequence 6, Appli
c 41	16	5.3	28958	3	US-09-028-934-6	Sequence 6, Appli
c 42	16	5.3	49377	1	US-08-764-233A-6	Sequence 99, Appli
c 43	15	5.0	171	4	US-09-020-956-99	Sequence 99, Appli
c 44	15	5.0	171	4	US-09-030-607-99	Sequence 99, Appli
c 45	15	5.0	171	4	US-09-439-313-99	Sequence 99, Appli

ALIGNMENTS

RESULT 1
US-08-340-011-1
: Sequence 1, Application US/08340011
: Patent No. 5776755
: GENERAL INFORMATION:
: APPLICANT: Alitalo, et al.
: TITLE OF INVENTION: FLT4, A NOVEL RECEPTOR TYROSIN KINASE
: NUMBER OF SEQUENCES: 20
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
: STREET: 6300 Sears Tower, 233 South Wacker Drive
: CITY: Chicago
: STATE: Illinois
: COUNTRY: United States of America
: ZIP: 60606-6402
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION NUMBER: US/08/340,011
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/959,951
: FILING DATE: 09-OCT-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: Meyers, Thomas C.
: REGISTRATION NUMBER: 36,989
: REFERENCE/DOCKET NUMBER: 32267
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312/474-6300
: TELEFAX: 312/474-0448
: TELEX: 25-3856
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 4195 base pairs
: TYPE: nucleic acid
: TOPOLOGY: linear
: MOLECULE TYPE: CDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 20..3916
: US-08-340-011-1

Query Match 100.0%; Score 303; DB 1; Length 4195;
Best Local Similarity 100.0%; Pred. No. 2.2e-140;

```
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 gagcgctgcacctgggagagtgctcggtacgagcgcccttcgggaagtggtggaagcc 60
Db 2546 GAGCGGCTGCACCTGGGAGAGTGCTCGGTACCGCCCTTCGGGAAGGTGGTGAAGCC 2605
Qy 61 tccgctttcggcatcccaaggagcagctgtgacaccctggtgacccgtgaaatgctgaaa 120
Db 2606 TCCGCTTTCCGCATCCCAAGGAGCAGCTGTGACACCGTGGCGGTGAAAATGCTGAAA 2665
Qy 121 gagggcgccagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcg 180
Db 2666 GAGGCGCCACCGCAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCG 2725
Qy 241 ctcatggtgatcgtggagttctgcaagtcagcgcaacctctccaaacttctcgcgcgcaag 300
Db 2786 CTCATGCTGATCGTGGAGTTCTGCAAGTACGGCAACCTCTCCAACCTTCCTCGCGCGCAAG 2845
Qy 301 cgg 303
Db 2846 CGG 2848

RESULT 2
US-08-901-710-1
: Sequence 1, Application US/08901710
: Patent No. 6107046
: GENERAL INFORMATION:
: APPLICANT: Alitalo, Kari
: APPLICANT: Aprelikova, Olga
: APPLICANT: Pajusola, Katri
: APPLICANT: Armstrong, Elina
: APPLICANT: Korhonen, Jaana
: APPLICANT: Kaipainen, Arja
: APPLICANT: Matikainen, Marja-Terttu
: TITLE OF INVENTION: FLT4 A RECEPTOR TYROSINE KINASE, AND USES
: TITLE OF INVENTION: THEREOF
: NUMBER OF SEQUENCES: 2
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
: STREET: 6300 Sears Tower, 233 South Wacker Drive
: CITY: Chicago
: STATE: Illinois
: COUNTRY: United States of America
: ZIP: 60606-6402
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: FILING DATE: US/08/901,710
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/340,011
: FILING DATE: 14-NOV-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/257,754
: FILING DATE: 09-JUL-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/959,951
: FILING DATE: 09-OCT-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: Gass, David A.
: REGISTRATION NUMBER: 38,153
: REFERENCE/DOCKET NUMBER: 28113/33824
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312/474-6300
```

```
: TELEFAX: 312/474-0448
: TELEX: 25-3856
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 4195 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 20..3916
: US-08-901-710-1

Query Match 100.0%; Score 303; DB 3; Length 4195;
Best Local Similarity 100.0%; Pred. No. 2.2e-140;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 gagcgctgcacctgggagagtgctcggtacgagcgcccttcgggaagtggtggaagcc 60
Db 2546 GAGCGGCTGCACCTGGGAGAGTGCTCGGTACCGCCCTTCGGGAAGGTGGTGAAGCC 2605
Qy 61 tccgctttcggcatcccaaggagcagctgtgacaccctggtgacccgtgaaatgctgaaa 120
Db 2606 TCCGCTTTCCGCATCCCAAGGAGCAGCTGTGACACCGTGGCGGTGAAAATGCTGAAA 2665
Qy 121 gagggcgccagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcg 180
Db 2666 GAGGCGCCACCGCAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCG 2725
Qy 181 atcggaaccacactcaagtggtgaccccttcgggagtggtgacccagcgagcgccccc 240
Db 2726 ATCGGCAACCACTCAACGTTGGTCAACCTCTCGGGCGGTGACCAAGCGCGAGGCCCC 2785
Qy 241 ctcatggtgatcgtggagttctgcaagtcagcgcaacctctccaaacttctcgcgcgcaag 300
Db 2786 CTCATGCTGATCGTGGAGTTCTGCAAGTACGGCAACCTCTCCAACCTTCCTCGCGCGCAAG 2845
Qy 301 cgg 303
Db 2846 CGG 2848

RESULT 3
US-08-795-430-1
: Sequence 1, Application US/08795430
: Patent No. 6130071
: GENERAL INFORMATION:
: APPLICANT: Alitalo, Kari
: APPLICANT: Joukov, Vladimir
: TITLE OF INVENTION: Vascular Endothelial Growth Factor C (VEGF-C)
: TITLE OF INVENTION: Protein and Gene, Mutants Thereof, and Uses Thereof
: NUMBER OF SEQUENCES: 57
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
: STREET: 6300 Sears Tower, 233 South Wacker Drive
: CITY: Chicago
: STATE: Illinois
: COUNTRY: United States of America
: ZIP: 60606-6402
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/795,430
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/FI96/00427
: FILING DATE: 01-AUG-1996
```


Sequence 31, Application PC/TUS9504228
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Bennett, Brian D.
APPLICANT: Goeddel, David
APPLICANT: Lee, James M.
APPLICANT: Matthews, William
APPLICANT: Tsai, Siao Ping
APPLICANT: Wood, William I.
TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04228
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/222616
FILING DATE: 04-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Wendy M. Lee
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 821P3PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/223-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 4425 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US95-04228-31

Query Match 100.0%; Score 303; DB 5; Length 4425;
Best Local Similarity 100.0%; Pred. No. 2.2e-140;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gagcggtgcacctggggagtgctcggctacggcgcttcgggaagtggtgaaagcc 60
DB 2557 GAGCGGCTGCACCTGGGGAGTGCTCGGCTACGGCGCTTCGGGAAGTGTTGGAAGCC 2616
OY 61 tccgctttcggcatccacaaaggcagcagctgtgacacccgtgcccgtgaaatcgtgaaa 120
DB 2617 TCCGCTTTTCGGCATCCACAAAGGCAGCAGCTGTGACACCGTGGCGCTGAAAATGCTGAAA 2676
OY 121 gagggcgacagggcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 180
DB 2677 GAGGGCGCCACGGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 2736
OY 181 atcggcaaccac 180
DB 2737 ATCGGCAACCACTCAACGTGGTCAACCTCTCTCGGGGGGTGCACCAAGCCGAGGGCCCC 2796
OY 241 ctcatggtgatcgtggagttctgcaagtaaggcaacacctctcaacctctcctcgtcgcccaag 300
DB 2797 CTCATGGTGATCGTGGAGTTCTGCAAGTACGGCAACCTCTTCCAACTTCTCTGGCGCCCAAG 2856
OY 301 cgg 303
|||

Db 2857 CGG 2859

RESULT 6

US-08-340-011-3
Sequence 3, Application US/08340011
Patent No. 5776755
GENERAL INFORMATION:
APPLICANT: Alitalo, et al.
TITLE OF INVENTION: FLT4, A NOVEL RECEPTOR TYROSIN KINASE
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/340,011
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/959,951
FILING DATE: 09-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Thomas C.
REGISTRATION NUMBER: 36,989
REFERENCE/DOCKET NUMBER: 32267
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 4795 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 20..4111
US-08-340-011-3

Query Match 100.0%; Score 303; DB 1; Length 4795;
Best Local Similarity 100.0%; Pred. No. 2.2e-140;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gagcggtgcacctggggagtgctcggcgcttcgggaagtggtgaaagcc 60
DB 2546 GAGCGGCTGCACCTGGGGAGAGTGCTCGGCTACGGCGCTTCGGGAAGTGTTGGAAGCC 2605
OY 61 tccgctttcggcatccacaaaggcagcagctgtgacacccgtgcccgtgaaatcgtgaaa 120
DB 2606 TCCGCTTTTCGGCATCCCAAGGGCAGCAGCTGTGACACCGTGGCGCTGAAAATGCTGAAA 2665
OY 121 gagggcgac 180
DB 2666 GAGGGCGCCACGGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 2725
OY 181 atcggcaaccac 240
DB 2726 ATCGGCAACCACTCAACGTGGTCAACCTCTCTCGGGGGGTGCACCAAGCCGAGGGCCCC 2785
OY 241 ctcatggtgatcgtggagttctgcaagtaaggcaacacctctcaacctctcctcgtcgcccaag 300
|||

Qy 100 gtggccgtgaaatgct 116
|||||
Db 2297 GTGGCCGTGAAATGCT 2313

RESULT 11
US-08-237-401A-19
: Sequence 19, Application US/08237401A
: Patent No. 5837448
: GENERAL INFORMATION:
: APPLICANT: Lemke Ph.D. et al., Greg E.
: TITLE OF INVENTION: PROTEIN-TYROSINE KINASE GENES
: NUMBER OF SEQUENCES: 54
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Fish & Richardson P.C.
: STREET: 4225 Executive Square, Suite 1400
: CITY: La Jolla
: STATE: CA
: COUNTRY: US
: ZIP: 92037
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/237,401A
: FILING DATE: 02-MAY-1994
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/884,486
: FILING DATE: 15-MAY-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: Haile Ph.D., Lisa A.
: REGISTRATION NUMBER: 38,347
: REFERENCE/DOCKET NUMBER: 07251/007001
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (619) 678-5070
: TELEFAX: (619) 678-5099
: INFORMATION FOR SEQ ID NO: 19:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3120 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA
: IMMEDIATE SOURCE:
: CLONE: Tyro-10
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 485..3047
US-08-237-401A-19

Query Match 5.6%; Score 17; DB 2; Length 3120;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 100 gtggccgtgaaatgct 116
|||||
Db 2297 GTGGCCGTGAAATGCT 2313

RESULT 12
US-09-098-707A-1
: Sequence 1, Application US/09098707A
: Patent No. 6204011
: GENERAL INFORMATION:
: APPLICANT: Kendall, Richard L.
: Thomas, Kenneth A.
: Mao, Xianzhi
: Tebben, Andrew J.

: TITLE OF INVENTION: HUMAN RECEPTOR TYROSINE KINASE, KDR
: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Merck & Co., Inc.
: STREET: P.O. Box 2000
: CITY: Rahway
: STATE: NJ
: COUNTRY: US
: ZIP: 07065-0907
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/098,707A
: FILING DATE: 17-Jun-1998
: CLASSIFICATION: <Unknown>
: ATTORNEY/AGENT INFORMATION:
: NAME: Hand, J. Mark
: REGISTRATION NUMBER: 36,545
: REFERENCE/DOCKET NUMBER: 19963PV
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 732/594-3905
: TELEFAX: 732/594-4720
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 4071 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-098-707A-1

Query Match 5.6%; Score 17; DB 4; Length 4071;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 163 ctcaagatctctcatcca 179
|||||
Db 2656 CTCAAGATCTCTCATCCA 2672

RESULT 13
US-09-483-539-1
: Sequence 1, Application US/09483539
: Patent No. 6359115
: GENERAL INFORMATION:
: APPLICANT: Kendall, Richard L.
: APPLICANT: Thomas, Kenneth A.
: APPLICANT: Mao, Xianzhi
: APPLICANT: Tebben, Andrew J.
: TITLE OF INVENTION: HUMAN RECEPTOR TYROSINE KINASE, KDR
: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Merck & Co., Inc.
: STREET: P.O. Box 2000
: CITY: Rahway
: STATE: NJ
: COUNTRY: US
: ZIP: 07065-0907
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/483,539
: FILING DATE:
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:

NAME: Hand, J. Mark
REGISTRATION NUMBER: 36,545
REFERENCE/DOCKET NUMBER: 19963PV
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732/594-3905
TELEFAX: 732/594-4720
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4071 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-483-539-1

Query Match 5.6%; Score 17; DB 4; Length 4071;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 163 ctcaagatcctcatcca 179
|||||
Db 2656 CTCAAGATCCTCATCCA 2672

RESULT 14
US-08-810-116-7
; Sequence 7, Application US/08810116
; Patent No. 5766860
; GENERAL INFORMATION:
; APPLICANT: Terman, Bruce I.
; APPLICANT: Carrion, Miguel E.
; TITLE OF INVENTION: Identification of a No. 5766860el Human Growth
; TITLE OF INVENTION: Factor Receptor
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07470

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,116
FILING DATE: 25-FEB-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/930,548
FILING DATE: 23-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Gordon, Alan M.
REGISTRATION NUMBER: 30,637
REFERENCE/DOCKET NUMBER: 31,298-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-831-3244
TELEFAX: 201-831-3305
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 4236 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..4068

US-08-810-116-7
; Sequence 9, Application US/08469005A
; Patent No. 5665874
; GENERAL INFORMATION:
; APPLICANT: KUHAJDA, FRANCIS P.
; APPLICANT: PASTERNAK, GARY A.
; TITLE OF INVENTION: CANCER RELATED ANTIGEN

Query Match 5.6%; Score 17; DB 1; Length 4236;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 163 ctcaagatcctcatcca 179
|||||
Db 2656 CTCAAGATCCTCATCCA 2672

RESULT 15
US-07-930-548A-7
; Sequence 7, Application US/07930548A
; Patent No. 5861301
; GENERAL INFORMATION:
; APPLICANT: Terman, Bruce I.
; APPLICANT: Carrion, Miguel E.
; TITLE OF INVENTION: Identification of a No. 5861301el Human Growth
; TITLE OF INVENTION: Factor Receptor
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07470

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/930,548A
FILING DATE: 23-NOV-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gordon, Alan M.
REGISTRATION NUMBER: 30,637
REFERENCE/DOCKET NUMBER: 31,298-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-831-3244
TELEFAX: 201-831-3305
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 4236 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..4068

Query Match 5.6%; Score 17; DB 2; Length 4236;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 163 ctcaagatcctcatcca 179
|||||
Db 2656 CTCAAGATCCTCATCCA 2672

RESULT 16
US-08-469-005A-9/c
; Sequence 9, Application US/08469005A
; Patent No. 5665874
; GENERAL INFORMATION:
; APPLICANT: KUHAJDA, FRANCIS P.
; APPLICANT: PASTERNAK, GARY A.
; TITLE OF INVENTION: CANCER RELATED ANTIGEN

```
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BAKER & BOTTS, L.L.P.
; STREET: 1299 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20004-2400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,005A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/188,426
; FILING DATE: 24-JAN-1994
; APPLICATION NUMBER: 08/096,908
; FILING DATE: 26-JUL-1993
; APPLICATION NUMBER: 07/917,716
; FILING DATE: 24-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Posorske, Laurence H
; REGISTRATION NUMBER: 34,698
; REFERENCE/DOCKET NUMBER: 082482-0113
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-639-7700
; TELEFAX: 202-639-7890
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8460 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 124..7650
; OTHER INFORMATION:
; US-08-469-005A-9

Query Match 5.6%; Score 17; DB 1; Length 8460;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 83 gcagcagctgtgacacc 99
|||||
Db 1738 GCAGCAGCTGTGACACC 1722

RESULT 17
US-09-261-907-1/c
; Sequence 1, Application US/09261907A
; Patent No. 6294364
; GENERAL INFORMATION:
; APPLICANT: ELLIS, CATHERINE
; APPLICANT: LONSDALE, JOHN
; APPLICANT: BERGSMAN, DEK J.
; APPLICANT: MOONEY, JEFFREY L.
; APPLICANT: DEPIERA, MEGAN E.
; APPLICANT: CHAPMAN, CONRAD
; TITLE OF INVENTION: HUMAN FAS
; FILE REFERENCE: GP-70603
; CURRENT APPLICATION NUMBER: US/09/261,907A
```

```
; CURRENT FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 8519
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-261-907-1

Query Match 5.6%; Score 17; DB 4; Length 8519;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 83 gcagcagctgtgacacc 99
|||||
Db 1770 GCAGCAGCTGTGACACC 1754

RESULT 18
US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match 5.6%; Score 17; DB 4; Length 4403765;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 29 gctacggcgcttcggg 45
|||||
Db 3179438 GCTACGGCGCCTTCGGG 3179422

RESULT 19
US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
```

```
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match      5.6%; Score 17; DB 4; Length 4411529;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 gctacggcgcccttcggg 45
|||||
Db 3185328 GCTACGGCGCCCTTCGGG 3185312

RESULT 20
5457037-7/c
; Patent No. 5457037
; APPLICANT: TOGNONI, ANGELO;CARRERA, PAOLO;CAMERINI, BARBARA;
; GALLI, GIULIANO;LUCCHESI, GIUSEPPE;GRANDI, GUIDO;DI GENNARO, CARLO
; TITLE OF INVENTION: CLONING OF THE GENE CODING THE ISOAMYLASE
; ENZYME AND ITS USE IN THE PRODUCTION OF SAID ENZYME
; NUMBER OF SEQUENCES: 7
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/1,797
; FILING DATE: 08-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 749,621
; FILING DATE: 19-AUG-1991
; APPLICATION NUMBER: 224,114
; FILING DATE: 25-JUL-1988
; SEQ ID NO:7:
; LENGTH: 78
; 5457037-7

Query Match      5.3%; Score 16; DB 6; Length 78;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 134 ccagcgagcaccgcgc 149
|||||
Db 53 CCAGCGAGCACC GC 38

RESULT 21
US-08-998-416-314/c
; Sequence 314, Application US/08998416
; Patent No. 6239264
; GENERAL INFORMATION:
; APPLICANT: Philippsen, Peter
; APPLICANT: Pohlmann, Rainer
; APPLICANT: Steiner, Sabine
; APPLICANT: Mohr, Christine
; APPLICANT: Wendland, Jurgén
; APPLICANT: Knechtle, Philipp
; APPLICANT: Rebschung, Corinne
; TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPIL
; NUMBER OF SEQUENCES: 1152
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NO. 6239264artis Corporation
; STREET: 3054 Cornwalis Road
; CITY: Research Triangle Park
; STATE: NO.6239264th Carolina
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/998.416
; FILING DATE: 24-DEC-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: CH 0016/97
; FILING DATE: 31-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: PF/5-30306/A/CCG1976
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 314:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 850 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: PAG1254UP
; US-08-998-416-314

Query Match      5.3%; Score 16; DB 4; Length 850;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 88 agctgtgacaccgtgg 103
|||||
Db 493 AGCTGTGACACCGTGG 478

RESULT 22
US-09-330-611-15/c
; Sequence 15, Application US/09330611
; Patent No. 6248874
; GENERAL INFORMATION:
; APPLICANT: FREY, Perry A.
; APPLICANT: RUZICKA, Frank J.
; TITLE OF INVENTION: DNA MOLECULES ENCODING BACTERIAL LYSINE 2,3-AMINOMUTASE
; FILE REFERENCE: 032026/0476
; CURRENT APPLICATION NUMBER: US/09/330,611
; CURRENT FILING DATE: 1999-06-11
; EARLIER APPLICATION NUMBER: US 09/198,942
; EARLIER FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 15
; LENGTH: 1065
; TYPE: DNA
; ORGANISM: Treponema pallidum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1065)
; US-09-330-611-15

Query Match      5.3%; Score 16; DB 4; Length 1065;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 138 cgagcaccgcgcgctg 153
|||||
Db 685 CGAGCACC GC GCTG 670

RESULT 23
US-07-681-704A-1/c
; Sequence 1, Application US/07681704A
; Patent No. 5279965
; GENERAL INFORMATION:
```


REFERENCE/DOCKET NUMBER: 18740/125/CACO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5300
TELEFAX: 202 672 5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2185 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 531..2069
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 531..902
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 903..2069
FEATURE:
NAME/KEY: misc_feature
LOCATION: 531..533
OTHER INFORMATION: /note= "Met at position -124
OTHER INFORMATION: represents fMet"
US-08-173-508-3

Query Match 5.3%; Score 16; DB 1; Length 2185;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 216 ggcgtgacccaagccg 231
Db 1943 GCGGTGCACCAAGCCG 1958

RESULT 26
US-08-265-310-3
Sequence 3, Application US/08265310
Patent No. 5856166
GENERAL INFORMATION:
APPLICANT: Bartfeld, Daniel
APPLICANT: Butler, Michael J.
APPLICANT: Hadary, Dany
APPLICANT: Jenish, David
APPLICANT: Krieger, Timothy
APPLICANT: Malek, Lawrence T.
APPLICANT: Soostmeyer, Gisela
APPLICANT: Walczyk, Eva
APPLICANT: Krygsman, Phyllis
APPLICANT: Garven, Shella
TITLE OF INVENTION: STREPTOMYCES PROTEASES AND IMPROVED
TITLE OF INVENTION: STREPTOMYCES STRAINS FOR EXPRESSION OF PEPTIDES AND
TITLE OF INVENTION: POLYPEPTIDES
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W.
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/265.310
FILING DATE: 24-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,508

FILING DATE: 23-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 18740/133/CACO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5300
TELEFAX: 202 672 5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2185 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 531..2069
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 531..902
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 903..2069
FEATURE:
NAME/KEY: misc_feature
LOCATION: 531..533
OTHER INFORMATION: /note= "Met at position -124
OTHER INFORMATION: represents fMet"
US-08-265-310-3

Query Match 5.3%; Score 16; DB 2; Length 2185;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 216 ggcgtgacccaagccg 231
Db 1943 GCGGTGCACCAAGCCG 1958

RESULT 27
US-08-951-742-3
Sequence 3, Application US/08951742
Patent No. 6127144
GENERAL INFORMATION:
APPLICANT: Bartfeld, Daniel
APPLICANT: Michael J. Butler
APPLICANT: Dany Hadary
APPLICANT: David Jenish
APPLICANT: Tim Krieger
APPLICANT: Lawrence T. Malek
APPLICANT: Gisela Soostmeyer
APPLICANT: Eva Walczyk
APPLICANT: Phyllis Krygsman
APPLICANT: Shella Garven
TITLE OF INVENTION: METHOD FOR EXPRESSION OF PROTEINS IN
TITLE OF INVENTION: BACTERIAL HOST CELLS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/951,742

US-08-403-545-1

Sequence 1, Application US/08403545
Patent No. 5656483
GENERAL INFORMATION:
APPLICANT: Sokatch, John R.
APPLICANT: Sykes, Pamela Joy
APPLICANT: Madhusudhan, K.T.
TITLE OF INVENTION: Genes Encoding Operon and Promoter for
TITLE OF INVENTION: Branched Chain Keto Acid Dehydrogenase of Pseudomonas putida
TITLE OF INVENTION: and Methods
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carolyn D. Moon
ADDRESSEE: Dunlap, Coddling, Perterson and Lee
STREET: 9400 N Broadway, Suite 420
CITY: Oklahoma City
STATE: Oklahoma
COUNTRY: USA
ZIP: 73114
COMPUTER TYPE: Diskette 5.25 inch, 360 Kb Storage
COMPUTER: IBM AT
OPERATING SYSTEM: MS-DOS Version 3.3
SOFTWARE: Professional Write 2.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/403,545
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 7/603/781
APPLICATION NUMBER: 07/172,148
FILING DATE: 23-003-1988
ATTORNEY/AGENT INFORMATION:
NAME: Carolyn D. Moon
REGISTRATION NUMBER: 33,022
REFERENCE/DOCKET NUMBER: 5820.101
TELECOMMUNICATION INFORMATION:
TELEPHONE: Attorney, (405) 478-5344
TELEFAX: Attorney, (405) 478-5349
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6122 base pairs
TYPE: Nucleic acid
STRANDEDNESS: Double stranded
TOPOLOGY: Circular
MOLECULE TYPE: Genomic DNA
DESCRIPTION: Seq ID No. 56564831 is genomic DNA from P. putida
DESCRIPTION: strain Pg2 which contains the control region regulating
DESCRIPTION: expression of the bkd operon and the four structural genes
DESCRIPTION: of the bkd operon, bkdA1, bkdA2, bkdB and lpdV.
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: No. 5656483 applicable
ORIGINAL SOURCE:
ORGANISM: Pseudomonas putida
STRAIN: Pg2
INDIVIDUAL ISOLATE: No. 5656483 applicable
DEVELOPMENTAL STAGE: No. 5656483 applicable
HAPLOTYPE: No. 5656483 applicable
TISSUE TYPE: No. 5656483 applicable
CELL TYPE: Gram negative, aerobic bacilli
CELL LINE: No. 5656483 applicable
ORGANELLE: No. 5656483 applicable
IMMEDIATE SOURCE:
LIBRARY: Genomic DNA from Pseudomonas putida
CLONE: pJRS54
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION: 35 Minutes
UNITS:
FEATURE:
NAME/KEY: Promoter plus leader

LOCATION: 1-792
IDENTIFICATION METHOD: By experiment
OTHER INFORMATION: The promoter plus leader are responsible
OTHER INFORMATION: for expression of the bkd operon in Pseudomonas putida
FEATURE:
NAME/KEY: bkdA1, Gene encoding branched-chain keto acid
NAME/KEY: dehydrogenase-decarboxylase E1 alpha subunit.
LOCATION: 805-2031. Initiating methionine codon is at
LOCATION: position 802, however mature peptide does not contain N-
LOCATION: terminal methionine.
IDENTIFICATION METHOD: By experiment
OTHER INFORMATION: The E1 component of branched chain keto
OTHER INFORMATION: acid dehydrogenase catalyzes the oxidative decarboxylation.
OTHER INFORMATION: of the keto acid substrate. E1 is composed of two subunits.
OTHER INFORMATION: E1 alpha and E1 beta.
FEATURE:
NAME/KEY: bkdA2, Gene encoding branched-chain keto acid
NAME/KEY: dehydrogenase-decarboxylase E1 beta subunit.
LOCATION: 2078-3091. Initiating methionine codon is position
LOCATION: 2075, however mature peptide does not contain N-terminal
LOCATION: methionine.
IDENTIFICATION METHOD: By experiment
OTHER INFORMATION: See description for Feature 2 above.
FEATURE:
NAME/KEY: bkdB Gene encoding the E2 component of branched
NAME/KEY: chain keto acid dehydrogenase
LOCATION: 3098-4363 Initiating methionine codon is position
LOCATION: 3095, however mature peptide does not contain N-terminal
LOCATION: methionine.
IDENTIFICATION METHOD: By experiment
OTHER INFORMATION: E2 catalyzes the transacylation of the
OTHER INFORMATION: fatty acyl group from the lipoyl residue of E2 to coenzym
OTHER INFORMATION: A. E2 is the core of the complex and binds E1 and E3
OTHER INFORMATION: components.
FEATURE:
NAME/KEY: lpdV, Gene encoding the E3 component of branched
NAME/KEY: chain keto acid dehydrogenase
LOCATION: 4369-5745. N-terminal methionine is present on
LOCATION: mature peptide.
IDENTIFICATION METHOD: By experiment
OTHER INFORMATION: E3 is LPD-val, the specific lipamide
OTHER INFORMATION: dehydrogenase which catalyzes oxidation of the
OTHER INFORMATION: dihydrolipoyl residue of the E2 component of branched cha
OTHER INFORMATION: keto acid dehydrogenase and the reduction of NAD+.
OTHER INFORMATION:
AUTHORS: Sokatch, John R.
AUTHORS: McCully, Vicki
AUTHORS: Gebrosky, Janet
AUTHORS: Sokatch, David, J.
TITLE: Isolation of a specific lipamide dehydrogenase
TITLE: for a branched-chain keto acid dehydrogenase
TITLE: from Pseudomonas putida
JOURNAL: Journal of Bacteriology
VOLUME: 148
ISSUE:
PAGES: 639-646
DATE: 1981
AUTHORS: Sokatch, John R.
AUTHORS: McCully, Vicki
AUTHORS: Roberts, C.M.
TITLE: Purification of a branched-chain keto acid
TITLE: dehydrogenase from Pseudomonas putida
JOURNAL: Journal of Bacteriology
VOLUME: 148
ISSUE:
PAGES: 647-652
DATE: 1981
AUTHORS: Sykes, Pamela
AUTHORS: Burns, Gayle
AUTHORS: Menard, Joan
AUTHORS: Hatter, Kenneth
AUTHORS: Sokatch, John R.
TITLE: Molecular cloning of genes encoding branched-chain

TITLE: keto acid dehydrogenase of Pseudomonas putida
JOURNAL: Journal of Bacteriology
VOLUME: 169
ISSUE: 1619-1625
PAGES: 1987
DATE: 1987
AUTHORS: Burns, Gayle
AUTHORS: Brown, Tracy
AUTHORS: Hatter, Kenneth
AUTHORS: Sokatch, John R.
TITLE: Comparison of the amino acid sequences of the
TITLE: transacylase components of branched-chain oxoacid
TITLE: dehydrogenase of Pseudomonas putida, and the pyruvate and 2-
TITLE: oxoglutarate dehydrogenases of Escherichia coli
JOURNAL: European Journal of Biochemistry
VOLUME: 176
ISSUE: 165-169
PAGES: 1988
DATE: 1988
AUTHORS: Burns, Gayle
AUTHORS: Brown, Tracy
AUTHORS: Hatter, Kenneth
AUTHORS: Idriss, John M.
AUTHORS: Sokatch, John R.
TITLE: Similarity of the E1 subunits of branched-chain-
TITLE: oxoacid dehydrogenase from Pseudomonas putida to the
TITLE: corresponding subunits of mammalian branched-chain-oxoacid
TITLE: and pyruvate dehydrogenases
JOURNAL: European Journal of Biochemistry
VOLUME: 176
PAGES: 311-317
DATE: 1988
AUTHORS: Burns, Gayle
AUTHORS: Brown, Tracy
AUTHORS: Hatter, Kenneth
AUTHORS: Sokatch, John R.
TITLE: Sequence analysis of the lpdV gene for lipoamide
Patent No. 5656483
TITLE: dehydrogenase of Pseudomonas putida
JOURNAL: European Journal of Biochemistry
VOLUME: 179
ISSUE: 61-69
PAGES: 1989
DATE: 1989
AUTHORS: Madhusudhan, K.T.
AUTHORS: Huang, G.
AUTHORS: Burns, Gayle
AUTHORS: Sokatch, J.R.
TITLE: Transcriptional analysis of the promoter region of
TITLE: the branched chain keto acid dehydrogenase operon of
TITLE: Pseudomonas putida
JOURNAL: Journal of Bacteriology
VOLUME: 172
ISSUE: October, 1990
Query Match 5.3%; Score 16; DB 1; Length 6122;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 192 cctcaacgtgtggtcaac 207
Db 1509 CcTCAACGGTGGTCAAC 1524
RESULT 32
US-08-404-381-1
Sequence 1, Application US/08404381
Patent No. 6168945
GENERAL INFORMATION:
APPLICANT: Sokatch, John R.
APPLICANT: Sykes, Pamela Joy
APPLICANT: Madhusudhan, K.T.

TITLE OF INVENTION: Genes Encoding Operon and Promoter for
TITLE OF INVENTION: Branched Chain Keto Acid Dehydrogenase of Pseudomonas putid
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carolyn D. Moon
ADDRESSEE: Dunlap, Coddling, Perterson and Lee
STREET: 9400 N. Broadway, Suite 420
CITY: Oklahoma City
STATE: Oklahoma
COUNTRY: USA
ZIP: 73114
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 5.25 Inch, 360 Kb Storage
COMPUTER: IBM AT
OPERATING SYSTEM: MS-DOS Version 3.3
SOFTWARE: Professional Write 2.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/404,381
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603,781
FILING DATE:
APPLICATION NUMBER: 07/172,148
FILING DATE: 23-003-1988
ATTORNEY/AGENT INFORMATION:
NAME: Carolyn D. Moon
REGISTRATION NUMBER: 33, 022
REFERENCE/DOCKET NUMBER: 5820.101
TELECOMMUNICATION INFORMATION: 478-5344
TELEPHONE: Attorney, (405) 478-5344
TELEFAX: Attorney, (405) 478-5349
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6122 base pairs
TYPE: Nucleic acid
STRANDEDNESS: Double stranded
TOPOLOGY: Circular
MOLECULE TYPE: Genomic DNA
DESCRIPTION: Seq ID No. 61689451 is genomic DNA from P. putida
DESCRIPTION: strain ppg2 which contains the control region regulating
DESCRIPTION: expression of the bkd operon and the four structural genes
DESCRIPTION: of the bkd operon, bkdA1, bkdA2, bkdB and lpdV.
HYPOTHETICAL: No
ANTI-SENSE: No
FRAGMENT TYPE: No. 6168945 applicable
ORIGINAL SOURCE:
ORGANISM: Pseudomonas putida
STRAIN: Ppg2
INDIVIDUAL ISOLATE: No. 6168945 applicable
DEVELOPMENTAL STAGE: No. 6168945 applicable
HAPLOTYPE: No. 6168945 applicable
TISSUE TYPE: No. 6168945 applicable
CELL TYPE: Gram negative, aerobic bacilli
CELL LINE: No. 6168945 applicable
ORGANELLE: No. 6168945 applicable
IMMEDIATE SOURCE:
LIBRARY: Genomic DNA from Pseudomonas putida
CLONE: pJRS54
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION: 35 Minutes
UNITS:
FEATURE:
NAME/KEY: Promoter plus leader
LOCATION: 1-792
IDENTIFICATION METHOD: By experiment
OTHER INFORMATION: The promoter plus leader are responsible
OTHER INFORMATION: for expression of the bkd operon in Pseudomonas putida
FEATURE:
NAME/KEY: bkdA1, Gene encoding branched-chain keto acid

NAME/KEY: dehydrogenase-decarboxylase E1 alpha subunit.
LOCATION: 805-2031. Initiating methionine codon is at
LOCATION: position 802, however mature peptide does not contain N-
IDENTIFICATION METHOD: terminal methionine.
IDENTIFICATION METHOD: By experiment
OTHER INFORMATION: The E1 component of branched chain keto
OTHER INFORMATION: acid dehydrogenase catalyzes the oxidative decarboxylation
OTHER INFORMATION: of the keto acid substrate. E1 is composed of two subunits,
OTHER INFORMATION: E1 alpha and E1 beta.
FEATURE:
NAME/KEY: bkdA2. Gene encoding branched-chain keto acid
NAME/KEY: dehydrogenase-decarboxylase E1 beta subunit
LOCATION: 2078-3091. Initiating methionine codon is position
LOCATION: 2075, however mature peptide does not contain N-terminal
LOCATION: methionine.
IDENTIFICATION METHOD: By experiment
OTHER INFORMATION: See description for Feature 2 above.
FEATURE:
NAME/KEY: bkdB Gene encoding the E2 component of branched
NAME/KEY: chain keto acid dehydrogenase
LOCATION: 3098-4363 Initiating methionine codon is position
LOCATION: 3095, however mature peptide does not contain N-terminal
LOCATION: methionine.
IDENTIFICATION METHOD: By experiment
OTHER INFORMATION: E2 catalyzes the transacylation of the
OTHER INFORMATION: fatty acyl group from the lipoyl residue of E2 to coenzyme
OTHER INFORMATION: A. E2 is the core of the complex and binds E1 and E3
OTHER INFORMATION: components.
FEATURE:
NAME/KEY: lpdV. Gene encoding the E3 component of branched
NAME/KEY: chain keto acid dehydrogenase.
LOCATION: 4369-5745. N-terminal methionine is present on
LOCATION: mature peptide.
IDENTIFICATION METHOD: By experiment
OTHER INFORMATION: E3 is lpd-val, the specific lipamide
OTHER INFORMATION: dehydrogenase which catalyzes oxidation of the
OTHER INFORMATION: dihydrolipoyl residue of the E2 component of branched chain
OTHER INFORMATION: keto acid dehydrogenase and the reduction of NAD+.
PUBLICATION INFORMATION:
AUTHORS: Sokatch, John R.
AUTHORS: McCully, Vicki
AUTHORS: Gebrosky, Janet
AUTHORS: Sokatch, David J.
TITLE: Isolation of a specific lipamide dehydrogenase
TITLE: for a branched-chain keto acid dehydrogenase
TITLE: from Pseudomonas putida
JOURNAL: Journal of Bacteriology
VOLUME: 148
ISSUE:
PAGES: 639-646
DATE: 1981
AUTHORS: Sokatch, John R.
AUTHORS: McCully, Vicki
AUTHORS: Roberts, C.M.
TITLE: Purification of a branched-chain keto acid
TITLE: dehydrogenase from Pseudomonas putida
JOURNAL: Journal of Bacteriology
VOLUME: 148
ISSUE:
PAGES: 647-652
DATE: 1981
AUTHORS: Sykes, Pamela
AUTHORS: Burns, Gayle
AUTHORS: Menard, Joan
AUTHORS: Hatter, Kenneth
AUTHORS: Sokatch, John R.
TITLE: Molecular cloning of genes encoding branched-chain
TITLE: keto acid dehydrogenase of Pseudomonas putida
JOURNAL: Journal of Bacteriology
VOLUME: 169
ISSUE:
PAGES: 1619-1625
DATE: 1987

AUTHORS: Burns, Gayle
AUTHORS: Brown, Tracy
AUTHORS: Hatter, Kenneth
AUTHORS: Sokatch, John R.
TITLE: Comparison of the amino acid sequences of the
TITLE: transacylase components of branched-chain oxoacid
TITLE: dehydrogenase of Pseudomonas putida, and the pyruvate and 2-
TITLE: oxoglutarate dehydrogenases of Escherichia coli
JOURNAL: European Journal of Biochemistry
VOLUME: 176
ISSUE:
PAGES: 165-169
DATE: 1988
AUTHORS: Burns, Gayle
AUTHORS: Brown, Tracy
AUTHORS: Hatter, Kenneth
AUTHORS: Idriss, John M.
AUTHORS: Sokatch, John R.
TITLE: Similarity of the E1 subunits of branched-chain-
TITLE: oxoacid dehydrogenase from Pseudomonas putida to the
TITLE: corresponding subunits of mammalian branched-chain-oxoacid
TITLE: and pyruvate dehydrogenases
JOURNAL: European Journal of Biochemistry
VOLUME: 176
ISSUE:
PAGES: 311-317
DATE: 1988
AUTHORS: Burns, Gayle
AUTHORS: Brown, Tracy
AUTHORS: Hatter, Kenneth
AUTHORS: Sokatch, John R.
TITLE: Sequence analysis of the lpdV gene for lipamide
Patent No. 6168945
TITLE: dehydrogenase of Pseudomonas putida
JOURNAL: European Journal of Biochemistry
VOLUME: 179
ISSUE:
PAGES: 61-69
DATE: 1989
AUTHORS: Madhusudhan, K.T.
AUTHORS: Huang, G.
AUTHORS: Burns, Gayle
AUTHORS: Sokatch, J.R.
TITLE: Transcriptional analysis of the promoter region of
TITLE: the branched chain keto acid dehydrogenase operon of
TITLE: Pseudomonas putida
JOURNAL: Journal of Bacteriology
VOLUME: 172

Query Match 5.3%; Score 16; DB 4; Length 6122;
Best Local Similarity 100.0%; Pred. No. 46;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 192 cctcaacgtggtcaac 207

|||||

Db 1509 CCTCAACGTGTCAC 1524

RESULT 33

US-08-258-261B-6/c

; Sequence 6, Application US/08258261B

; Patent No. 5635949

; GENERAL INFORMATION:

; APPLICANT: Schupp, Thomas

; APPLICANT: Ligon, James M.

; APPLICANT: Beck, James Joseph

; APPLICANT: Hill, Dwight Steven

; APPLICANT: Ryals, John Andrew

; APPLICANT: Gaffney, Thomas Deane

; APPLICANT: Lam, Stephen Ting

; APPLICANT: Hammer, Phillip E.

; APPLICANT: Uknes, Scott Joseph

; TITLE OF INVENTION: Genes for the synthesis of

```

; TITLE OF INVENTION: antipathogenic substances
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ciba-Geigy Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/258,261B
; FILING DATE: 08-JUN-1994
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/457,205
; FILING DATE: 01-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: CGC 1506/CIP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8614
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28958 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-258-261B-6

Query Match 5.3%; Score 16; DB 1; Length 28958;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 126 cgcacgcccagcgag 141
|||||
Db 18696 CGCCAGCCGCGAG 18681

RESULT 34
US-08-456-837-6/c
; Sequence 6, Application US/08456837
; Patent No. 5643774
; GENERAL INFORMATION:
; APPLICANT: Schupp, Thomas
; APPLICANT: Ligon, James M.
; APPLICANT: Beck, James Joseph
; APPLICANT: Hill, Dwight Steven
; APPLICANT: Ryals, John Andrew
; APPLICANT: Gaffney, Thomas Deane
; APPLICANT: Lam, Stephen Ting
; APPLICANT: Hammer, Phillip E.
; APPLICANT: Uknes, Scott Joseph
; TITLE OF INVENTION: Genes for the synthesis of
; TITLE OF INVENTION: antipathogenic substances
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ciba-Geigy Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,342
; FILING DATE: 01-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/457,205
; FILING DATE: 01-JUN-1995
; APPLICATION NUMBER: 08/258,261
; FILING DATE: 08-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: CGC 1506/CIP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8614
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28958 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-456-837-6
```

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/456,837
; FILING DATE: 01-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/457,205
; FILING DATE: 01-JUN-1995
; APPLICATION NUMBER: 08/258,261
; FILING DATE: 08-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: CGC 1506/CIP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8614
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28958 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-456-837-6

Query Match 5.3%; Score 16; DB 1; Length 28958;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 126 cgcacgcccagcgag 141
|||||
Db 18696 CGCCAGCCGCGAG 18681

RESULT 35
US-08-457-342-6/c
; Sequence 6, Application US/08457342
; Patent No. 5662898
; GENERAL INFORMATION:
; APPLICANT: Schupp, Thomas
; APPLICANT: Ligon, James M.
; APPLICANT: Beck, James Joseph
; APPLICANT: Hill, Dwight Steven
; APPLICANT: Ryals, John Andrew
; APPLICANT: Gaffney, Thomas Deane
; APPLICANT: Lam, Stephen Ting
; APPLICANT: Hammer, Phillip E.
; APPLICANT: Uknes, Scott Joseph
; TITLE OF INVENTION: Genes for the synthesis of
; TITLE OF INVENTION: antipathogenic substances
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ciba-Geigy Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,342
```

; FILING DATE: 01-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA: US 08/457,205
; FILING DATE: 01-JUN-1995
; APPLICATION NUMBER: 08/258,261
; FILING DATE: 08-Jun-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8614
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28958 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-457-342-6

Query Match 5.3%; Score 16; DB 1; Length 28958;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 126 cgccacggccagcgag 141
|||||

Db 18696 CGCCACGCCAGCGAG 18681

RESULT 36
US-08-457-646A-6/c
; Sequence 6, Application US/08457646A
; Patent No. 5679560
; GENERAL INFORMATION:
; APPLICANT: Schupp, Thomas
; APPLICANT: Ligon, James M.
; APPLICANT: Beck, James Joseph
; APPLICANT: Hill, Dwight Steven
; APPLICANT: Ryals, John Andrew
; APPLICANT: Gaffney, Thomas Deane
; APPLICANT: Lam, Stephen Ting
; APPLICANT: Hammer, Phillip E.
; APPLICANT: Uknes, Scott Joseph
; TITLE OF INVENTION: Genes for the synthesis of
; TITLE OF INVENTION: antipathogenic substances
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ciba-Geigy Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,646A
; FILING DATE: 01-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/457,205
; FILING DATE: 01-JUN-1995
; APPLICATION NUMBER: 08/258,261
; FILING DATE: 08-Jun-1994

; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: CGC 1506/CIP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8614
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28958 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-457-646A-6

Query Match 5.3%; Score 16; DB 1; Length 28958;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 126 cgccacggccagcgag 141
|||||

Db 18696 CGCCACGCCAGCGAG 18681

RESULT 37
US-08-458-076A-6/c
; Sequence 6, Application US/08458076A
; Patent No. 5698425
; GENERAL INFORMATION:
; APPLICANT: Schupp, Thomas
; APPLICANT: Ligon, James M.
; APPLICANT: Beck, James Joseph
; APPLICANT: Hill, Dwight Steven
; APPLICANT: Ryals, John Andrew
; APPLICANT: Gaffney, Thomas Deane
; APPLICANT: Lam, Stephen Ting
; APPLICANT: Hammer, Phillip E.
; APPLICANT: Uknes, Scott Joseph
; TITLE OF INVENTION: Genes for the synthesis of
; TITLE OF INVENTION: antipathogenic substances
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ciba-Geigy Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,076A
; FILING DATE: 01-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/457,205
; FILING DATE: 01-JUN-1995
; APPLICATION NUMBER: 08/258,261
; FILING DATE: 08-Jun-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: CGC 1506/CIP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8614
; TELEFAX: 919-541-8689

; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28958 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-458-076A-6

Query Match 5.3%; Score 16; DB 1; Length 28958;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 126 cgcacgcccagcgag 141
|||||

DB 18696 CCCACGCCACGCGAG 18681

RESULT 38

US-08-764-233A-4/c
; Sequence 4, Application US/08764233A
; Patent No. 5716849
; GENERAL INFORMATION:
; APPLICANT: Ligon, James M.
; APPLICANT: Schupp, Thomas
; APPLICANT: Beck, James J.
; APPLICANT: Hill, Dwight S.
; APPLICANT: Neff, Snezana
; APPLICANT: Ryals, John A.
; TITLE OF INVENTION: Genes For The Biosynthesis Of Soraphen
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ciba-Geigy Corporation
; STREET: 520 White Plains Road, P.O. Box 2005
; CITY: Tarrytown
; STATE: NY
; COUNTRY: USA
; ZIP: 10591

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/764,233A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/729,214
; FILING DATE: 09-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/258,261
; FILING DATE: 08-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: 1506/CIP6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8587
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28958 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Sorangium cellulosum
; IMMEDIATE SOURCE:

; CLONE: p98/1
US-08-764-233A-4

Query Match 5.3%; Score 16; DB 1; Length 28958;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 126 cgcacgcccagcgag 141
|||||

DB 18696 CCCACGCCACGCGAG 18681

RESULT 39

US-08-457-335A-6/c
; Sequence 6, Application US/08457335A
; Patent No. 5723759
; GENERAL INFORMATION:
; APPLICANT: Schupp, Thomas
; APPLICANT: Ligon, James M.
; APPLICANT: Beck, James Joseph
; APPLICANT: Hill, Dwight Steven
; APPLICANT: Ryals, John Andrew
; APPLICANT: Gaffney, Thomas Deane
; APPLICANT: Lam, Stephen Ting
; APPLICANT: Hammer, Phillip E.
; APPLICANT: Uknes, Scott Joseph

; TITLE OF INVENTION: Genes for the synthesis of
; antipathogenic substances
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ciba-Geigy Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,335A
; FILING DATE: 01-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/457,205
; FILING DATE: 01-JUN-1995
; APPLICATION NUMBER: 08/258,261
; FILING DATE: 08-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: CGC 1506/CIP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8614
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28958 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO

Query Match 5.3%; Score 16; DB 1; Length 28958;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 126 cgcacggccgcgag 141
|||||
Db 18696 CGCCAGCGCCAGCAG 18681

RESULT 40
US-08-729-214-6/C
; Sequence 6, Application US/08729214
; Patent No. 5817502
; GENERAL INFORMATION:
; APPLICANT: Ligon, James M.
; APPLICANT: Hill, Dwight Steven
; APPLICANT: Ryals, John Andrew
; APPLICANT: Hammer, Phillip E.
; APPLICANT: van Pee, Karl-Heinz
; TITLE OF INVENTION: Genes for the synthesis of
; TITLE OF INVENTION: antipathogenic substances
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ciba-Geigy Corporation
; STREET: 520 White Plains Road
; CITY: Tarrytown
; STATE: NY
; COUNTRY: USA
; ZIP: 10591
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/729,214
; FILING DATE: TBA
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: CGC 1506/CIP5
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28958 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-729-214-6

Query Match 5.3%; Score 16; DB 1; Length 28958;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 126 cgcacggccgcgag 141
|||||
Db 18696 CGCCAGCGCCAGCAG 18681

RESULT 41
US-09-028-934-6/c
; Sequence 6, Application US/09028934
; Patent No. 6117670
; GENERAL INFORMATION:
; APPLICANT: Ligon, James M.
; APPLICANT: Hill, Dwight S.
; APPLICANT: Lam, Steven T.
; APPLICANT: Hammer, Phillip E.

; APPLICANT: van Pee, Karl-Heinz
; APPLICANT: Kirner, Sabine
; APPLICANT: Young, Thomas R.
; TITLE OF INVENTION: Pyrrolnitrin Biosynthesis Genes and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NO. 6117670artis Corporation
; STREET: 3054 Cornwalls Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/028,934
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/729,214
; FILING DATE: 09-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/258,261
; FILING DATE: 08-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: CGC1506/CIP7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28958 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-09-028-934-6

Query Match 5.3%; Score 16; DB 3; Length 28958;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 126 cgcacggccgcgag 141
|||||
Db 18696 CGCCAGCGCCAGCAG 18681

RESULT 42
US-08-764-233A-1/c
; Sequence 1, Application US/08764233A
; Patent No. 5716849
; GENERAL INFORMATION:
; APPLICANT: Ligon, James M.
; APPLICANT: Schupp, Thomas
; APPLICANT: Beck, James J.
; APPLICANT: Hill, Dwight S.
; APPLICANT: Neff, Snezana
; APPLICANT: Ryals, John A.
; TITLE OF INVENTION: Genes For The Biosynthesis Of Soraphen
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ciba-Geigy Corporation
; STREET: 520 White Plains Road, P.O. Box 2005
; CITY: Tarrytown

```

; LOCATION: 24638..30820
; OTHER INFORMATION: /product= "Module 2 of SorB"
;
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 30881..35446
; OTHER INFORMATION: /product= "Module 3 of SorB"
;
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 35528..40114
; OTHER INFORMATION: /product= "Module 4 of SorB"
;
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 40190..46318
; OTHER INFORMATION: /product= "Module 5 of SorB"
;
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 46851..47891
; OTHER INFORMATION: /product= "SorM"
;
; OTHER INFORMATION: /note= "The protein encoded by the sorM gene is highly homologous to the methyltransferase from Streptomyces hygroscopicus that is involved in the synthesis of the polyketide rapamycin."
;
US-08-764-233A-1

Query Match          5.3%; Score 16; DB 1; Length 49377;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 126 cgcacggcgccagcgaq 141
      |||||
Db 34999 CGCCACGCCGCGAG 34984

RESULT 43
US-09-020-956-99
; Sequence 99, Application US/09020956
; Patent No. 6261562
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillin, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHYLTRANSFERASE INHIBITORS
; NUMBER OF SEQUENCES: 178
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/020,956
; FILING DATE: 09-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Makl, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.427C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 99:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 171 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA

```

; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-09-020-956-99

Query Match 5.0%; Score 15; DB 4; Length 171;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 229 ccgcaggggccccctc 243
|||||
Db 28 CCGCAGGGCCCCCTC 42

RESULT 44

US-09-030-607-99
; Sequence 99, Application US/09030607
; Patent No. 6262245
; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
; NUMBER OF SEQUENCES: 224
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/030,607
; FILING DATE: 25-FEB-1998

CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.427C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031

; INFORMATION FOR SEQ ID NO: 99:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 171 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:

; ORGANISM: Homo sapiens
US-09-030-607-99

Query Match 5.0%; Score 15; DB 4; Length 171;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 229 ccgcaggggccccctc 243
|||||
Db 28 CCGCAGGGCCCCCTC 42

RESULT 45

US-09-439-313-99

; Sequence 99, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqui
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 99
; LENGTH: 171
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-439-313-99

Query Match 5.0%; Score 15; DB 4; Length 171;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 229 ccgcaggggccccctc 243
|||||
Db 28 ccgcaggggccccctc 42

Search completed: July 15, 2002, 23:07:17
Job time: 22970 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 15, 2002, 23:09:35 ; Search time 932.4 Seconds
(without alignments)
557.942 Million cell updates/sec

Title: US-09-375-248-1_COPY_2546_2848
Perfect score: 303
Sequence: 1 gagcggtgcacctggggag.....actlctctgcgcgccaagcgg 303

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1736436 seqs, 858457221 residues

Word size : 0
Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :	N_Geneseq_032802.*
1:	/SIDSI/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.*
2:	/SIDSI/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.*
3:	/SIDSI/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.*
4:	/SIDSI/gcgdata/geneseq/geneseq-emb1/NA1983.DAT.*
5:	/SIDSI/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.*
6:	/SIDSI/gcgdata/geneseq/geneseq-emb1/NA1985.DAT.*
7:	/SIDSI/gcgdata/geneseq/geneseq-emb1/NA1986.DAT.*
8:	/SIDSI/gcgdata/geneseq/geneseq-emb1/NA1987.DAT.*
9:	/SIDSI/gcgdata/geneseq/geneseq-emb1/NA1988.DAT.*
10:	/SIDSI/gcgdata/geneseq/geneseq-emb1/NA1989.DAT.*
11:	/SIDSI/gcgdata/geneseq/geneseq-emb1/NA1990.DAT.*
12:	/SIDSI/gcgdata/geneseq/geneseq-emb1/NA1991.DAT.*
13:	/SIDSI/gcgdata/geneseq/geneseq-emb1/NA1992.DAT.*
14:	/SIDSI/gcgdata/geneseq/geneseq-emb1/NA1993.DAT.*
15:	/SIDSI/gcgdata/geneseq/geneseq-emb1/NA1994.DAT.*
16:	/SIDSI/gcgdata/geneseq/geneseq-emb1/NA1995.DAT.*
17:	/SIDSI/gcgdata/geneseq/geneseq-emb1/NA1996.DAT.*
18:	/SIDSI/gcgdata/geneseq/geneseq-emb1/NA1997.DAT.*
19:	/SIDSI/gcgdata/geneseq/geneseq-emb1/NA1998.DAT.*
20:	/SIDSI/gcgdata/geneseq/geneseq-emb1/NA1999.DAT.*
21:	/SIDSI/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.*
22:	/SIDSI/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
23:	/SIDSI/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24:	/SIDSI/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	303	100.0	4111	21	Human Flt4/VEGFR-3
2	303	100.0	4111	22	Human Flt4/VEGFR-3
3	303	100.0	4195	17	FLT4 receptor tyro
4	303	100.0	4195	21	Human Flt4 recepto
5	303	100.0	4195	21	Human tyrosine kin
6	303	100.0	4425	16	Protein tyrosine-k
7	303	100.0	4795	21	Human Flt4 recepto
8	303	100.0	4795	21	Human tyrosine kin
9	303	100.0	9108	16	Plasmid PRK5.tk1-1

10	252	83.2	4450	21	AAC62210	Nucleotide sequenc
11	20	6.6	7680	23	AAS70286	DNA encoding novel
12	18	5.9	3351	20	AAZ31552	S. rochei strain E
13	17	5.6	17	18	AAAT71396	Human KDR VEGF rec
14	17	5.6	218	17	AAT14887	Thermus thermophil
15	17	5.6	272	22	ABAI1580	Human nervous syst
16	17	5.6	768	22	ABAI1580	Human CDNA clone (
17	17	5.6	813	22	AAH06553	Human CDNA clone (
18	17	5.6	1101	22	AAS22655	Human CDNA encodin
19	17	5.6	1116	23	AAS85415	DNA encoding novel
20	17	5.6	1116	23	AAS91079	DNA encoding novel
21	17	5.6	1233	23	AAS85413	DNA encoding novel
22	17	5.6	1302	23	AAS83501	Human polynucleoti
23	17	5.6	1406	22	AAH91319	Nucleotide sequenc
24	17	5.6	1417	22	AAH75162	Human CDNA sequenc
25	17	5.6	1767	22	AAH15398	Human CDNA sequenc
26	17	5.6	1824	22	AAI03231	Human reproductive
27	17	5.6	1901	22	ABA15613	Human nervous syst
28	17	5.6	2484	23	AAS83500	DNA encoding novel
29	17	5.6	2624	22	AAH14499	Human CDNA sequenc
30	17	5.6	2863	22	AAS22891	Human CDNA encodin
31	17	5.6	3120	19	AAV53895	Receptor protein t
32	17	5.6	3120	20	AAV65317	Receptor protein t
33	17	5.6	4008	22	AAS22909	DNA encoding novel
34	17	5.6	4071	13	AAQ28272	A novel type III R
35	17	5.6	4071	20	AAV99829	Human receptor tyr
36	17	5.6	4225	22	AAF83308	Human VEGFR-2 enco
37	17	5.6	4236	19	AAV34763	Human KDR genomic
38	17	5.6	5414	22	AAK78291	Human immune/haema
39	17	5.6	5656	23	ABL10071	Drosophila melanog
40	17	5.6	6730	24	ABI99504	Mouse ischaemic co
41	17	5.6	8460	18	AAT88206	CDNA for protein (
42	17	5.6	8470	21	AAZ95007	Cancer specific ge
43	17	5.6	8519	21	AAZ37760	Human fatty acid s
44	17	5.6	8864	22	AAK79882	Human immune/haema
45	17	5.6	9889	23	ABL10070	Drosophila melanog

ALIGNMENTS

RESULT 1	
AAAC62405	
ID	AAAC62405 standard; cDNA: 4111 BP.
XX	
AC	AAAC62405;
XX	
DT	31-JAN-2001 (first entry)
XX	
DE	Human Flt4/VEGFR-3 coding sequence.
XX	
KW	Human: Flt4; fms-like tyrosine kinase 4; lymphoedema;
KW	vascular endothelial growth factor receptor 3; VEGFR-3;
KW	Milroy-Nonne syndrome; lymphoedema praecox; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO200058511-A1.
XX	
PD	05-OCT-2000.
XX	
PF	26-MAR-1999; 99WO-US06133.
XX	
PR	26-MAR-1999; 99WO-US06133.
XX	
PA	(LUDW-) LUDWIG INST CANCER RES.
PA	(UYHE-) UNIV HELSINKI LICENSING LTD OY.
XX	(UYPI-) UNIV PITTSBURGH.
PI	Ferrell RE, Alitalo K, Finegold DN, Karkkainen M;
XX	WPI; 2000-679298/66.
DR	P-PSDB; AAB29047.
DR	

XX Screening a human subject for increased risk of developing a lymphatic
PT disorder, comprises assaying a nucleic acid to determine a mutation
PT altering the sequence of a vascular endothelial growth factor
PT receptor-3 -
XX
PS Claim 14; Page 46-52; 76pp; English.
XX
CC The present sequence is the coding sequence for the human vascular
CC endothelial growth factor receptor 3 (VEGFR-3, also known as Flt4 or
CC fms-like tyrosine kinase 4). It was used in the methods of the invention,
CC which involve the screening of individuals to determine which VEGFR-3
CC alleles they possess and thus their likelihood of developing hereditary
CC lymphoedema. Conditions associated with lymphoedema include Milroy-Nonne
CC syndrome, which is early onset lymphoedema and lymphoedema praecox, which
CC is late onset.
XX
SQ Sequence 4111 BP; 846 A; 1273 C; 1298 G; 694 T; 0 other;

Query Match 100.0%; Score 303; DB 21; Length 4111;
Best Local Similarity 100.0%; Pred. No. 1.6e-141;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 gagcggtgcacctgggagagtgctcggtacgctcgccgttcgggaagtggtggaagcc 60
Db |||||
QY 61 tcgcttttcggcatcccaaggcagcgtgtgacacgtggccgtgaaatgctgaaa 120
Db |||||
QY 121 gagggcgccacggcagcagccgcgctgtgctgagtcgagctcaagatcctcattcac 180
Db |||||
QY 241 ctcatggtgatcgtggagtgctgcaagtacggcaacctctccaacttctcgcgcgccaag 300
Db |||||
QY 301 cgg 303
Db 2846 cgg 2848

RESULT 2
AAC68952
ID AAC68952 standard; cDNA; 4111 BP.
XX
AC AAC68952;
XX
DT 27-FEB-2001 (first entry)
XX
DE Human Flt4/VEGFR-3 coding sequence.
XX
KW Human; gene therapy; lymphatic disorder; hereditary lymphoedema; Flt4;
KW vascular endothelial growth factor receptor-3; VEGFR-3; VEGF-D;
KW fms-like tyrosine kinase 4; ss.
XX
OS Homo sapiens.
XX

Key Location/Qualifiers
FH CDS 20..4111
FT /*tag= a
FT /product= "Human Flt4/VEGFR-3"
XX
XX CA2283470-A1.
PN
XX 26-SEP-2000.
PD

XX 29-SEP-1999; 99CA-2283470.
PF
XX 26-MAR-1999; 99WO-US06133.
PR
XX 16-AUG-1999; 99US-0375248.
PR
XX (UYPI-) UNIV PITTSBURGH.
PA (UYHE-) UNIV HELSINKI LICENSING LTD OY.
PA (LUDW-) LUDWIG INST CANCER RES.
XX
XX Alitalo K, Ferrell RE, Finegold DN, Karkkainen M;
PI
XX WPI; 2001-007762/02.
DR
XX P-PSDB; AAB37604.
DR
XX
PT Screening a human for an increased risk of developing lymphatic
PT disorder comprises assaying nucleic acid for alterations in the
PT sequences expressing vascular endothelial growth factor receptor-3 -
PT
XX Claim 15; Pages 48-54; 99pp; English.
PS
XX
CC The present invention relates to a method for screening a human subject
CC for an increased risk of developing a lymphatic disorder e.g. hereditary
CC lymphoedema. The method comprises assaying nucleic acid of a human
CC subject to determine a presence or an absence of a mutation altering the
CC sequence or expression of vascular endothelial growth factor receptor-3
CC (VEGFR-3)/fms-like tyrosine kinase 4 (Flt4) allele and determining an
CC increased risk of developing lymphatic disorder from presence or absence
CC of the mutation. The present sequence is the coding sequence for human
CC VEGFR-3/Flt4. The presence of a mutation altering the encoded amino acid
CC sequence or expression of at least 1 VEGFR-3 allele in the nucleic acid
CC correlates with an increased risk of developing a lymphatic disorder.
CC Treatment for hereditary lymphoedema can be provided through the
CC administration of VEGF-C and VEGF-D genes (via gene therapy) and
CC proteins.
XX
SQ Sequence 4111 BP; 846 A; 1272 C; 1299 G; 694 T; 0 other;

Query Match 100.0%; Score 303; DB 22; Length 4111;
Best Local Similarity 100.0%; Pred. No. 1.6e-141;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 gagcggtgcacctgggagagtgctcggtacgctcgcccttcgggaagtggtggaagcc 60
Db |||||
QY 2546 gagcggtgcacctgggagagtgctcggtacgctcgcccttcgggaagtggtggaagcc 2605
Db |||||
QY 61 tcgcttttcggcatcccaaggcagcagcgtgtgacacgtggccgtgaaatgctgaaa 120
Db |||||
QY 2606 tcgcttttcggcatcccaaggcagcagcgtgtgacacgtggccgtgaaatgctgaaa 2665
Db |||||
QY 121 gagggcgccacggcagcagccgcgctgtgctgagtcgagctcaagatcctcattcac 180
Db |||||
QY 2666 gagggcgccacggcagcagccgcgctgtgctgagtcgagctcaagatcctcattcac 2725
Db |||||
QY 181 atcggcaacacctcaacgtggtcaacctcctcggcgctgacccaagcgcaggggcccc 240
Db |||||
QY 2726 atcggcaacacctcaacgtggtcaacctcctcggcgctgacccaagcgcaggggcccc 2785
Db |||||
QY 241 ctcatggtgatcgtggagtgctgcaagtacggcaacctctccaacttctcgcgcgccaag 300
Db |||||
QY 2786 ctcatggtgatcgtggagtgctgcaagtacggcaacctctccaacttctcgcgcgccaag 2845
Db |||||
QY 301 cgg 303
Db 2846 cgg 2848

RESULT 3
AAT12068
ID AAT12068 standard; DNA; 4195 BP.
XX
AC AAT12068;


```

XX      Sequence 4195 BP; 889 A; 1279 C; 1305 G; 722 T; 0 other;
SQ
      Query Match      100.0%; Score 303; DB 21; Length 4195;
      Best Local Similarity 100.0%; Pred. No. 1.6e-141;
      Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 gagcggtgcacctggggagagtgctcggtcacgcgcttcgcggaaagtggtggaagcc 60
DB      2546 gagcggtgcacctggggagagtgctcggtcacgcgcttcgcggaaagtggtggaagcc 2605
QY      61 tccgctttcgcattccacaaggcagcagctgtgacaccgtggccgtgaaatgctgaaa 120
DB      2606 tccgctttcggcatccacaaggcagcagctgtgacaccgtggccgtgaaatgctgaaa 2665
QY      121 gagggcgccacggcgacgagcagcgcgctgctgagctcgagctcaagatcctcatcac 180
DB      2666 gagggcgccacggcgacgagcagcgctgctgagctcgagctcaagatcctcatcac 2725
QY      181 atcggcaaccactcaacgtggtgtaacctctcctggggcggtgcaccaagcgcagggcccc 240
DB      2726 atcggcaaccactcaacgtggtgtaacctctcctggggcggtgcaccaagcgcagggcccc 2785
QY      241 cteatggtgactggtgagttctcgaagtacggcaacctctccaacttctcgcgcgccaag 300
DB      2786 cteatggtgactggtgagttctcgaagtacggcaacctctccaacttctcgcgcgccaag 2845
QY      301 cgg 303
DB      2846 cgg 2848

RESULT 5
AAZ52333
ID      AAZ52333 standard; cDNA; 4195 BP.
XX
XX      AAZ52333;
DT      17-AUG-2000 (first entry)
XX
DE      Human tyrosine kinase receptor Flt4-short form cDNA.
XX
KW      Human; receptor tyrosine kinase; RTK; Flt4; fms-like tyrosine kinase 4;
KW      VEGFR-3; vascular endothelial growth factor receptor-3; chromosome 5q35;
KW      cytosolic; tumour imaging; anti-tumour therapy; treatment; diagnosis;
KW      neoplastic disease; lymphoma; carcinoma; breast; squamous cell; melanoma;
KW      sarcoma; malignancy; ss.
XX
OS      Homo sapiens.
XX
XX      Key      Location/Qualifiers
XX      CDS      20..3916
XX      FT      /*tag= a
XX      FT      /product= "Flt4 receptor-short form"
XX      FT      /note= "The start codon is surrounded by typical
XX      FT      consensus kozak sequence"
XX      FT      20..79
XX      FT      sig_peptide /*tag= b
XX      FT      /note= "Directs protein to endoplasmic reticulum"
XX      FT      mat_peptide 80..3913
XX      FT      /*tag= c
XX      FT      /product= "Mature Flt4 receptor-short form"
XX
XX      WO200021560-A1.
XX
XX      20-APR-2000.
XX
XX      08-OCT-1999; 99WO-US23525.
XX
XX      09-OCT-1998; 98US-0169079.
XX
XX      {LUDWIG INST CANCER RES.
XX

```


FT	/*tag= a
FT	/product= "flt-4"
FT	/transl_except= (pos: 55..57, aa: Trp)
FT	/transl_except= (pos: 58..60, aa: Leu)
FT	/transl_except= (pos: 61..63, aa: Cys)
FT	/transl_except= (pos: 64..66, aa: Leu)
FT	/transl_except= (pos: 67..69, aa: Gly)
FT	/transl_except= (pos: 70..72, aa: Leu)
FT	/transl_except= (pos: 73..75, aa: Leu)
FT	/transl_except= (pos: 76..78, aa: Asp)
FT	/transl_except= (pos: 79..81, aa: Gly)
FT	/transl_except= (pos: 82..84, aa: Leu)
FT	/transl_except= (pos: 85..87, aa: Val)
FT	/transl_except= (pos: 88..90, aa: Ser)
FT	/transl_except= (pos: 91..93, aa: Asp)
FT	/transl_except= (pos: 94..96, aa: Tyr)
FT	/transl_except= (pos: 97..99, aa: Ser)
FT	/transl_except= (pos: 1639..1641, aa: Lys)
FT	/transl_except= (pos: 2236..2238, aa: Arg)
FT	/transl_except= (pos: 3508..3510, aa: Ser)
FT	/transl_except= (pos: 3598..3600, aa: Ser)
FT	/transl_except= (pos: 3796..3798, aa: Phe)
XX	
PN	WO200062063-A1.
XX	
PD	19-OCT-2000.
XX	
PF	13-APR-1999; 99WO-US08079.
XX	
PR	13-APR-1999; 99WO-US08079.
XX	
PA	(NMWI-) NORTHWEST BIOTHERAPEUTICS INC.
XX	
PI	Su SL;
XX	
DR	WPT: 2000-687067/67.
DR	P-PSDB; AAB30542.
XX	
PT	Detecting metastatic potential, diagnosing metastatic prostate cancer
PT	or determining the prognosis of a subject with prostate cancer
PT	comprises detecting the expression of flt-4 in a prostate cell -
XX	
PS	Claim 6; Fig 1A-F; 78pp; English.
XX	
CC	The present sequence encodes human flt-4. Flt-4 is a receptor type
CC	tyrosine kinase with 7 Ig-like domains similar to other VEGF receptors.
CC	Flt-4 may play a role in lymphangiogenesis. Antisense oligonucleotides
CC	can be used for detecting the metastatic potential, diagnosing
CC	metastatic prostate cancer or determining the prognosis of a subject
CC	with prostate cancer. The method comprises identifying the prostate
CC	cell in a body fluid sample and detecting the expression of flt-4 in
CC	the cell. Expression of flt-4 in a prostate cell indicates that the
CC	cell is a cancerous prostate cell that has metastatic potential or is
CC	a secondary tumour metastasis of a primary prostate tumour.
XX	
QQ	Sequence 4450 BP; 968 A; 1352 C; 1349 G; 781 T; 0 other:
Query Match	83.2%; Score 252; DB 21; Length 4450;
Best Local Similarity	99.7%; Pred. No. 4.4e-116;
Matches 30;	Conservative 0; Mismatches 1; Indels 0; Gaps
QY	1 gagcggctgcacctgggagagtgctcggtcacggcgcccttcgggaaggtggtggaagcc 60
Db	2548 gagcggctgcacctgggagagtgctcggtcacggcgcccttcgggaaggtggtggaagcc 2607
QY	61 tcgcgcttcggatccacaaagggcagcagctgtgacaccgtggccgtgaaatgctgaaa 120
Db	2608 tcgcgcttcggatccacaaagggcagcagctgtgacaccgtggccgtgaaatgctgaaa 2667
QY	121 gagggcgccacggccagcagaccgcgcgctgatgctggagctcaagatccctcatcac 180
Db	2668 gagggcgccacggccagcagaccgcgcgctgatgctggagctcaagatccctcatcac 2727

Oy 181 atcggcaaccactcaacgtggtcaacctctcgtcggtggtgcacccaagcgcagggccccc 240
Db 2728 atcggcaaccactcaacgtggtcaacctctcgtcggtggtgcacccaagcgcagggccccc 2787
Oy 241 ctcatggtgatcgtggagttctgcaagtacaggcaacctctccaacttccctgctgcgcgccaag 300
Db 2788 ctcatggtgatcgtggagttctgcaagtacaggcaacctctccaacttccctgctgcgcgccaag 2847
Oy 301 cgg 303
Db 2848 cgg 2850

RESULT 11
AAS70286
ID AAS70286 standard; cDNA; 7680 BP.
XX
AC AAS70286;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #6090.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN W0200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
DR WPI: 2001-639362/73.
DR P-PSDB: ABC06099.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
XX biodiversity -
PS Claim 1: SEQ ID NO 6090; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX
SQ Sequence 7680 BP; 2279 A; 1661 C; 1739 G; 2001 T; 0 other;

Query Match 6.6%; Score 20; DB 23; Length 7680;
Best Local Similarity 100.0%; Pred. No. 2.6; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0;

Oy 106 gtgaaatgctgaagagg 125
Db 2827 gtgaaatgctgaagagg 2846

RESULT 12
AAZ31552
ID AAZ31552 standard; DNA; 3351 BP.
XX
AC AAZ31552;
XX
DT 10-JAN-2000 (first entry)
XX
DE S. rochei strain E87 inulin-degrading enzyme coding sequence.
XX
KW Inulin-degrading enzyme; IDE; inulotetraose production;
KW inulotriose preparation; raffinose purification; ketose decomposition;
KW ss.
XX
OS Streptomyces rochei.
XX
PN JP11243962-A.
XX
PD 14-SEP-1999.
XX
PF 27-FEB-1998; 98JP-0061957.
XX
PR 27-FEB-1998; 98JP-0061957.
XX
PA (NIPT) NIPPON TENSAI SEITO KK.
XX
DR WPI: 1999-603711/52.
DR P-PSDB: AAY43179.
XX
PT New inulin-degrading enzyme gene - useful for preparation of
PT inulotetraose and/or inulotriose
XX
PS Claim 1; Page 9-12; 15pp; Japanese.
XX
CC This sequence encodes the Streptomyces rochei strain E87 inulin-degrading
CC enzyme (IDE) of the invention. The IDE is useful for the preparation of
CC inulotetraose and/or inulotriose by treating inulin with the IDE. The IDE
CC can also be used in a method for the purification of raffinose in which
CC ketoses contained in a raffinose solution is selectively decomposed by
CC using the IDE and raffinose is maintained as it is.
XX
SQ Sequence 3351 BP; 619 A; 1309 C; 1003 G; 420 T; 0 other;

Query Match 5.9%; Score 18; DB 20; Length 3351;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 67 ttccggcatccacaaggc 84
Db 3133 ttccggcatccacaaggc 3150

RESULT 13
AAX71396
ID AAX71396 standard; RNA; 17 BP.
XX
AC AAX71396;
XX
DT 28-JUL-1999 (first entry)

```

XX DE Human KDR VEGF receptor hammerhead ribozyme substrate #408.
XX KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1;
XX KW flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
XX KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
XX KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
XX KW foetal liver kinase 1; ss.
OS Homo sapiens.
XX KW WO9715662-A2.
XX PD 01-MAY-1997.
XX PF 25-OCT-1996; 96WO-US17480.
XX PR 11-JAN-1996; 96US-0584040.
XX PR 26-OCT-1995; 95US-0005974.
XX PA (CHIR ) CHIRON CORP.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PI Escobedo J, McSwiggen J, Pavco P, Stinchcomb D;
XX DR WPI; 1997-259017/23.
XX PT Nucleic acid molecule modulating VEGF receptor(s) gene expression or
XX PT mRNA stability - useful for treating e.g. tumour angiogenesis,
XX PT psoriasis, rheumatoid arthritis, etc., in a human patient
XX PS Claim 4; Page 109; 218pp; English.
XX CC The present invention describes nucleic acid molecules which modulate
XX CC the synthesis, expression and/or stability of a mRNA encoding 1 or more
XX CC receptors of vascular endothelial growth factor (VEGF). A patient
XX CC (preferably human) having a condition associated with the level of the
XX CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
XX CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
XX CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can
XX CC be treated by administering the nucleic acid molecule or the expression
XX CC vector to the patient. AAX7275 to AAX7572 represent specific examples
XX CC of nucleic acid molecules from the present invention.
XX SQ Sequence 17 BP; 5 A; 6 C; 1 G; 5 U; 0 other;

Query Match 5.6%; Score 17; DB 18; Length 17;
Best Local Similarity 70.6%; Pred. No. 95;
Matches 12; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

OY 163 ctcaagatctctattca 179
DB 1 cucaagaauccauca 17
1:|||||:|:|:|:|

RESULT 14
AAT14887/c
ID AAT14887 standard; DNA; 218 BP.
XX AC AAT14887;
XX DT 17-SEP-1996 (first entry)
XX DE Thermus thermophilus HB27 218 bp DNA fragment with promoter function.
XX KW Base pair; bp; promoter; thermostable; Thermus sp.; ds.
XX OS Thermus thermophilus HB27.
XX PN JP08070868-A.
XX PD 19-MAR-1996.

```

```

XX PF 02-SEP-1994; 94JP-0210153.
XX PR 02-SEP-1994; 94JP-0210153.
XX PA (MITU ) MITSUBISHI CHEM CORP.
XX DR WPI; 1996-203149/21.
XX PT DNA fragment with promoter function derived from Thermus sp.
XX PT bacteria - useful in the prodn. of thermostable enzymes and
XX PT proteins
XX PS Claim 1; Page 8; 9pp; Japanese.
XX CC AAT14881-T14888 are DNA fragments derived from Thermus thermophilus
XX CC HB27. The fragments all have a promoter function and are useful for
XX CC the prodn. of DNA with a thermostable promoter. The DNA improves
XX CC Thermus bacteria stability and hence improves the prodn. process for
XX CC thermostable enzymes and proteins.
XX SQ Sequence 218 BP; 41 A; 59 C; 80 G; 38 T; 0 other;

Query Match 5.6%; Score 17; DB 17; Length 218;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 33 cggcgccttcgggaagg 49
DB 182 CGGCGCCTTCGGGAAGG 166
|||||

RESULT 15
ABAI1580
ID ABAI1580 standard; cDNA; 272 BP.
XX AC ABAI1580;
XX DT 23-JAN-2002 (first entry)
XX DE Human nervous system related polynucleotide SEQ ID NO 587.
XX KW Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
XX KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnery;
XX KW antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer;
XX KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
XX KW antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal;
XX KW antiparasitic; cardiant; immune disorder; cardiovascular disorder;
XX KW neurological disease; infection; nephrotropic; gene therapy; vaccine; ss.
XX OS Homo sapiens.
XX PN WO200159063-A2.
XX PD 16-AUG-2001.
XX PF 17-JAN-2001; 2001WO-US01334.
XX PR 31-JAN-2000; 2000US-0179065.
XX PR 04-FEB-2000; 2000US-0180628.
XX PR 24-FEB-2000; 2000US-0184664.
XX PR 02-MAR-2000; 2000US-0186350.
XX PR 16-MAR-2000; 2000US-0189874.
XX PR 17-MAR-2000; 2000US-0190076.
XX PR 18-APR-2000; 2000US-0198123.
XX PR 19-MAY-2000; 2000US-0205515.
XX PR 07-JUN-2000; 2000US-0209467.
XX PR 28-JUN-2000; 2000US-0214886.
XX PR 30-JUN-2000; 2000US-0215135.
XX PR 07-JUL-2000; 2000US-0216647.
XX PR 07-JUL-2000; 2000US-0216880.
XX PR 11-JUL-2000; 2000US-0217487.

```


CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
 CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
 CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
 CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
 CC and parasitic infections.

CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 272 BP; 58 A; 79 C; 87 G; 47 T; 1 other;

Query Match 5.6%; Score 17; DB 22; Length 272;

Best Local Similarity 100.0%; Pred. No. 89;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 276 cctctcccaactctctgc 292

|||||

Db 190 cctctcccaactctctgc 206

RESULT 16

AAH03972

ID AAH03972 standard; cDNA; 768 BP.

AC AAH03972;

DT 26-JUN-2001 (first entry)

XX Human cDNA clone (5'-primer) SEQ ID NO:807.

DE Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.

KW Homo sapiens.

OS EPI074617-A2.

PN 07-FEB-2001.

PD 28-JUL-2000; 2000EP-0116126.

PF 29-JUL-1999; 99JP-0248036.

PR 27-AUG-1999; 99JP-0300253.

PR 11-JAN-2000; 2000JP-0118776.

PR 02-MAY-2000; 2000JP-0183767.

PR 09-JUN-2000; 2000JP-0241899.

XX (HELI-) HELIX RES INST.

XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;

PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

XX WPI; 2001-318749/34.

XX Primer sets for synthesizing polynucleotides, particularly the 5602

PT full-length cDNAs defined in the specification, and for the detection

PT and/or diagnosis of the abnormality of the proteins encoded by the

XX full-length cDNAs -

XX Claim 1; SEQ ID 807; 2537pp + CD ROM; English.

XX The present invention describes primer sets for synthesising 5602

CC full-length cDNAs defined in the specification. Where a primer set

CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary

CC to the complementary strand of a polynucleotide which comprises one of

CC the 5602 nucleotide sequences defined in the specification, where the

CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination

CC of an oligonucleotide comprising a sequence complementary to the

CC complementary strand of a polynucleotide which comprises a 5'-end

CC sequence and an oligonucleotide comprising a sequence complementary to a

CC polynucleotide which comprises a 3'-end sequence, where the

CC oligonucleotide comprises at least 15 nucleotides and the combination of

CC the 5'-end sequence/3'-end sequence is selected from those defined in

CC the specification. The primer sets can be used in antisense therapy and
 CC in gene therapy. The primers are useful for synthesising polynucleotides,
 CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
 CC AAH13633 to AAH18742 represent human cDNA sequences. AAB92446 to
 CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
 CC represent oligonucleotides, all of which are used in the exemplification
 CC of the present invention.

XX Sequence 768 BP; 175 A; 222 C; 207 G; 161 T; 3 other;

Query Match 5.6%; Score 17; DB 22; Length 768;

Best Local Similarity 100.0%; Pred. No. 87;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 catccacaaggcgca 88

|||||

Db 221 catccacaaggcgca 237

RESULT 17

AAH06553

ID AAH06553 standard; cDNA; 813 BP.

XX AAH06553;

XX 26-JUN-2001 (first entry)

XX Human cDNA clone (5'-primer) SEQ ID NO:3388.

DE Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.

KW Homo sapiens.

OS EPI074617-A2.

PN 07-FEB-2001.

PD 28-JUL-2000; 2000EP-0116126.

PF 29-JUL-1999; 99JP-0248036.

PR 27-AUG-1999; 99JP-0300253.

PR 11-JAN-2000; 2000JP-0118776.

PR 02-MAY-2000; 2000JP-0183767.

PR 09-JUN-2000; 2000JP-0241899.

XX (HELI-) HELIX RES INST.

XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;

PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

XX WPI; 2001-318749/34.

XX Primer sets for synthesizing polynucleotides, particularly the 5602

PT full-length cDNAs defined in the specification, and for the detection

PT and/or diagnosis of the abnormality of the proteins encoded by the

XX full-length cDNAs -

XX Claim 1; SEQ ID 3388; 2537pp + CD ROM; English.

XX The present invention describes primer sets for synthesising 5602

CC full-length cDNAs defined in the specification. Where a primer set

CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary

CC to the complementary strand of a polynucleotide which comprises one of

CC the 5602 nucleotide sequences defined in the specification, where the

CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination

CC of an oligonucleotide comprising a sequence complementary to the

CC complementary strand of a polynucleotide which comprises a 5'-end

CC sequence and an oligonucleotide comprising a sequence complementary to a

CC polynucleotide which comprises a 3'-end sequence, where the

CC oligonucleotide comprises at least 15 nucleotides and the combination of

CC the 5'-end sequence/3'-end sequence is selected from those defined in

CC oligonucleotide comprises at least 15 nucleotides and the combination of
 CC the 5'-end sequence/3'-end sequence is selected from those defined in
 CC the specification. The primer sets can be used in antisense therapy and
 CC in gene therapy. The primers are useful for synthesising polynucleotides,
 CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
 CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
 CC represent oligonucleotides, all of which are used in the exemplification
 CC of the present invention.
 XX
 XX Sequence 813 BP; 209 A; 188 C; 203 G; 209 T; 4 other;

Query Match 5.6%; Score 17; DB 22; Length 813;
 Best Local Similarity 100.0%; Pred. No. 87;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 ctgcacctggggagagt 23
 |||||
 Db 27 ctgcacctggggagagt 43

RESULT 18
 AAS22655
 ID AAS22655 standard; cDNA: 1101 BP.
 XX
 AC AAS22655;
 XX
 DT 24-OCT-2001 (first entry)
 XX
 DE Human cDNA encoding a novel human protein #221.
 XX
 KW Human: novel protein; ss: Antianaemic; osteopathic; antiinflammatory;
 KW immunomodulatory; cytostatic; neuroprotective; vulnery; nootropic;
 KW anticonvulsant; antiallergic; cerebroprotective; antifungal; antiviral;
 KW antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic;
 KW thrombolytic; immunogen; antibody; gene therapy; neurological disorder;
 KW Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
 KW tissue regeneration; immune disorder.
 XX
 OS Homo sapiens.
 XX
 XX WO200155437-A2.
 PN
 XX
 PD 02-AUG-2001.
 XX
 XX 25-JAN-2001; 2001WO-US02623.
 PF
 XX 25-JAN-2000; 2000US-0491404.
 PR
 XX (HYSE-) HYSEQ INC.
 PA
 XX Tang YT, Liu C, Drmanac RT;
 PI
 XX WPI: 2001-451939/48.
 DR
 XX P-PSDB; AAU14350.
 XX
 PT Isolated polypeptides useful for treating anti-inflammatory diseases,
 PT nervous system disorders, and for regenerating bone and cartilage.
 PT
 PS Claim 1: Page 493-494; 894pp; English.
 XX

CC The invention relates to polynucleotides encoding novel human
 CC proteins or their active domains. The polypeptides, polynucleotides and
 CC antibodies raised against the polypeptides are used in a method of
 CC treatment of a mammal and prevention of disorders caused by the aberrant
 CC protein expression or activity. The polypeptides can be used as
 CC molecular weight markers, food supplements, and in antibody production.
 CC The polypeptides are used to identify compounds which bind to the
 CC polypeptides. Polynucleotides of the invention are used as probes and

CC primers, for sequencing, for chromosome or gene mapping, in the
 CC production of recombinant proteins, and in generating anti-sense DNA or
 CC RNA and in gene therapy. Polypeptides of the invention can be used to
 CC target drugs to a tumour, in assays to determine biological activity, to
 CC raise antibodies/elicite an immune response, to determine quantitative
 CC protein levels, as tissue markers, and to isolate receptors or ligands.
 CC Polypeptides of the invention may also be useful in treating platelet
 CC disorders, stem cell disorders, regenerating bone, cartilage, tendon,
 CC ligament and/or nerve tissue, wound healing, treating burns, promoting
 CC the proliferation, differentiation and survival of stem cells, as a
 CC contraceptive, treating osteoporosis and osteoarthritis, anaemia,
 CC Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral
 CC sclerosis, stroke, immune deficiencies resulting from bacterial, viral or
 CC fungal infection or from autoimmunity, cancer, allergy, asthma,
 CC graft-versus-host disease, eczema, haemophilia, thrombosis,
 CC anti-inflammatory diseases, nervous system disorders, and infection.
 CC The present sequence encodes a protein of the invention.

XX Sequence 1101 BP; 286 A; 266 C; 335 G; 214 T; 0 other;

Query Match 5.6%; Score 17; DB 22; Length 1101;
 Best Local Similarity 100.0%; Pred. No. 86;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 197 acgtggtcaacctctc 213
 |||||
 Db 311 acgtggtcaacctctc 327

RESULT 19
 AAS85415
 ID AAS85415 standard; cDNA: 1116 BP.
 XX
 AC AAS85415;
 XX
 DT 13-FEB-2002 (first entry)
 XX
 DE DNA encoding novel human diagnostic protein #21219.
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO200175067-A2.
 PN
 XX
 PD 11-OCT-2001.
 XX
 XX 30-MAR-2001; 2001WO-US08631.
 PF
 XX 31-MAR-2000; 2000US-0540217.
 PR
 XX 23-AUG-2000; 2000US-0649167.
 XX
 XX (HYSE-) HYSEQ INC.
 PA
 XX Drmanac RT, Liu C, Tang YT;
 PI
 XX WPI: 2001-639362/73.
 DR
 XX P-PSDB; ABG21228.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.
 PT
 PS Claim 1: SEQ ID No 21219; 103pp; English.

CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags

CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAS64197-AAS94564 represent novel human
 CC diagnostic coding sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 1116 BP; 272 A; 340 C; 299 G; 205 T; 0 other;

Query Match 5.6%; Score 17; DB 23; Length 1116;
 Best Local Similarity 100.0%; Pred. No. 86;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 274 aacctctccaacttct 290
 |||||
 Db 626 aacctctccaacttct 642

RESULT 20

AAS91079
 ID AAS91079 standard; cDNA; 1116 BP.

XX AAS91079;

DT 13-FEB-2002 (first entry)

DE DNA encoding novel human diagnostic protein #26883.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.

XX Homo sapiens.

PN WO200175067-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US08631.

XX 31-MAR-2000; 2000US-0540217.

PR 23-AUG-2000; 2000US-0649167.

XX (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

DR P-PSDB; ABG26892.

XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -

XX Claim 1; SEQ ID NO 26883; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags.
 CC for identifying expressed genes. (I) is useful in gene therapy techniques

CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAS64197-AAS94564 represent novel human
 CC diagnostic coding sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 1116 BP; 272 A; 340 C; 299 G; 205 T; 0 other;

Query Match 5.6%; Score 17; DB 23; Length 1116;
 Best Local Similarity 100.0%; Pred. No. 86;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 274 aacctctccaacttct 290
 |||||
 Db 626 aacctctccaacttct 642

RESULT 21

AAS85413

ID AAS85413 standard; cDNA; 1233 BP.

XX AAS85413;

DT 13-FEB-2002 (first entry)

DE DNA encoding novel human diagnostic protein #21217.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.

XX Homo sapiens.

PN WO200175067-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US08631.

XX 31-MAR-2000; 2000US-0540217.

PR 23-AUG-2000; 2000US-0649167.

XX (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

DR P-PSDB; ABG21226.

XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -

XX Claim 1; SEQ ID NO 21217; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving

CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAS64197-AAS94564 represent novel human
 CC diagnostic coding sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 1233 BP; 316 A; 373 C; 317 G; 227 T; 0 other;

Query Match 5.6%; Score 17; DB 23; Length 1233;
 Best Local Similarity 100.0%; Pred. No. 86;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 274 aacctctccaacttct 290
 |||||
 Db 680 aacctctccaacttct 696

RESULT 22

AAS83501
 ID AAS83501 standard; cDNA; 1302 BP.

AC AAS83501;

DT 13-FEB-2002 (first entry)

DE DNA encoding novel human diagnostic protein #19305.

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.

OS Homo sapiens.

PN WO200175067-A2.

PD 11-OCT-2001.

PF 30-MAR-2001; 2001WO-US08631.

PR 31-MAR-2000; 2000US-0540217.

PR 23-AUG-2000; 2000US-0649167.

XX (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

XX WPI: 2001-639362/73.

DR P-PSDB; ABG19314.

XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -

XX Claim 1; SEQ ID No 19305; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or

CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAS64197-AAS94564 represent novel human
 CC diagnostic coding sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX

SQ Sequence 1302 BP; 324 A; 402 C; 343 G; 233 T; 0 other;

Query Match 5.6%; Score 17; DB 23; Length 1302;
 Best Local Similarity 100.0%; Pred. No. 86;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 274 aacctctccaacttct 290
 |||||
 Db 680 aacctctccaacttct 696

RESULT 23

AAC91319

ID AAC91319 standard; cDNA; 1406 BP.

XX AAC91319;

DT 16-MAR-2001 (first entry)

DE Human polynucleotide for diagnostics and therapeutics, SEQ ID NO: 19.

KW Human; diagnostics and therapeutics; dithp; cytostatic;
 KW immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic;
 KW hepatotropic; antidiabetic; antinflammatory; antitumor; vulnary;
 KW anticonvulsant; antibacterial; antifungal; antiparasitic; cardiac;
 KW cancer; immune disorder; cardiovascular disorder; neurological disease;
 KW infection; endocrine disorder; metabolic disorder; ss.

OS Homo sapiens.

PN WO200073509-A2.

XX 07-DEC-2000.

PF 31-MAY-2000; 2000WO-US15404.

XX 01-JUN-1999; 99US-0137161.

PR 02-JUN-1999; 99US-0137109.

PR 02-JUN-1999; 99US-0137113.

PR 02-JUN-1999; 99US-0137114.

PR 02-JUN-1999; 99US-0137173.

PR 02-JUN-1999; 99US-0137258.

PR 02-JUN-1999; 99US-0137259.

PR 02-JUN-1999; 99US-0137260.

PR 03-JUN-1999; 99US-0137337.

PR 03-JUN-1999; 99US-0137396.

PR 03-JUN-1999; 99US-0137411.

PR 03-JUN-1999; 99US-0137417.

PR 04-AUG-1999; 99US-0137377.

PR 04-AUG-1999; 99US-0137436.

PR 05-AUG-1999; 99US-0137500.

PR 05-AUG-1999; 99US-0137520.

PR 05-AUG-1999; 99US-0137527.

PR 05-AUG-1999; 99US-0137530.

PR 05-AUG-1999; 99US-0137536.

PR 05-AUG-1999; 99US-0137541.

PR 05-AUG-1999; 99US-0137542.

PR 05-AUG-1999; 99US-0137547.

```

PR 05-AUG-1999; 99US-0137549.
PR 05-AUG-1999; 99US-0137824.
XX
XX (INCY-) INCYTE GENOMICS INC.
XX
XX Hodgson DM, Lincoln SE, Russo FD, Spiro PA, Banville SC;
PI Bratcher SR, Dufour GE, Cohen HJ, Rosen BH, Hillman JL;
PI Jones AL, Yu JY, Greenawalt LB, Panzer SR, Roseberry AM;
PI Wright RJ, Daniels SE;
XX
XX WPI: 2001-016511/02.
XX
XX Fifty two human polynucleotides, referred to as DITHP polynucleotides,
XX useful in the diagnosis and treatment of cancer, immune disorders and
XX neurological diseases .
XX
XX Claim 1: Page 245-246; 263pp; English.
XX
XX The present sequence is one of fifty-two human polynucleotides for
XX diagnostics and therapeutics. The polynucleotides are referred to as
XX DITHP polynucleotides. The DITHP polynucleotides and polypeptides are
XX useful for diagnosing and treating diseases such as cancer, particularly
XX breast and ovarian cancer, and other cancers of the adrenal gland, bone,
XX bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
XX immune disorders such as Addison's disease, allergies, autoimmune
XX haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
XX disease, multiple sclerosis, rheumatoid arthritis and ulcerative
XX colitis; cardiovascular disorders such as myocardial ischaemias;
XX neurological diseases such as cerebral palsy and epilepsy; infectious
XX diseases such as viral, bacterial, fungal and parasitic infections; and
XX endocrine disorders (e.g. disorders of hypothalamus), disorders
XX associated with hypothyroidism and hyperthyroidism, pancreatic
XX disorders (e.g. diabetes mellitus) and metabolic disorders.
XX The DITHP polynucleotides are useful for screening for molecules that
XX bind to or are bound by the encoded polypeptides. The anti-DITHP
XX antibodies are useful in diagnostic assays.
XX
XX Sequence 1406 BP: 278 A; 481 C; 395 G; 251 T; 1 other;

Query Match 5.6%; Score 17; DB 22; Length 1406;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 276 cctctcccaacttcctgc 292
Db 227 cctctcccaacttcctgc 243

RESULT 24
AAH75162
ID AAH75162 standard; cDNA: 1417 BP.
XX
XX AAH75162;
XX
XX 13-NOV-2001 (first entry)
XX
XX Nucleotide sequence of a human enzyme.
XX
XX Human; enzyme: cancer; neurological disorder; epilepsy; stroke;
XX Alzheimer's disease; Pick's disease; Huntington's disease; dementia;
XX multiple sclerosis; Parkinson's disease; amyotrophic lateral sclerosis;
XX meningitis; schizophrenia; neuroskeletal disorder; allergy;
XX addison's disease; autoimmune disease; anemia; asthma; Crohn's disease;
XX adult respiratory distress syndrome; atopic dermatitis; psoriasis;
XX diabetes mellitus; osteoporosis; pancreatitis; rheumatoid arthritis;
XX infection; genetic disorder; muscular dystrophy; Gaucher's disease;
XX Huntington's chorea; sickle cell anemia; thalassemia; atherosclerosis;
XX Von Willebrand's disease; Wilms' tumour; cell proliferative disorder;
XX leukemia; hepatitis; cirrhosis; arteriosclerosis; gene therapy; ss.
XX
XX Homo sapiens.
XX

```

```

FH Key Location/Qualifiers
FT CDS 250..1359
FT /*tag= a
FT /product= "enzyme"
XX
XX WO200164896-A2.
XX
XX 07-SEP-2001.
XX
XX 01-MAR-2001; 2001WO-US06806.
XX
XX 01-MAR-2000; 2000US-0186307.
XX 28-MAR-2000; 2000US-0192532.
XX 30-MAR-2000; 2000US-0193578.
XX
XX (INCY-) INCYTE GENOMICS INC.
XX
XX Tang YH, Lu DAM, Bandman O, Yue H, Azimzai Y, Lal P, Burford N;
XX Baughn MR;
XX
XX WPI: 2001-550184/61.
XX P-PSDB; AAG67134.
XX
XX Novel human enzyme molecule useful for treating and preventing, e.g.,
XX cancer, genetic disorders, neurological disorders, autoimmune and
XX inflammatory disorders .
XX
XX Claim 5; Page 144; 154pp; English.
XX
XX The present sequence encodes a human enzyme. The enzyme polynucleotide
XX and polypeptide are useful for diagnosis, treatment and prevention of
XX cancers, neurological disorders (e.g. epilepsy, stroke, Alzheimer's
XX disease, Pick's disease, Huntington's disease, dementia, multiple
XX sclerosis, Parkinson's disease, amyotrophic lateral sclerosis, bacterial
XX and viral meningitis, schizophrenic disorders and neuroskeletal
XX disorders), autoimmune/inflammatory disorders (e.g. allergies,
XX addison's disease, autoimmune diseases, adult respiratory distress
XX syndrome, anemia, asthma, Crohn's disease, atopic dermatitis, diabetes
XX mellitus, osteoporosis, pancreatitis, psoriasis, rheumatoid arthritis,
XX and viral, bacterial, fungal, parasitic, protozoal and helminthic
XX infections), genetic disorder (e.g. Duchenne and Becker muscular
XX dystrophy, Gaucher's disease, Huntington's chorea, sickle cell anemia,
XX thalassemia, Von Willebrand's disease and Wilms' tumour), and cell
XX proliferative disorder (e.g. atherosclerosis, leukemia, hepatitis,
XX cirrhosis, and arteriosclerosis). The polynucleotide is also useful in
XX somatic or germline gene therapy.
XX
XX Sequence 1417 BP; 292 A; 479 C; 396 G; 250 T; 0 other;

Query Match 5.6%; Score 17; DB 22; Length 1417;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 276 cctctcccaacttcctgc 292
Db 227 cctctcccaacttcctgc 243

RESULT 25
AAH15398
ID AAH15398 standard; cDNA: 1767 BP.
XX
XX AAH15398;
XX
XX 26-JUN-2001 (first entry)
XX
XX Human cDNA sequence SEQ ID NO:13599.
XX
XX Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
XX Homo sapiens.
XX

```


PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-465570/50.
XX Isolated nucleic acid molecule encoding a reproductive system antigen -
is used in preventing, treating or ameliorating a medical condition -
XX Disclosure; SEQ ID NO 5919; 1297pp + Sequence Listing; English.
XX The present invention provides the protein and coding sequences of a
number of human reproductive system related antigens. These can be used
CC in the prevention and treatment of reproductive system disorders,
CC including cancer. The present sequence is a genomic sequence encoding a
CC protein of the invention.
XX
SQ Sequence 1824 BP; 380 A; 499 C; 488 G; 457 T; 0 other;

Query Match 5.6%; Score 17; DB 22; Length 1824;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 33 cggcgcccttcgggaagg 49
|||||
Db 1442 CGCGCCCTCGGGAAGG 1426

RESULT 27
ABAI5613
ID ABAI5613 standard; DNA; 1901 BP.
XX
AC ABAI5613;
XX
DT 23-JAN-2002 (first entry)
XX
DE Human nervous system related polynucleotide SEQ ID NO 7944.
XX
KW Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;
antiparkinsonian; antispasmodic; antianemic; antithrombotic; cancer;
antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
antiallergic; antidiabetic; antitumor; anticonvulsant; antifungal;
KW antiparasitic; cardiant; immune disorder; cardiovascular disorder;
neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
OS Homo sapiens.
XX
PN WO200159063-A2.
XX
PD 16-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01334.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 11-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 14-JUL-2000; 2000US-0217496.
PR 26-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.

PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226686.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0233423.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0242221.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249266.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250391.
PR 01-DEC-2000; 2000US-0251160.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 06-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-541565/60.
XX
XX Nucleic acids encoding 3224 human nervous system antigen polypeptides,
XX useful for preventing, diagnosing and/or treating nervous system
XX cancers and metastases -
XX
XX Disclosure; SEQ ID NO 7944; 1701pp + Sequence Listing; English.
XX
XX The invention relates to novel genes (AB11004-ABA21534) and proteins
XX (AB114678-AB18001) useful for preventing, treating or ameliorating
XX medical conditions e.g. by protein or gene therapy. The genes are
XX isolated from a range of human tissues disclosed in the specification.
XX The nucleic acids, proteins, antibodies and (antagonists are useful
XX in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
XX and ovarian cancer and other cancers of the adrenal gland, bone, bone
XX marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
XX (b) immune disorders e.g. Addison's disease, allergies, autoimmune
XX haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
XX disease, multiple sclerosis, rheumatoid arthritis and ulcerative
XX colitis; (c) cardiovascular disorders such as myocardial ischaemia;
XX (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
XX epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
XX and parasitic infections.

CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 1901 BP; 373 A; 619 C; 573 G; 336 T; 0 other;

Query Match 5.68; Score 17; DB 22; Length 1901;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 276 cctctcccaacttcctgc 292
|||||
Db 620 cctctcccaacttcctgc 636

RESULT 28
AAS83500
ID AAS83500 standard; cDNA: 2484 BP.
XX
AC AAS83500;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #19304.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR P-PSDB; ABG19313.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 1; SEQ ID No 19304; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed

CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 2484 BP; 611 A; 686 C; 672 G; 515 T; 0 other;

Query Match 5.68; Score 17; DB 23; Length 2484;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 274 aacctctcccaacttcct 290
|||||
Db 1994 aacctctcccaacttcct 2010

RESULT 29
AAH14499
ID AAH14499 standard; cDNA: 2624 BP.
XX
AC AAH14499;
XX
DT 26-JUN-2001 (first entry)
XX
DE Human cDNA sequence SEQ ID NO:12018.
XX
KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN EP1074617-A2.
XX
PD 07-FEB-2001.
XX
PF 28-JUL-2000; 2000EP-0116126.
XX
PR 29-JUL-1999; 99JP-0248036.
PR 27-AUG-1999; 99JP-0300253.
PR 11-JAN-2000; 2000JP-0118776.
PR 02-MAY-2000; 2000JP-0183767.
PR 09-JUN-2000; 2000JP-0241899.
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX
DR WPI; 2001-318749/34.
XX
PT Primer sets for synthesizing polynucleotides, particularly the 5602
PT full-length cDNAs defined in the specification, and for the detection
PT and/or diagnosis of the abnormality of the proteins encoded by the
PT full-length cDNAs -
XX
PS Claim 8; SEQ ID 12018; 2537pp + CD ROM; English.
XX
CC The present invention describes primer sets for synthesising 5602
CC full-length cDNAs defined in the specification. Where a primer set
CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
CC to the complementary strand of a polynucleotide which comprises one of
CC the 5602 nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in
CC the specification. The primer sets can be used in antisense therapy and
CC in gene therapy. The primers are useful for synthesising polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and

CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
CC represent oligonucleotides, all of which are used in the exemplification
CC of the present invention.

XX Sequence 2624 BP; 662 A; 684 C; 654 G; 624 T; 0 other;

Query Match 5.6%; Score 17; DB 22; Length 2624;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 7 ctgcacctggggagagt 23
|||||
Db 27 ctgcacctggggagagt 43

RESULT 30
AAS22891/c
ID AAS22891 standard; cDNA; 2663 BP.

AC AAS22891;

XX 24-OCT-2001 (first entry)

DE Human cDNA encoding a novel human protein #457.

XX Human; novel protein; ss; Antianaemic; osteopathic; antiinflammatory;
KW immunomodulatory; cytostatic; neuroprotective; vulnery; nootropic;
KW anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral;
KW antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic;
KW thrombolytic; immunogen; antibody; gene therapy; neurological disorder;
KW Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
KW tissue regeneration; immune disorder.

XX Homo sapiens.

XX WO200155437-A2.

XX 02-AUG-2001.

XX 25-JAN-2001; 2001WO-US02623.

XX 25-JAN-2000; 2000US-0491404.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Drmanac RT;

XX WPI; 2001-451939/48.

XX P-PSDB; AAU14586.

PT Isolated polypeptides useful for treating anti-inflammatory diseases,
PT nervous system disorders, and for regenerating bone and cartilage -

XX Claim 1; Page 776-777; 894pp; English.

PS The invention relates to polynucleotides encoding novel human
CC proteins or their active domains. The polypeptides, polynucleotides and
CC antibodies raised against the polypeptides are used in a method of
CC treatment of a mammal and prevention of disorders caused by the aberrant
CC protein expression or activity. The polypeptides can be used as
CC molecular weight markers, food supplements, and in antibody production.
CC The polypeptides are used to identify compounds which bind to the
CC polypeptides. Polynucleotides of the invention are used as probes and
CC primers, for sequencing, for chromosome or gene mapping, in the
CC production of recombinant proteins, and in generating anti-sense DNA or
CC RNA and in gene therapy. Polypeptides of the invention can be used to
CC target drugs to a tumour, in assays to determine biological activity, to
CC raise antibodies/elicite an immune response, to determine quantitative
CC protein levels, as tissue markers, and to isolate receptors or ligands.
CC Polypeptides of the invention may also be useful in treating platelet
CC disorders, stem cell disorders, regenerating bone, cartilage, tendon,

CC ligament and/or nerve tissue, wound healing, treating burns, promoting
CC the proliferation, differentiation and survival of stem cells, as a
CC contraceptive, treating osteoporosis and osteoarthritis, anaemia,
CC Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral
CC sclerosis, stroke, immune deficiencies resulting from bacterial, viral or
CC fungal infection or from autoimmunity, cancer, allergy, asthma,
CC graft-versus-host disease, eczema, haemophilia, thrombosis,
CC anti-inflammatory diseases, nervous system disorders, and infection.
CC The present sequence encodes a protein of the invention.

XX Sequence 2663 BP; 510 A; 805 C; 667 G; 681 T; 0 other;

Query Match 5.6%; Score 17; DB 22; Length 2663;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 197 acgtgggtcaacctctc 213
|||||
Db 1013 ACGTGGTCAACCTCCTC 997

RESULT 31
AAV55895
ID AAV55895 standard; DNA; 3120 BP.

XX AAV55895;

AC 19-NOV-1998 (first entry)

XX Receptor protein tyrosine kinase (PTK) subtype tyro-10 encoding DNA.

XX PTK; receptor; protein tyrosine kinase; brain tissue; ss.

XX Rattus sp.

XX Key Location/Qualifiers

XX CDS 485..3049

XX /*tag= a

XX /*product= *PTK subtype tyro-10*

XX US5811516-A.

XX 22-SEP-1998.

XX 02-JUN-1995; 95US-0456647.

XX 15-MAY-1992; 92US-0884486.

XX 02-MAY-1994; 94US-0237401.

XX 02-JUN-1995; 95US-0456647.

XX (SALK) SALK INST BIOLOGICAL STUDIES.

XX Lai CHC, Lemke GE;

XX WPI; 1998-530939/45.

XX P-PSDB; AAW79152.

XX Receptor protein tyrosine kinase polypeptide, tyro-3 - preferably
XX expressed in brain tissue

XX Example 2; Columns 53-60; 46pp; English.

XX This DNA encodes a novel receptor protein tyrosine kinase (PTK)

XX polypeptide subtype tyro-10. The invention provides polynucleotide

XX sequences encoding novel PTK polypeptide subtypes tyro-1 to tyro-13.

XX The PTK subtypes are found expressed predominantly in the brain tissue.

XX Sequence 3120 BP; 760 A; 786 C; 830 G; 744 T; 0 other;

Query Match 5.6%; Score 17; DB 19; Length 3120;
Best Local Similarity 100.0%; Pred. No. 84;

Matches 17: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 100 gtggccgtgaaatgct 116
|||||
Db 2297 gtggccgtgaaatgct 2313

RESULT 32
AAV65317
ID AAV65317 standard; DNA: 3120 BP.

XX AC AAV65317;
XX DT 22-JAN-1999 (first entry)

XX DE Receptor protein tyrosine kinase (PTK) subtype tyro-10 encoding DNA.

XX KW PTK: receptor; protein tyrosine kinase; recombinant; grafting;
KW diagnosis; tumour; skin transplant; connective tissue; tyro-10; ss.
XX Rattus sp.

XX FH Key Location/Qualifiers
FT CDS 485..3049
FT /*tag= a
FT /product= "PTK subtype tyro-10"

XX US5837448-A.

XX PN 17-NOV-1998.

XX PF 02-MAY-1994; 94US-0237401.

XX PR 15-MAY-1992; 92US-0884486.

XX PR 02-MAY-1994; 94US-0237401.

XX PA (SALK) SALK INST BIOLOGICAL STUDIES.

XX PI Lai CHC, Lemke GE;

XX WPI: 1999-023436/02.

XX P-PSDB; AAW81409.

XX Nucleic acids encoding protein tyrosine kinase subtypes - for
PT identification of new sub:types and treatment of diseases associated
PT with the kinase

XX Claim 1: Columns 53-58; 47pp; English.

XX This DNA encodes a receptor protein tyrosine kinase (PTK) subtype
CC tyro-10. The invention provides sequences AAV65308 to AAV65313, AAV65315,
CC and AAV65317 to AAV65319 that encode proteins having a tyrosine kinase
CC domain and a tissue expression pattern of a receptor PTK subtype selected
CC from tyro-1, tyro-2, tyro-3, tyro-4, tyro-5, tyro-6, tyro-8, tyro-10,
CC tyro-11, and tyro-12, respectively. The polynucleotides are useful for
CC the detection of tyrosine kinase domain sequences and detection of
CC tissue expression patterns of PTK subtypes. The cDNAs can also be
CC injected into oocytes, the protein expressed, and expression products
CC screened for using antibodies against tyrosine kinase epitopes. These
CC subtypes sequences can be used for the design of oligonucleotides, for
CC use in amplification reactions to isolate other subtype sequences. These
CC detection protocols are used in the diagnosis of diseases associated
CC with (receptor) PTKs. Recombinant vectors expressing the subtypes can be
CC used to treat related diseases e.g. tumours, by introduction of the
CC vectors into skin transplants, then grafting these into the connective
CC tissue of the dermis, thus specifically targeting tumours as the
CC proteins are released from the matrix.

XX Sequence 3120 BP; 760 A; 786 C; 830 G; 744 T; 0 other;

Query Match 5.6%; Score 17; DB 20; Length 3120;
Best Local Similarity 100.0%; Pred. No. 84;

Matches 17: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 100 gtggccgtgaaatgct 116
|||||
Db 2297 gtggccgtgaaatgct 2313

RESULT 33

AA522909
ID AAS22909 standard; DNA: 4008 BP.

XX AC AAS22909;

XX DT 24-OCT-2001 (first entry)

XX DE DNA encoding novel bone marrow polypeptide #3.

XX KW Bone marrow; diagnostic; therapeutic; gene therapy; antigenic;
KW haematopoiesis; myeloid; lymph cell disorder; tissue regeneration;
KW wound healing; nutritional supplement; immune disorder;
KW severe combined immunodeficiency; SCID; ds.

XX OS Homo sapiens.

XX WO200157187-A2.

XX PN 09-AUG-2001.

XX PD 05-FEB-2001; 2001WO-US03782.

XX PF 03-FEB-2000; 2000US-0496914.

XX PR 20-JUN-2000; 2000US-0598075.

XX PR 19-JUL-2000; 2000US-0620325.

XX PR 30-NOV-2000; 2000US-0250683.

XX PA (HYSE-) HYSEQ INC.

XX Ford JE, Boyle BJ, Tang YT, Liu C, Asundi V, Zhou P, Xue AJ;
PI Ren F, Drmanac RT;

XX WPI: 2001-488875/53.

XX P-PSDB; AAU14604.

XX Nucleic acids encoding bone marrow polypeptides, useful in diagnostic
PT and gene therapy -

XX Claim 1: Page 151-152; 392pp; English.

XX AAS22907-AAS23099 represent nucleic acids encoding novel bone marrow
CC polypeptides. The nucleic acids and corresponding proteins may be used
CC in the prevention, diagnosis and treatment of diseases associated with
CC inappropriate bone marrow polypeptide expression. For example, to treat
CC disorders associated with decreased expression by rectifying mutations
CC or deletions in a patient's genome that affect the activity of the
CC polypeptides by expressing inactive proteins or to supplement the
CC patient's own production of the polypeptide. Additionally, the nucleic
CC acids may be used to produce the polypeptides, by inserting the nucleic
CC acids into a host cell and culturing the cell to express the protein.
CC The nucleic acid and its complementary sequences may also be used as
CC probes in diagnostic assays to detect and quantitate the presence of
CC similar nucleic acid sequences in samples, and therefore which patients
CC may be in need of restorative therapy. The proteins may also be used as
CC antigens in the production of antibodies against bone marrow proteins
CC and in assays to identify modulators of their expression and activity.
CC The anti-bone marrow protein antibodies and antagonists may also be used
CC to down regulate expression and activity. The antibodies may also be used
CC as diagnostic agents for detecting the presence of the protein in samples
CC (e.g. by enzyme linked immunosorbent assay (ELISA)). The proteins
CC may be used to regulate haematopoiesis activity, and consequently in the
CC treatment of myeloid or lymph cell disorders; in tissue regeneration,
CC such as wound healing; as a nutritional supplement; and in treatment of
CC immune disorders such as severe combined immunodeficiency (SCID).

XX

SQ Sequence 4008 BP; 860 A; 1183 C; 1140 G; 824 T; 1 other;

Query Match 5.6%; Score 17; DB 22; Length 4008;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 276 cctctccaactctctgc 292
|||||
DB 2796 cctctccaactctctgc 2812

RESULT 34

ID AAQ28272 standard; cDNA: 4071 BP.

XX AC AAQ28272;

XX DT 15-FEB-1993 (first entry)

XX DE A novel type III RTK gene - the KDR gene.

XX KW Receptor tyrosine kinase; vascular endothelial cell growth factors;
XX KW cancer; tumour; diagnosing; monitoring; ss.
XX OS Homo sapiens.

XX FH Key Location/Qualifiers
XX FT CDS 1..4068
XX FT /*tag= a

XX PN W09214748-A.

XX PD 03-SEP-1992.

XX PF 20-FEB-1992; 92WO-US01300.

XX PR 22-FEB-1991; 91US-0657236.

XX PA (AMCY) AMERICAN CYANAMID CO.

XX PI Carrion ME, Terman BI;

XX WPI: 1992-316117/38.
XX P-PSDB: AAR26999.

XX PT DNA encoding type III receptor tyrosine kinase - useful for
XX PT diagnosing the onset of cancer

XX PS Claim 3; Fig 7; 101pp; English.

XX CC This sequence represents a novel type III receptor tyrosine kinase
XX CC gene. A labelled EcoRI-BamHI DNA segment derived from clone B7II1081.8
XX CC was used as a probe to rescreen a human endothelial cDNA library
XX CC (HL10246) for 5' full length DNA segments of the gene from which the
XX CC insert portion of B7II1081.8 is derived. A synthetic probe designed
XX CC from nucleotides 3297-3325 of B7II1081.8 is then used to isolate
XX CC more 3' full length clones. One of the clones, designated B7II1200.2
XX CC is cloned into pLucscript KS and the synthetic oligonucleotide
XX CC TCGACGCGCG ATG GAG cloned, which contains the initial sequence Met-
XX CC Glu, the first two amino acids encoded by the KDR gene, forming
XX CC B7IV140, which is then purified on a CsCl density gradient. This
XX CC was sequenced, together with B7II1081.8, and B7II129.5 to comprise
XX CC the entire ORF of 4,068 nucleotides of the KDR gene.

XX SQ Sequence 4071 BP; 1172 A; 894 C; 1024 G; 981 T; 0 other;

Query Match 5.6%; Score 17; DB 13; Length 4071;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 163 ctcaagatcctcattca 179

DB 2656 ctcaagatcctcattca 2672
|||||

RESULT 35

AAV99829 standard; cDNA: 4071 BP.

XX AC AAV99829;

XX DT 12-APR-1999 (first entry)

XX DE Human receptor tyrosine kinase KDR cDNA.

XX KW KDR; receptor tyrosine kinase; human; signal transduction;
XX KW mitogen; neovascularization; angiogenesis; diabetic retinopathy;
XX KW breast cancer; brain cancer; inflammation; rheumatoid arthritis;
XX KW psoriasis; contact dermatitis; hypersensitivity; antagonist;
XX KW gene therapy; ds.

XX OS Homo sapiens.

XX PN W09858053-A1.

XX PD 23-DEC-1998.

XX PF 17-JUN-1998; 98WO-US12569.

XX PR 18-JUN-1997; 97US-0050962.

XX PA (MERI) MERCK & CO INC.

XX PI Kendall RL, Mao X, Tebben A, Thomas KA;

XX WPI: 1999-095333/08.
XX P-PSDB: AAW80997.

XX PT Human receptor tyrosine kinase protein, KDR - useful e.g. to screen
XX PT for antagonists useful to treat diseases involving neovascularization
XX PT e.g. diabetic retinal vascularization, cancers

XX PS Claim 1; Fig 1a; 69pp; English.

XX CC This nucleotide sequence encodes a novel receptor tyrosine kinase,
XX CC termed KDR (see AAW80997), that is expressed on human endothelial
XX CC cells. KDR is activated by vascular endothelial growth factor and
XX CC mediates a mitogenic signal. It is implicated in clinical
XX CC neovascularization. KDR cDNA was isolated from a human umbilical vein
XX CC endothelial cell lambda phage cDNA library using a 576-bp DNA probe
XX CC that had been generated by PCR (see also AAV99850-53). The predicted
XX CC protein product has amino acid differences from the previously
XX CC published KDR sequence at positions 498 (Ala to Glu), 772 (Thr to
XX CC Ala), 787 (Gly to Arg), 835 (Asn to Lys), 848 (Glu to Val) and 1347
XX CC (Thr to Ser), producing a protein predicted by computer modeling to
XX CC have higher activity and functionality. The invention also relates
XX CC to recombinant vectors and recombinant hosts which contain a DNA
XX CC fragment encoding human KDR, a DNA fragment encoding the
XX CC intracellular portion of KDR with or without a membrane anchor
XX CC sequence, purified forms of associated human KDR, and human mutant
XX CC forms of KDR. KDR, fusion proteins or fragments can be used in
XX CC assays to identify antagonists and agonists of human KDR (claimed).
XX CC Antagonists of KDR useful for treating diseases involving
XX CC neovascularization e.g. diabetic retinal vascularization, cancers
XX CC (e.g. brain, breast, etc.) and forms of inflammation e.g. rheumatoid
XX CC arthritis, psoriasis, contact dermatitis and hypersensitivity
XX CC reactions. The polynucleotides are useful to screen for KDR
XX CC antagonists/agonists and for gene therapy (e.g. by introducing a
XX CC gene portion encoding a KDR protein containing functional ligand
XX CC binding and membrane anchoring moieties but not tyrosine kinase
XX CC activity). They are also useful to measure levels of human KDR.

XX SQ Sequence 4071 BP; 1169 A; 894 C; 1027 G; 981 T; 0 other;

Query Match 5.6%; Score 17; DB 20; Length 4071;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 163 ctcaagatcctcattca 179
|||||
Db 2656 ctcaagatcctcattca 2672

RESULT 36
AAFB3308
ID AAFB3308 standard; DNA: 4225 BP.
XX
AC AAFB3308;
XX
DT 09-JUL-2001 (first entry)
XX
DE Human VEGFR-2 encoding DNA.
XX
KW Receptor protein; vascular endothelial growth factor receptor-2;
KW VEGFR-2; neuropilin-1; NP-1; co-receptor; human; angiogenic; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 70..4140
FT /*tag= a
FT /product= "VEGFR-2"
FT misc_feature 71..2350
FT /*tag= b
FT /*note= "extracellular domain coding fragment (AAFB3310)"
XX
PN WO200131346-A2.
XX
PD 03-MAY-2001.
XX
PF 26-OCT-2000; 2000WO-US29579.
XX
PR 28-OCT-1999; 98US-0162367.
XX
PA (PROC) PROCTER & GAMBLE CO.
XX
PI Rosenbaum JS, Whitaker GB, Limberg BJ;
XX WPI: 2001-308686/32.
DR P-PSDB; AAB62475.
XX
PT Determining compounds which bind to a complex comprising vascular
PT endothelial growth factor receptor-2 and Neuropilin-1 to provide
PT superior pro- and anti-angiogenic agents -
XX Example 1; Page 32-39; 82pp; English.
XX
CC The invention relates to determining whether a compound is capable of
CC binding to a receptor protein complex comprising a vascular endothelial
CC growth factor receptor-2 (VEGFR-2) receptor protein and a neuropilin-1
CC (NP-1) receptor protein. One method comprises introducing a sample
CC comprising the compound to the receptor protein and allowing the
CC compound to bind to the complex. Signaling through VEGFR-2 is enhanced
CC in the presence of the NP-1 co-receptor. The methods of the invention
CC can be used for identifying novel pro- and anti-angiogenic compounds.
CC The present sequence represents the DNA encoding a human VEGFR-2.
XX
SQ Sequence 4225 BP; 1204 A; 940 C; 1067 G; 1014 T; 0 other;

Query Match 5.6%; Score 17; DB 22; Length 4225;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 163 ctcaagatcctcattca 179
|||||

Db 2725 ctcaagatcctcattca 2741
RESULT 37
AAV34763
ID AAV34763 standard; DNA: 4236 BP.
XX
AC AAV34763;
XX
DT 27-AUG-1998 (first entry)
XX
DE Human KDR genomic DNA.
XX
KW Kinase insert domain containing receptor; KDR; screening; inhibitor;
KW vascular endothelial growth factor; VEGF; angiogenesis; treatment;
KW cancer; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..4071
FT /*tag= a
FT /product= KDR
FT /*note= "kinase insert domain containing receptor"
XX
PN US5766860-A.
XX
PD 16-JUN-1998.
XX
PF 25-FEB-1997; 97US-0810116.
XX
PR 23-NOV-1992; 92US-0930548.
PR 25-FEB-1997; 97US-0810116.
XX
PA (AMCY) AMERICAN CYANAMID CO.
XX
PI Carrion ME, Terman BI;
XX WPI: 1998-361682/31.
DR P-PSDB; AAW59275.
XX
PT Screening assay for vascular endothelial cell growth factor
PT antagonists - using recombinant cells expressing receptor protein
XX Claim 1; Fig 7A-W; 51pp; English.
XX
CC This sequence encodes a novel human growth factor receptor, kinase
CC insert domain containing receptor or KDR. This receptor is capable of
CC binding to the vascular endothelial cell growth factor, VEGF and is
CC used in a screening assay which identifies compounds that inhibit VEGF
CC action on KDR. Such compounds which inhibit binding of VEGF to the KDR
CC may inhibit angiogenesis and thus be useful for treating cancer.
XX
SQ Sequence 4236 BP; 1216 A; 938 C; 1062 G; 1020 T; 0 other;

Query Match 5.6%; Score 17; DB 19; Length 4236;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 163 ctcaagatcctcattca 179
|||||
Db 2656 ctcaagatcctcattca 2672

RESULT 38
AAK78291
ID AAK78291 standard; DNA: 5414 BP.
XX
AC AAK78291;
XX
DT 07-NOV-2001 (first entry)
XX

DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33103.
XX Human: immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.
XX Homo sapiens.
OS
PN WO200157182-A2.
XX
PD 09-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01354.
XX
XX 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 26-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 06-DEC-2000; 2000US-0256719.
PR 08-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.

PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-483426/52.
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis -
XX
XX
PS Disclosure: SEQ ID NO 33103; 3071pp + Sequence Listing; English.
XX
CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins, and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patients own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent
CC diagnosis and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC represent sequences used in the exemplification of the present invention.
XX
SQ Sequence 5414 BP; 1287 A; 1382 C; 1330 G; 1415 T; 0 other;

Query Match 5.6%; Score 17; DB 22; Length 5414;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 ctgcacctggggagagt 23
|||||
Db 2804 ctgcacctggggagagt 2820

RESULT 39
ABL10071/c
ID ABL10071 standard; cDNA: 5656 BP.

XX ABL10071;

XX 26-MAR-2002 (first entry)

XX Drosophila melanogaster expressed polynucleotide SEQ ID NO 24695.

XX Drosophila: developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ss.

XX Drosophila melanogaster.

XX WO200171042-A2.

XX 27-SEP-2001.

XX 23-MAR-2001; 2001WO-US09231.

XX 23-MAR-2000; 2000US-191637p.

XX 11-JUL-2000; 2000US-0614150.

XX (PEKE) PE CORP NY.

XX Venter JC, Adams M, Li PWD, Myers EW;

XX WPI; 2001-656860/75.
DR P-PSDB; ABB65968.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
XX Claim 1; SEQ ID NO 24695; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABU16175) and the encoded proteins
CC (ABB57737-ABB72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 5656 BP; 1364 A; 1607 C; 1375 G; 1310 T; 0 other;

Query Match 5.6%; Score 17; DB 23; Length 5656;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 248 tgatcgtggagttctgc 264
|||||
Db 1058 TGATCGTGGAGTTCTGC 1042

RESULT 40

ABI99504
ID ABI99504 standard; cDNA: 6730 BP.

XX ABI99504;

XX 07-MAR-2002 (first entry)

XX Mouse ischaemic condition related cDNA sequence SEQ ID NO:479.

XX Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;
KW vasospastic ischaemia; ischaemic condition; ischaemic disease; ss.

XX Mus musculus.

XX WO200188188-A2.

XX 22-NOV-2001.

XX 18-MAY-2001; 2001WO-JP04192.

XX 18-MAY-2000; 2000JP-0145977.

XX (UYNT-) UNIV NIHON SCHOOL JURIDICAL PERSON.

XX Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;

XX WPI; 2002-034733/04.

XX P-PSDB; ABB57196.

XX Examining the ischemic condition (e.g. occlusive ischemia) by measuring
PT expression levels of particular genes defined in the specification or
PT by determining the expression profile of a gene group comprising these
PT genes -

XX Claim 2; Page 1319-1331; 2690pp; English.

XX The present invention describes a method for examining ischaemic
CC conditions, comprising measuring the expression levels of particular

CC genes (1) in a test sample or determining the expression profile of a
 CC gene group in the sample comprising genes selected from (1). The method
 CC is useful for examining the ischaemic condition (e.g. compressive
 CC ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring
 CC expression levels of particular genes (ABI99202 to ABI99912, encoding
 CC the protein sequences in ABB57020 to ABB57374) or by determining the
 CC expression profile of a gene group comprising these genes. The
 CC expression levels or expression profiles produced by these genes are
 CC used as an indicator when screening for ischaemic condition-improving
 CC drugs or therapeutics for ischaemic diseases. ABI99913 and ABI99914
 CC represent PCR primers for a mouse ischaemic condition related sequence,
 CC which are used in the exemplification of the present invention.
 XX
 SQ Sequence 6730 BP; 1656 A; 1850 C; 1740 G; 1482 T; 2 other;

Query Match 5.6%; Score 17; DB 24; Length 6730;
 Best Local Similarity 100.0%; Pred. No. 82;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 72 catccacaagggcagca 88
 |||||
 Db 5829 catccacaagggcagca 5845

RESULT 41
 AAT88206/c
 ID AAT88206 standard; cDNA: 8460 BP.

AC AAT88206;

XX 16-JAN-1998 (first entry)

XX cDNA for protein (OA-519) cross-reactive with hpr gene product.

XX OA-519; cross-reaction; haptoglobin related; hpr; antibody;
 KW epitope; haptoglobin 1; haptoglobin 2; cancer; breast cancer;
 KW prognosis assay; ss.

XX Homo sapiens.

XX Key Location/Qualifiers
 FT CDS 124..7653
 FT /*tag= a

FT /product= OA-519

XX US5665874-A.

XX 09-SEP-1997.

XX 17-JAN-1989; 89US-0297722.

XX 24-JAN-1994; 94US-0188426.

XX 17-JAN-1989; 89US-0297722.

XX 04-DEC-1990; 90US-0622407.

XX 26-JUL-1991; 91US-0735522.

XX 24-JUL-1992; 92US-0917716.

XX 26-JUL-1993; 93US-0096908.

XX 05-JUN-1995; 95US-0469005.

XX (UYJO) UNIV JOHNS HOPKINS.

XX KuhaJda FP, Pasternack CR;

XX WPI; 1997-469516/43.

XX P-PSDB; AAW32881.

XX DNA encoding protein cross-reactive with hpr gene product - useful
 PT to raise antibodies reactive with epitope(s) found on hpr gene
 PT product, useful in cancer, especially breast cancer, prognosis
 PT assays

XX Claim 2; Columns 43-60; 68pp; English.

XX The present sequence encodes a protein (OA-519) cross-reactive with
 CC the haptoglobin related (hpr) gene product. OA-519 can be used to
 CC raise antibodies reactive with epitopes found on the hpr gene
 CC product, but not on haptoglobin 1 or 2, useful in cancer,
 CC especially breast cancer, prognosis assays.

XX Sequence 8460 BP; 1453 A; 2864 C; 2655 G; 1487 T; 1 other;

Query Match 5.6%; Score 17; DB 18; Length 8460;
 Best Local Similarity 100.0%; Pred. No. 82;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 83 gcagcagctgtgacacc 99
 |||||
 Db 1738 GCAGCAGCTGTGACACC 1722

RESULT 42
 AAZ95007/c
 ID AAZ95007 standard; cDNA: 8470 BP.

XX AAZ95007;

XX 15-AUG-2000 (first entry)

XX Cancer specific gene Prol10 useful as prostate cancer marker.

XX Prostate cancer; cancer specific gene; CSG; diagnosis; monitoring;
 KW staging; imaging; therapy; metastasis; marker; human; Prol10; ds.

XX Homo sapiens.

XX WO200023111-A1.

XX 27-APR-2000.

XX 19-OCT-1999; 99WO-US24331.

XX 19-OCT-1998; 98US-0104737.

XX (DIAD-) DIADEXUS LLC.

XX Salceda S, Recipon H, Cafferkey R;

XX WPI; 2000-339531/29.

XX Diagnosing, staging and monitoring the presence and metastases of
 PT prostate cancer especially useful for treating prostate cancer
 PT comprises measuring changes in cancer specific gene levels -

XX Claim 7; Page 59-62; 74pp; English.

XX The present sequence is that of a full-length contig for cancer
 CC specific gene (CSG) Prol10 (clone 3277219H1); a corresponding
 CC expressed sequence tag is given in AAZ95006. The CSG was identified
 CC in a database search using the data mining Cancer Leads Automatic
 CC Search Package (CLASP), which allows the identification of highly
 CC expressed organ and cancer specific genes. Although not tissue
 CC specific, Prol10 expression is upregulated in prostate cancer
 CC tissues. It can be used as a diagnostic marker for prostate
 CC cancer, and may also be a diagnostic marker for other types of
 CC cancer. The invention provides ESTs and full-length contigs for
 CC prostate CSGs (see AAZ94998-295017). The CSGs, polypeptides encoded
 CC by them, and antibodies that specifically bind CSG are used in new,
 CC claimed methods for detecting, diagnosing, monitoring, staging,
 CC imaging and treating prostate cancer. The new methods provide
 CC earlier diagnosis for the presence and metastasis of prostate
 CC cancer, and can be used to determine if a cancer has metastasized,
 CC or to monitor the progress or stage of the disease when it has not
 CC metastasized.

SQ Sequence 8470 BP; 1461 A; 2863 C; 2658 G; 1485 T; 3 other;

Query Match 5.6%; Score 17; DB 21; Length 8470;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

JY 83 gcagcagctgtgacacc 99
|||||
Db 1740 GCAGCAGCTGTGACACC 1724

RESULT 43
AAA37760/C
ID AAA37760 standard; DNA; 8519 BP.

XX
AC AAA37760;

DT 04-DEC-2000 (first entry)

DE Human fatty acid synthase (FAS) coding sequence.

KW Human; FAS; fatty acid synthase; infection; cancer; gene therapy; ds.

XX Homo sapiens.

FH Key Location/Qualifiers

FT CDS 156..7691

FT /*tag= a

XX /product= fatty_acid_synthase

XX WO200051430-A1.

PD 08-SEP-2000.

PF 25-FEB-2000; 2000WO-US04825.

XX 03-MAR-1999; 99US-0261907.

XX (SMIK) SMITHKLINE BEECHAM CORP.

PI Bergsma DJ, Chapman C, Deptera ME, Ellis CE, Lonsdale J;

PI Mooney JL;

XX WPI; 2000-594133/56.

DR p-PSDB; AAY90349.

PT Novel fatty acid synthase polypeptides and polynucleotides encoding

them, for diagnosing and treating cancer and bacterial infections -

PS Claim 2; Page 28-30; 38pp; English.

XX This sequence encodes the human fatty acid synthase (FAS) of the
CC invention. The DNA, protein, antibodies against it, and antagonists and
CC agonists of FAS are useful for diagnosing and treating abnormal
CC expression of FAS. The FAS sequences are useful for treating cancers and
CC bacterial infections. The DNA sequence is also useful in gene therapy.

SQ Sequence 8519 BP; 1477 A; 2871 C; 2680 G; 1491 T; 0 other;

Query Match 5.6%; Score 17; DB 21; Length 8519;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 83 gcagcagctgtgacacc 99
|||||
Db 1770 GCAGCAGCTGTGACACC 1754

RESULT 44
AAK79882/C
ID AAK79882 standard; DNA; 8864 BP.

XX AAK79882;
AC 07-NOV-2001 (first entry)
DT Human immune/haematopoietic antigen genomic sequence SEQ ID NO:34694.
DE Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytosolic; gene therapy; vaccine; metastasis; ds.
XX Homo sapiens.
OS
PN WO200157182-A2.
XX 09-AUG-2001.
PD
PF 17-JAN-2001; 2001WO-US01354.
XX 31-JAN-2000; 2000US-0179065.
XX 04-FEB-2000; 2000US-0180628.
XX 24-FEB-2000; 2000US-0184664.
XX 02-MAR-2000; 2000US-0186350.
XX 16-MAR-2000; 2000US-0189874.
XX 17-MAR-2000; 2000US-0190076.
XX 18-APR-2000; 2000US-0198123.
XX 19-MAY-2000; 2000US-0205515.
XX 07-JUN-2000; 2000US-0209467.
XX 28-JUN-2000; 2000US-0214886.
XX 30-JUN-2000; 2000US-0215135.
XX 07-JUL-2000; 2000US-0216647.
XX 07-JUL-2000; 2000US-0216880.
XX 11-JUL-2000; 2000US-0217487.
XX 14-JUL-2000; 2000US-0217496.
XX 26-JUL-2000; 2000US-0220963.
XX 26-JUL-2000; 2000US-0220964.
XX 14-AUG-2000; 2000US-0224518.
XX 14-AUG-2000; 2000US-0224519.
XX 14-AUG-2000; 2000US-0225213.
XX 14-AUG-2000; 2000US-0225214.
XX 14-AUG-2000; 2000US-0225266.
XX 14-AUG-2000; 2000US-0225267.
XX 14-AUG-2000; 2000US-0225268.
XX 14-AUG-2000; 2000US-0225370.
XX 14-AUG-2000; 2000US-0225447.
XX 14-AUG-2000; 2000US-0225757.
XX 14-AUG-2000; 2000US-0225758.
XX 14-AUG-2000; 2000US-0225759.
XX 18-AUG-2000; 2000US-0226279.
XX 22-AUG-2000; 2000US-0226681.
XX 22-AUG-2000; 2000US-0226868.
XX 22-AUG-2000; 2000US-0227182.
XX 23-AUG-2000; 2000US-0227009.
XX 30-AUG-2000; 2000US-0228924.
XX 01-SEP-2000; 2000US-0229287.
XX 01-SEP-2000; 2000US-0229343.
XX 01-SEP-2000; 2000US-0229344.
XX 01-SEP-2000; 2000US-0229345.
XX 05-SEP-2000; 2000US-0229509.
XX 05-SEP-2000; 2000US-0229513.
XX 06-SEP-2000; 2000US-0230437.
XX 06-SEP-2000; 2000US-0230438.
XX 08-SEP-2000; 2000US-0231242.
XX 08-SEP-2000; 2000US-0231243.
XX 08-SEP-2000; 2000US-0231244.
XX 08-SEP-2000; 2000US-0231413.
XX 08-SEP-2000; 2000US-0231414.
XX 08-SEP-2000; 2000US-0232080.
XX 08-SEP-2000; 2000US-0232081.
XX 12-SEP-2000; 2000US-0231968.
XX 14-SEP-2000; 2000US-0232397.
XX 14-SEP-2000; 2000US-0232398.
XX 14-SEP-2000; 2000US-0232399.

PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249246.
PR 17-NOV-2000; 2000US-0249247.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-02556719.

PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251858.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-483426/52.
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
XX useful for preventing, diagnosing and/or treating cancers and
XX metastasis -
XX
XX Disclosure: SEQ ID NO 34694; 3071pp + Sequence Listing; English.
XX
XX AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
XX amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
XX activity, and can be used in gene therapy and vaccine production. (I)
XX proteins and polynucleotides may be used in the prevention, diagnosis and
XX treatment of diseases associated with inappropriate (I) expression. For
XX example, they may be used to treat disorders associated with decreased
XX expression by rectifying mutations or deletions in a patient's genome
XX that affect the activity of (I) by expressing inactive proteins or to
XX supplement the patients own production of (I). Additionally, (I)
XX polynucleotides may be used to produce the secreted (I), by inserting
XX the nucleic acids into a host cell and culturing the cell to express the
XX protein. (I) proteins and polynucleotides may be used to prevent,
XX diagnose and treat immune/hematopoietic-related diseases, especially
XX cancers and cancer metastases of haematopoietic-derived cells. AAK64703
XX to AAK87694 represent human immune/hematopoietic antigen genomic
XX sequences from the present invention. AAK54942 to AAK54950 and AAM82169
XX represent sequences used in the exemplification of the present invention.
XX
XX Sequence 8864 BP; 1897 A; 2376 C; 2556 G; 2035 T; 0 other;

Query Match 5.6%; Score 17; DB 22; Length 8864;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 197 acgtggtaaacctctc 213
|||||||
Db 8790 ACGTGGTCAACCTCTC 8774

RESULT 45
ABLI0070/c
ID ABLI0070 standard; cDNA; 9889 BP.
XX
XX ABLI0070;
XX
XX
XX 26-MAR-2002 (first entry)
XX
XX
XX Drosophila melanogaster expressed polynucleotide SEQ ID NO 24692.
XX
XX Drosophila; developmental biology; cell signalling; insecticide;
XX pharmaceutical; gene; ss.
XX
XX Drosophila melanogaster.
XX
XX WO200171042-A2.
XX
XX
XX 27-SEP-2001.
XX
XX
XX 23-MAR-2001; 2001WO-US09231.
XX
XX 23-MAR-2000; 2000US-191637P.

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 15, 2002, 23:22:29 : Search time 9532.94 Seconds
(without alignments)
665.140 Million cell updates/sec

Title: US-09-375-248-1_COPY_2546_2848

Perfect score: 303

Sequence: 1 gagcgctgcacctggggag.....acttcctgcgcgcaagcgg 303

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1797656 seqs, 10463268293 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : GenEmbl.*

- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pi.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sv.*
- 13: gb_un.*
- 14: gb_vi.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
- 20: em_om.*
- 21: em_or.*
- 22: em_ov.*
- 23: em_pat.*
- 24: em_ph.*
- 25: em_pi.*
- 26: em_ro.*
- 27: em_sts.*
- 28: em_un.*
- 29: em_vi.*
- 30: em_htg_hum.*
- 31: em_htg_inv.*
- 32: em_htg_other.*
- 33: em_htg_inv.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description

Query Match 100.0%; Score 303; DB 6; Length 4195;

1	303	100.0	4195	6	AR016568	AR016568 Sequence
2	303	100.0	4195	6	AR106405	AR106405 Sequence
3	303	100.0	4416	6	AR112506	AR112506 Sequence
4	303	100.0	4416	6	HSFLT4	X68203 H.sapiens m
5	303	100.0	4425	6	I44520	I44520 Sequence 31
6	303	100.0	4425	9	HSU43143	U43143 Human recep
7	303	100.0	4795	6	AR016569	AR016569 Sequence
8	303	100.0	4795	6	AR106406	AR106406 Sequence
9	252	83.2	4450	9	HSFLT4X	X69878 H.sapiens F
10	117	38.6	130129	2	AC108083	AC108083 Homo sapi
11	117	38.6	168347	2	AC025336	AC025336 Homo sapi
12	106	35.0	127488	2	AC022095	AC022095 Homo sapi
13	106	35.0	173341	2	AC106813	AC106813 Homo sapi
14	23	7.6	5284	10	MUSRTKA	L07296 Mus musculu
15	23	7.6	260266	2	AL646088	AL646088 Mus muscu
16	21	6.9	4254	10	AF402786	AF402786 Rattus no
17	21	6.9	4360	10	AF402785	AF402785 Rattus no
18	21	6.9	161580	2	AC098957	AC098957 Rattus no
19	20	6.6	4017	9	AF063657	AF063657 Homo sapi
20	20	6.6	4272	5	AB065372	AB065372 Gallus ga
21	20	6.6	7680	9	HSFLT	X51602 Human flt m
22	20	6.6	31360	1	SC9C7	AL035161 Streptomy
23	20	6.6	208304	2	AC108477	AC108477 Homo sapi
24	19	6.3	78210	1	AB070949	AB070949 Streptomy
25	19	6.3	80908	9	HS524E15	Z84485 Human DNA s
26	19	6.3	119916	2	AC105566	AC105566 Rattus no
27	19	6.3	155825	2	AC106084	AC106084 Rattus no
28	18	5.9	561	11	AF207872	AF207872 Ovis arie
29	18	5.9	621	9	HSA330119	AJ330119 Homo sapi
30	18	5.9	827	14	HAUNKTRP	Z16420 Human astro
31	18	5.9	1307	1	RSU62291	U62291 Rhodobacter
32	18	5.9	1519	3	AB025557	AB025557 Branchios
33	18	5.9	2065	9	AF049459	AF049459 Homo sapi
34	18	5.9	2329	9	AF049460	AF049460 Homo sapi
35	18	5.9	2405	9	AF049461	AF049461 Pan trogl
36	18	5.9	3614	5	AF188842	AF188842 Gallus ga
37	18	5.9	4784	8	NEUATPPM	J02602 Neurospora
38	18	5.9	5359	8	NEUATPASE	M14085 N.crassa pl
39	18	5.9	6813	14	HA1CAPNS	Z25771 Human astro
40	18	5.9	10003	1	U67544	U67544 Methanococc
41	18	5.9	39314	1	SGR300302	AJ300302 Streptomy
42	18	5.9	71769	2	AC102135	AC102135 Mus muscu
43	18	5.9	74586	2	AC060793	AC060793 Homo sapi
44	18	5.9	76072	8	NCB1D1	AL355927 Neurospor
45	18	5.9	84481	9	AL136378	AL136378 Human DNA

ALIGNMENTS

RESULT	1					
AR016568						
LOCUS	AR016568	Sequence 1	from patent US 5776755.	4195 bp	DNA	linear PAT 05-DEC-1998
DEFINITION	AR016568	Sequence 1	from patent US 5776755.			
ACCESSION	AR016568					
VERSION	AR016568.1	GI:3972845				
KEYWORDS						
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 4195)					
AUTHORS	Alitalo,K., Aprelikova,O., Pajusola,K., Korhonen,J. and Kaipainen,A.					
TITLE	FLT4, a receptor tyrosine kinase					
JOURNAL	Patent: US 5776755-A 1 07-JUL-1998;					
FEATURES	Location/Qualifiers					
source	1..4195					
	/organism="unknown"					
BASE COUNT	889 a 1279 c 1305 g 722 t					
ORIGIN						

```
Best Local Similarity 100.0%; Pred. No. 4e-152;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gagcggctgcacctgggagagtgctcggtacgagcgcttcgggaagtggtggaagcc 60
Db 2546 GAGCGGCTGCACCTGGGGAGAGTCTCGGCTACGGCGCCTTCGGGAAGTGTGGGAAGCC 2605

Qy 61 tcgcgttcggcatccacaaaggcagcagctgtgacacggtgcccgtgaaatgctgaaa 120
Db 2606 TCCGCTTTTCGGCATCCACAAAGGCGACAGCTGTGACACCGTGGCCGTGAAATGCTGAAA 2665

Qy 121 gagggcgcaacgcccagcagcagcagcagcagcagcagcagcagcagcagcagcagc 180
Db 2666 GAGGGCGCCACGGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 2725

Qy 181 atcggaacacacctcaacgtgggtcaacctctcctcgggcggtgacacagcgagggccc 240
Db 2726 ATCGGAACACCACTCAACGTGGTCAACCTCTCGGGCGCTGCACCAAGCGGCGGCC 2785

Qy 241 ctcatggtgatcgtggagtgctgcaagtcagcagcagcagcagcagcagcagcagcagc 300
Db 2786 CTCATGTTGATCGTGGAGTCTTCAAGTACGGCAACCTCTCCAACTTCTCTCGCGCCAAG 2845

Qy 301 cgg 303
Db 2846 CGG 2848

RESULT 2
LOCUS AR106405
DEFINITION Sequence 1 from patent US 6107046.
ACCESSION AR106405
VERSION AR106405.1 GI:12820935
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Alicalco,K., Aprelikova,O., Pajusola,K., Armstrong,E., Korhonen,J.,
TITLE Antibodies to Flt4, a receptor tyrosine kinase and uses thereof
JOURNAL
FEATURES
LOCATION/Qualifiers
SOURCE
1. .4195
/organism="unknown"

BASE COUNT 889 a 1279 c 1305 g 722 t
ORIGIN

Query Match 100.0%; Score 303; DB 6; Length 4195;
Best Local Similarity 100.0%; Pred. No. 4e-152;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gagcggctgcacctgggagagtgctcggtacgagcgcttcgggaagtggtggaagcc 60
Db 2546 GAGCGGCTGCACCTGGGGAGAGTCTCGGCTACGGCGCCTTCGGGAAGTGTGGGAAGCC 2605

Qy 61 tcgcgttcggcatccacaaaggcagcagctgtgacacggtgcccgtgaaatgctgaaa 120
Db 2606 TCCGCTTTTCGGCATCCACAAAGGCGACAGCTGTGACACCGTGGCCGTGAAATGCTGAAA 2665

Qy 121 gagggcgcaacgcccagcagcagcagcagcagcagcagcagcagcagcagcagcagc 180
Db 2666 GAGGGCGCCACGGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 2725

Qy 181 atcggaacacacctcaacgtgggtcaacctctcctcgggcggtgacacagcgagggccc 240
Db 2726 ATCGGAACACCACTCAACGTGGTCAACCTCTCGGGCGCTGCACCAAGCGGCGGCC 2785

Qy 241 ctcatggtgatcgtggagtgctgcaagtcagcagcagcagcagcagcagcagcagcagc 300
Db 2786 CTCATGTTGATCGTGGAGTCTTCAAGTACGGCAACCTCTCCAACTTCTCTCGCGCCAAG 2845

Qy 301 cgg 303
Db 2846 CGG 2848

RESULT 3
LOCUS AR112506
DEFINITION Sequence 1 from patent US 6130071.
ACCESSION AR112506
VERSION AR112506.1 GI:14092406
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Alitalo,K. and Joukov,V.
TITLE Vascular endothelial growth factor C (VEGF-C) .DELTA.Cys.sub.156
protein and gene, and uses thereof
JOURNAL
FEATURES
LOCATION/Qualifiers
SOURCE
1. .4416
/organism="unknown"

BASE COUNT 941 a 1345 c 1355 g 774 t
ORIGIN

Query Match 100.0%; Score 303; DB 6; Length 4416;
Best Local Similarity 100.0%; Pred. No. 4e-152;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gagcggctgcacctgggagagtgctcggtacgagcgcttcgggaagtggtggaagcc 60
Db 2546 GAGCGGCTGCACCTGGGGAGAGTCTCGGCTACGGCGCCTTCGGGAAGTGTGGGAAGCC 2605

Qy 61 tcgcgttcggcatccacaaaggcagcagctgtgacacggtgcccgtgaaatgctgaaa 120
Db 2606 TCCGCTTTTCGGCATCCACAAAGGCGACAGCTGTGACACCGTGGCCGTGAAATGCTGAAA 2665

Qy 121 gagggcgcaacgcccagcagcagcagcagcagcagcagcagcagcagcagcagcagc 180
Db 2666 GAGGGCGCCACGGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 2725

Qy 181 atcggaacacacctcaacgtgggtcaacctctcctcgggcggtgacacagcgagggccc 240
Db 2726 ATCGGAACACCACTCAACGTGGTCAACCTCTCGGGCGCTGCACCAAGCGGCGGCC 2785

Qy 241 ctcatggtgatcgtggagtgctgcaagtcagcagcagcagcagcagcagcagcagcagc 300
Db 2786 CTCATGTTGATCGTGGAGTCTTCAAGTACGGCAACCTCTCCAACTTCTCTCGCGCCAAG 2845

Qy 301 cgg 303
Db 2846 CGG 2848

RESULT 4
LOCUS HSFLT4
DEFINITION H.sapiens mRNA for FLT4, class III receptor tyrosine kinase.
ACCESSION X68203
VERSION X68203.1 GI:31433
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Aprelikova,O.
TITLE Direct Submission
JOURNAL
Submitted (01-SEP-1992); O. Aprelikova, University of Helsinki,
Cancer Biology Laboratory, Dept of Pathology, Haartmaninkatu 3,
```

00290 Helsinki, FINLAND
2 (bases 1 to 4416)
Aprelikova,O., Pajusola,K., Partanen,J., Armstrong,E., Alitalo,R.,
Bailey,S.K., McMahon,J., Wasmuth,J., Huebner,K. and Alitalo,K.
FLT4, a novel class III receptor tyrosine kinase in chromosome
5q33-qter
Cancer Res. 52 (3), 746-748 (1992)
92119639
Related sequence: X51602.
Location/Qualifiers
source
1..4416
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5q35"
/haplotype="erythroleukemia cells"
/cell_line="HEL"
<1..>4416
/gene="FLT4"
1..4416
/gene="FLT4"
<1..3916
/gene="FLT4"
/note="class III tyrosine kinase"
/codon_start=2
/product="FLT4"
/protein_id="CAA48290.1"
/db_xref="GI:388522"
/db_xref="SWISS-PROT:P35916"
/translation="HAORPEMORGAAALCLRLWLCLGLDLVSGVSMPTPTLITEES
HYIDGDSLSISCRGHLEWAWPQAEAPATGDKDSEDGVVRCDEGTDAKYCKVL
LHUEVHNDTGSVCYIKYIKARIEGTAAASYVFEVDFEQPIFNKPTDLLVRKDDAM
WYPLVSLPGLNVLWSDQVWDDRRGMLVSTPLLHLYLCQETTWGD
QDFLNPEFLVHTGELYDIQLPRKSLLELLVGEKVLNCTVWAEFNFGVTFDMQPG
KOAERGVWPPERSQOHTTELSILTINVSQHDLCVCKANNGIORFRESTEVIH
ENPFIQSVMLKGPILLEATAGDELKVLKLAAYPPEFQWYKCKALSGRSHALVL
KEYTEASTGTYTLALWNSAAGLRNLSILELVNVPQIHEXEAASPSIYSRHSRALTL
CTAYGVPLSTQWHRPWTCKMFAQSLRRKQDQDLMPCRDRWAVTTQDANPIE
SLDTWTEFEVGNKTSKLVITQNAVVSAMYSKVSNGYQDERLIYFYVTTIPDFTI
ESKSEELLEGOPVLLSCQADSYKYEHLRWYRLNLSTLHDAHGNPLLLDCKNHLFAT
PLAASLEEVAPCARHLLSLSTPRVAPAEHGYVCEVODRSHDKHCHKYLSVOALE
APRLTQNTDLLVNVSDSLEMOCLVAGAHAPSIYVYKDERLLEKSGVDLADSNOKLS
IQRVEEDAGRYLCSVCNAKGVNSSASVAVEGEDKGSMEIVILVGGVTAFFWVL
LLLIIFCNRRAHAPADIKTYLISIMDPGEVPLEEOCEYLSYDASQWEPRELRHLGRV
LYGAFGVAFSAFTHKSGSDTVAVMKLEKATASEHRLMSCLKLIHIGNHLN
VYNLIGACTKQGPLMVAIFECYKGNLSNFKRAKDAFSPCAEKSPEDRGVFRAMVEL
ARLDRRRGSSDRVLFAFNSKTEGARASPDQAEADLWLSPLTMEDLVGYSFQVARG
MEFLASRVCIIHRDLAARNLILLESADVVKICDFGLARDIYKDPDYVRKGSARLPKQWA
PESIFDKVYTTQSDVMSFQVLLWELFSLGASPYPCQVINBEFCORLDRCTMRAPELA
TPAIRIMLNCWSDPKARPAFSELVEILGDLLOGRLOEEVEVCMAPRSSOSSEEGS
FSQVSTMALHIAQADAEDSPSLORHLSLAARYNMVSPGCLARGAETRGSSRMKTFE
EFPMTPTTYKGVSDNOTDSGMVLASEEFEQIESRHRQESGR"
BASE COUNT 941 a 1345 c 1355 g 774 t 1 others
ORIGIN

Query Match 100.0%; Score 303; DB 9; Length 4416;
Best Local Similarity 100.0%; Pred. No. 4e-152;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gaagcgctacacgtggagagtgctcggtacgagcgcttcggaagtggtggaagcc 60
|||||
Db 2546 GAGCGGCTCGACCTGGGAGAGTGCTCGGCTACGGCGCTTCGGAAAGTGCTGGAAGCC 2605
|||||

QY 61 tcgcgtttcggcatcaccaaggcgagcagctgtgacacagcggtgcaaatgctgaaa 120
|||||
Db 2606 TCCGCTTTCCGCATCACAAAGGCGACGACCTGTGACACCGTGGCGTGAAAATGCTGAAA 2665
|||||

QY 121 gagggcgccagcgagcgagcagcgctgtgctgagtgagtgagtgagtgagtgagtc 180
|||||
Db 2666 GAGGGCGCCACGCCAGCGAGCAGCGCGCTGATGTCGGAGCTCAAGATCTCATTCAC 2725
|||||

QY 181 atcggcaaccactcaagtggtgaacctctcgaggcggtgaccaaagcgagggccccc 240
|||||
BASE COUNT 941 a 1345 c 1355 g 774 t 1 others
ORIGIN

Query Match 100.0%; Score 303; DB 9; Length 4416;
Best Local Similarity 100.0%; Pred. No. 4e-152;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gaagcgctacacgtggagagtgctcggtacgagcgcttcggaagtggtggaagcc 60
|||||
Db 2546 GAGCGGCTCGACCTGGGAGAGTGCTCGGCTACGGCGCTTCGGAAAGTGCTGGAAGCC 2605
|||||

QY 61 tcgcgtttcggcatcaccaaggcgagcagctgtgacacagcggtgcaaatgctgaaa 120
|||||
Db 2606 TCCGCTTTCCGCATCACAAAGGCGACGACCTGTGACACCGTGGCGTGAAAATGCTGAAA 2665
|||||

QY 121 gagggcgccagcgagcgagcagcgctgtgctgagtgagtgagtgagtgagtc 180
|||||
Db 2666 GAGGGCGCCACGCCAGCGAGCAGCGCGCTGATGTCGGAGCTCAAGATCTCATTCAC 2725
|||||

QY 181 atcggcaaccactcaagtggtgaacctctcgaggcggtgaccaaagcgagggccccc 240
|||||

Db 2726 ATCGGCAACCACTCAACGTGGTCAACCTCTCGGGGGGTGCACCAAGCCGCGAGGCCCC 2785
QY 241 ctcatgggtgatcgtgagttctgcaagtacgcaacctctcaactctctcgcgcccaag 300
|||||
Db 2786 CTCATGGGTGATCGTGGAGTTCGTCAAGTACGGCAACCTCTCCAACCTCTCTCGCGCCCAAG 2845
QY 301 cgg 303
|||||
Db 2846 CGG 2848
|||||

RESULT 5
LOCUS I44520
DEFINITION Sequence 31 from patent US 5635177. DNA linear PAT 07-OCT-1997
ACCESSION I44520
VERSION I44520.1 GI:2469233
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 4425)
AUTHORS Bennett,B.D., Goeddel,D. and Matthews,W.
TITLE Protein tyrosine kinase agonist antibodies
JOURNAL Patent: US 5635177-A 31 03-JUN-1997;
FEATURES Location/Qualifiers
source 1..4425
/organism="unknown"
BASE COUNT 939 a 1348 c 1361 g 777 t
ORIGIN

Query Match 100.0%; Score 303; DB 6; Length 4425;
Best Local Similarity 100.0%; Pred. No. 4e-152;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gagcgctgcacctggggagagtgctcggtctacgagcgcttcggaagtggtggaagcc 60
|||||
Db 2557 GAGCGGCTGCACCTGGGAGAGTGCTCGGCTACGGCGCTTCGGAAAGTGCTGGAAGCC 2616
|||||

QY 61 tcgcgtttcggcatcaccaaggcgagcagctgtgacacagcggtgcaaatgctgaaa 120
|||||
Db 2617 TCCGCTTTCCGCATCACAAAGGCGACGACCTGTGACACCGTGGCGTGAAAATGCTGAAA 2676
|||||

QY 121 gagggcgccagcgagcgagcagcgctgtgctgagtgagtgagtgagtgagtc 180
|||||
Db 2677 GAGGGCGCCACGCCAGCGAGCAGCGCGCTGATGTCGGAGCTCAAGATCTCATTCAC 2736
|||||

QY 181 atcggcaaccactcaagtggtgaacctctcgaggcggtgaccaaagcgagggccccc 240
|||||
Db 2737 ATCGGCAACCACTCAACGTGGTCAACCTCTCGGGGGGTGCACCAAGCCGCGAGGCCCC 2796
|||||

QY 241 ctcatgggtgatcgtgagttctgcaagtacgcaacctctcaactctctcgcgcccaag 300
|||||
Db 2797 CTCATGGGTGATCGTGGAGTTCGTCAAGTACGGCAACCTCTCCAACCTCTCTCGCGCCCAAG 2856
QY 301 cgg 303
|||||
Db 2857 CGG 2859
|||||

RESULT 6
LOCUS HSU43143
DEFINITION Human receptor tyrosine kinase Flt4 (short form) mRNA, complete cds.
ACCESSION U43143
VERSION U43143.1 GI:1150990
KEYWORDS human.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 4425)
AUTHORS Lee,J., Gray,A., Yuan,J., Luoh,S.-M., Avraham,H. and Wood,W.I.
TITLE Vascular Endothelial Growth Factor Related Protein (VRP): A Ligand and Specific Activator of the Tyrosine Kinase Receptor Flt4
JOURNAL Proc. Natl. Acad. Sci. U.S.A. (1996) In press
REFERENCE 2 (bases 1 to 4425)
AUTHORS Wood,W.I.
TITLE Direct Submission
JOURNAL Submitted (12-DEC-1995) William I. Wood, Molecular Biology, Genentech, Inc., 460 Pt. San Bruno Blvd., S. San Francisco, CA 94080, USA

FEATURES
source
Location/Qualifiers
1..4425
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="combined from clones tk1.94, tk1.65, and tk1.4"
/cell_line="megakaryocyte lines CMK11-5 and DAM1"
31..3927
/function="receptor for vascular endothelial growth factor related protein (VRP); receptor tyrosine kinase"
/note="also called SAL-S1 or tk1"
/codon_start=1
/product="Flt4"
/protein_id="AAA85215.1"
/db_xref="GI:1150991"
/translation="MORCAALCLRLWLCLGLDLVSCYSMTPTLNITRESHVIDTG
DSLISCRGHPLEWAPCAQEPATGDKDSEDGVYVDRDCEGTDAKPYCKVLLHEVH
ANDTGYCYKYKIKARIEGTAASSVYVDFQPIFKPDTLLNKNKDAWVPCLV
SPGLNVTLSOSSVLPDQGVVWDRGMLVSTPLLDALYLQCTTTGDDQDFLSN
PFLVHTINELYDITLPRKLELLVGEKLYLNGTYWAEFNSGVTFDWDYPGKQAEKRG
KWPERRSQOHTLELSITLTHNSQHDLSYGVCKANNQIQRFFRESYEVIVHNPFLIS
VEMLKGPILAEATAGDELVKLPVLAAYPPPEFOWYKDGKALSGRHSFHALVKEVTEA
STGYTTLALMSAAGLRNLSLELVVNPPOIHEKEASSPSIYSRHSQALICTAYGV
PLPLSIOMHNPWPCKMFAQRLRRQOQDLMFQCDRWRAVITQDAVNPISLDTWT
EFVEGKNITVSKLQIANVNSAMTKCVNVKVGQDERLIYVITPIDGFTIESKPSE
ELLEGQVLLSCDYSKYRHLRYRLNLSLTHDAHGNPLLLDCKNHLFATPLAASL
EEVAPGARHATLSLIPRVAPEHEGYVCEYQDRRSHDKHKRYLSVQALEAPRLTO
NLTLVVLEASLQMLCVAGAHAPSIVWYKDERLLEKSGVDLADSNOKLSIQVRVE
EDAGRYLCSVCNAGVNSASVAVESGDKSMETVILVGTGVIANVFVFWVLLILIC
NMRRPAHDIKTGLYSIIMDPCEVPLEQCEYLSYDASQWEPFRERHLGRVLYGAF
CKVPEASAFGIHKSSCDTVAVKMLKEGATSEHRLMSELKILIHGINHLNVNLLG
ACTPQGPLMIVFEFCYKGNLSNLRARADPAESCAEKSPQGRFRAMVLEARDLR
RPGSSDRVLFARFCEGGARRAPDQEDLMSPLTMDLVYCSFQVARGMFEFLAS
RKTITRDUAARNILLESDDVYKICDFGLARDIYKDPDYVRKGSARLPKWMAPESIFD
KVVYTTDSVFGVLLWEIFSLGASPYGVQVINEFCORLRDGTMRAPELATPAIR
IMLNCSGDPKARPAFSELVEILGDLLQGLQEEVEECVMAPRSSQSEGSFSQVST
MALHIQDADEDSPPSLQRHSLAARYYNWVSPQCLARGAETGRSSRNKTFEFPMP
TTYKGSVDNQDSGMVLASBEFEQIESHRHRESGFR"

BASE COUNT 939 a 1348 c 1361 g 777 t
ORIGIN

Query Match 100.0%; Score 303; DB 9; Length 4425;
Best Local Similarity 100.0%; Pred. No. 4e-152;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gagcggtcacctgggagagtgctcggtacgagcgcttcggaagtggtggaagcc 60
|||||
Db 2557 GAGCGGCTGCACTGGGAGAGTGTCTGGCTACGGCGCTTCGGGAAGTGTGGAAGCC 2616
|||||

Qy 61 tcgcgtttcggcatccacaaggcagcagctgtgacacccgtggtgaaatgctgaaa 120
|||||
Db 2617 TCCGCTTCGGCATCCACAGGCGACGAGCTGTGACACCGTGGCGCTGAAATGCTGAAA 2676
|||||

Qy 121 gagggcgccagcgagcagcagcagcagcagcagcagcagcagcagcagcagc 180
|||||
Db 2677 GAGGCGCCACGCGGCGAGCAGCGCGCTGTGTCGGAGCTCAAGATCTCATTAC 2736
|||||

Qy 181 atcggaaccacccacagtggtcaacctctcgggcggtgacacacccctctccaa 240
|||||
Db 2737 ATCGGCAACCACTCAACGTGTGTAACCTCTTCGGGGCGTGCACCAAGCCGAGGCC 2796
|||||

Qy 241 ctcatggtgatcgtgagtgcttctgcaaglacggaacacctctccaaacctctc 300
|||||
Db 2796 CTATGGTGTATCGTGGAGTCTTCTGCAAGTACGGCAACCTCTCCAACTTCTCGCGCC 2845
|||||

Qy 301 cgg 303
|||
Db 2846 CGG 2848
|||

RESULT 8
AR106406
LOCUS AR106406
DEFINITION Sequence 3 from patent US 6107046.
ACCESSION AR106406
VERSION AR106406
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 4795)
AUTHORS Alitalo,K., Aprelikova,O., Pajusola,K., Armstrong,E., Korhonen,J.,
Kaipainen,A. and Matikainen,M.
TITLE Antibodies to Flt4, a receptor tyrosine kinase and uses thereof

Db 2797 CTCATGGTGATCGTGGAGTCTTGTCAAGTACGGCAACCTCTCCAACTTCTCGCGCC 2856
Qy 301 cgg 303
|||
Db 2857 CGG 2859
|||

RESULT 7
AR016569
LOCUS AR016569
DEFINITION Sequence 3 from patent US 5776755.
ACCESSION AR016569
VERSION AR016569.1 GI:3972846
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 4795)
AUTHORS Alitalo,K., Aprelikova,O., Pajusola,K., Armstrong,E., Korhonen,J.,
and Kaipainen,A.
TITLE JOURNAL
PATENT: US 5776755-A 3 07-JUL-1998;
FEATURES Location/Qualifiers
Source 1..4795
/organism="unknown"
BASE COUNT 977 a 1490 c 1494 g 834 t
ORIGIN

Query Match 100.0%; Score 303; DB 6; Length 4795;
Best Local Similarity 100.0%; Pred. No. 4e-152;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gagcggtgcacctgggagagtgctcggtacgagcgcttcggaagtggtggaagcc 60
|||||
Db 2546 GAGCGGCTGCACTGGGAGAGTGTCTGGCTACGGCGCTTCGGGAAGTGTGGAAGCC 2605
|||||

Qy 61 tcgcgtttcggcatccacaaggcagcagcagcagcagcagcagcagcagcagcagc 120
|||||
Db 2606 TCCGCTTCGGCATCCACAGGCGAGCAGCTGTGACACCGTGGCGCTGAAAATGCTGAAA 2665
|||||

Qy 121 gagggcgccagcgagcagcagcagcagcagcagcagcagcagcagcagcagc 180
|||||
Db 2666 GAGGCGCCACGCGGCGAGCAGCAGCGCGCTGTGTCGGAGCTCAAGATCTCATTAC 2725
|||||

Qy 181 atcggaaccacccacagtggtggtcaacctctcgggcggtgacacacccctctccaa 240
|||||
Db 2726 ATCGGCAACCACTCAACGTGTGTAACCTCTTCGGGGCGTGCACCAAGCCGAGGCC 2785
|||||

Qy 241 ctcatggtgatcgtgagtgcttctgcaaglacggaacacctctccaaacctctc 300
|||||
Db 2786 CTATGGTGTATCGTGGAGTCTTCTGCAAGTACGGCAACCTCTCCAACTTCTCGCGCC 2845
|||||

Qy 301 cgg 303
|||
Db 2846 CGG 2848
|||

RESULT 8
AR106406
LOCUS AR106406
DEFINITION Sequence 3 from patent US 6107046.
ACCESSION AR106406
VERSION AR106406.1 GI:12820936
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 4795)
AUTHORS Alitalo,K., Aprelikova,O., Pajusola,K., Armstrong,E., Korhonen,J.,
Kaipainen,A. and Matikainen,M.
TITLE Antibodies to Flt4, a receptor tyrosine kinase and uses thereof

JOURNAL Patent: US 6107046-A 3 22-AUG-2000;
FEATURES Location/Qualifiers
1. .4795
/organism="unknown"
BASF COUNT 977 a 1490 c 1494 g 834 t
ORIGIN

Query Match 100.0%; Score 303; DB 6; Length 4795;
Best local Similarity 100.0%; Pred. No. 4e-152;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 gagcggtgcacctgggagagtgctcgctacgagcgcttcgggaggtgggtggaagcc 60
|||||
Db 2546 GAGCGGCTGCACCTGGGAGAGTGCTCGCTACCGCGCTTCGGGAAGTGGTGGGAAGCC 2605
|||||
Oy 61 tccgcttcggcatcaccaaggagcagcagctgtgacacagcggtggaatcttgaaa 120
|||||
Db 2606 TCCGCTTTCGGCATCCACAAAGGCAGCAGCTGTGCACACCTGGCGCTGAAAATGCTTCAA 2665
|||||
Oy 121 gagggcgccagcgagcagcgagcgagcgctgagcagctcagatcagatcctcattcac 180
|||||
Db 2666 GAGCGGCCACGCGCAGCAGCAGCAGCGCGCTGATGTCGGAGCTCAAGATCTCATTTAC 2725
|||||
Oy 181 atcggaacacacctcaacgtgggtcaacctctcctcgggcggtgcaacagcgagggcccc 240
|||||
Db 2726 ATCGGAACACCTCAACGTGGTCAACCTCTCGCGCGGTGCACCAAGCGCAGGCGCCCC 2785
|||||
Oy 241 ctcagtgatcgtgagttctcagagtcagagtcagagtcacactctcagctcgcgccaag 300
|||||
Db 2786 CTCATGTCATGTCGTGGAGTTCTCAAGTAGCGCAACCTCTCCAACCTCTCGCGCGCAAG 2845
|||||
Oy 301 cgg 303
|||
Db 2846 CGG 2848
|||

RESULT 9
HSFLT4X HSFLT4X 4450 bp mRNA linear PRI 29-NOV-1993
LOCUS H.sapiens Flt4 mRNA for transmembrane tyrosine kinase.
DEFINITION X69878.559182
ACCESSION X69878.1 GI:297049
VERSION transmembrane tyrosine kinase; tyrosine kinase.
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 4450)
AUTHORS Galland,F., Karaymsheva,A., Pebusque,M.J., Borg,J.P., Rottapel,R.,
Dubreuil,P., Rosnet,O. and Birnbaum,D.
TITLE The FLT4 gene encodes a transmembrane tyrosine kinase related to
the vascular endothelial growth factor receptor
JOURNAL Oncogene 8 (5), 1233-1240 (1993)
MEDLINE 93241723
REFERENCE 2 (bases 776 to 1200)
AUTHORS Galland,F., Karaymsheva,A., Mattei,M.G., Rosnet,O., Marchetto,S.
and Birnbaum,D.
TITLE Chromosomal localization of FLT4, a novel receptor-type tyrosine
kinase gene
JOURNAL Genomics 13 (2), 475-478 (1992)
MEDLINE 92307693
REFERENCE 3 (bases 1 to 4450)
AUTHORS Galland,F.
TITLE Direct Submission
JOURNAL Submitted (28-DEC-1992) F. Galland, INSERM, Unite 119, 27 Bd Lei
Roure, Marseille 13009, FRANCE
FEATURES Location/Qualifiers
1. .4450
/organism="Homo sapiens"
source /db_xref="taxon:9606"
sig_peptide 22. .87
CDS 22. .3918

/function="tyrosine kinase"
/note="unnamed protein product"
/citation=[1]
/codon_start=1
/protein_id="CAA49505.1"
/db_xref="GI:297050"
/db_xref="SWISS-PROT:P35916"
/translation="MORGAALCLRLWCLGLGLDGLVSDYSMTPTLNITESHVIDTG
DSLISCRGHPLEWAWPCQAQEPATGDKDSEDTGVVRCDCGTGTPYCKVLLHLEH
ANDTGSVYCYKIKARIEGTAASSVYVDFEQPIINKPDTLLVNRKDDAWVPCLV
SIPGLNVLRSQSSVLPWDCQEVVWDDRGMLVSTPLLDALYLOCTWGDQDFLSN
PFLVHITNELYDIDLOLPKRLSELVLLGKLVNCTVMAEFNSGVTFDDHYDCKAERC
KWVPRRSQOHTTELSILTTHNSQHDLSYVCKANNIGQRFRETEVIVHENPFI
STGYTLALNWSAAGLRNLSLELVNVPPOIHERKEASSPSIYSRHSQALTCYAGV
VEMLKPTILEATAGDELKLPVLAAPPEFQYKDGKALSGRSHALYKVEYTEA
PLPLSIOWHWRPWTCKFAORSLRRROQDLMPOCRDMRAVTTQDAVNPITSLDTWT
EFVEGKNKTVSKLYIQANVSNMYKCVSNKVGQDERLIYFYVTTIPDGFITSEKPS
ELLEGPVLLSCQADSYKIEHLRWTLNLSTLHDHGNPLLDCKNVLHFLATPLAASL
EEVAPGARHATLSLSIPRAPEHGHVYCEVDRRSHDKCHKYLSVOALEAPRLTQ
NLDTLLNVSDSLMOCLVAGAHAPSIWYKDERLEEKSGVDLADSNOKLSIORVRE
EDAGPYLCVCRPKGVNNSASVAVEGSEDKGMEIVILVGTGVIATVFWVLLLLIFC
NMRPAHADIKTGYSIITDPCEVPLEQCEYLSYDASQWEEPRERLHGRVLYGAF
GKVPASAFGIHKGSCDTAVKMLKEGATASEQALMSSELKILIHGNHNLNVNLLG
ACTPQGPLMIVIFECYGNLSNLRARDAFSPCAEKSPEORGRFAMVELARDLR
RPGSDRVLFARFKEGARRASPDQAEIDLWLSPLTMEDLVCSYFQVARGMEFLAS
RKCTHRLAARNILISESDVYKICDFGLARDYKDPDYVRKGSARLPKMWAPESIFD
KVYTTQSDVWSFGVLLWEIFSLGASPYPGVOINEEFCVRDGTMRAPELATPAIRH
IMLNCSGDPKARPAFSDLVLEIGDLLOGRGLQEEVEYCMAPRSOSSSEGSFSQVST
MALHIAQADADESPSLQRHSLAARYINWSPFCCCLARGAETRGSSRMKKTPEEFPMT
TTYKGSVDNQTDGSMVLASEEFEQIESRHRQESGFR"
22. .2346
/citation=[1]
/product="extracellular domain"
160. .366
/citation=[1]
/function="IG-like domain 1"
481. .651
/citation=[1]
/function="IG-like domain 2"
763. .963
/citation=[1]
/function="IG-like domain 3"
1072. .1230
/citation=[1]
/function="IG-like domain 4"
1342. .1635
/citation=[1]
/function="IG-like domain 5"
1741. .1992
/citation=[1]
/function="IG-like domain 6"
2104. .2277
/citation=[1]
/product="IG-like domain 7"
2347. .2412
/citation=[1]
/product="transmembrane domain"
2413. .2547
/citation=[2]
/citation=[1]
/product="juxtamembrane domain"
2548. .2853
/citation=[2]
/citation=[1]
/product="tyrosine kinase domain 1"
2854. .3048
/citation=[2]
/citation=[1]
/product="kinase insert"
3049. .3558
/citation=[2]
/citation=[1]

```
BASE COUNT      960 a 1350 c 1354 g 786 t
ORIGIN
Query Match      83.2%; Score 252; DB 9; Length 4450;
Best Local Similarity 99.7%; Pred. No. 1.2e-124;
Matches 302; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 gagcggtcgacacgtggagagtgctcgctacgagcgcttcggggaagtggtggaagcc 60
|||||
Db 2548 GAGCGGCTGCACCTGGGAGAGTGTCTCGGCTACGGCGCCTTCGGGAAGTGTGTGAAGCC 2607
|||||

Qy 61 tcgctttcggtatcacaaaggacagcagctgtgacacgtggtgacctgaaatgctgaaa 120
|||||
Db 2608 TCGCGTTCGGCATCCACAAAGGCGACAGCTGTGACACCGTGGCCGTGAAATGCTGAAA 2667
|||||

Qy 121 gagggcgccacgagcgagcagccgcgcgtgatctgagagctcaagatcctcattcac 180
|||||
Db 2668 GAGGCGGCCACGCCAGCAGCAGCGCGCTGATCGGAGCTCAAGATCCTCATTTAC 2727
|||||

Qy 181 atcgggaaccacacacgaactggtgtaacacctctcggggcggtgacccaagcgagggcccc 240
|||||
Db 2728 ATCGGAACACACCTCAACGTTGGTCAACCTCTCTCGGGCGGTGCACCAAGCGCAGGGCCCC 2787
|||||

Qy 241 ctcatgtgatctgagtgagttctcaagtagcagcaacctctccaactctcctgcgcgccaag 300
|||||
Db 2788 CTATGCTGATCGTGGAGTTCTGCAAGTAGCGCAACCTCTCCAACATTCCTCGCGGCCAAG 2847
|||||

Qy 301 cgg 303
Db 2848 CGG 2850

RESULT 10
AC108083
LOCUS      Homo sapiens chromosome 5 clone CTD-2013L15, linear HTG 25-JAN-2002
DEFINITION AC108083
SEQUENCE, 4 unordered pieces.
ACCESSION AC108083.1 GI:18369929
VERSION
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE      human.
ORGANISM    Homo sapiens
REFERENCE    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE        DOE Joint Genome Institute.
JOURNAL      Sequencing of Human Chromosome 5
AUTHORS      Unpublished
REFERENCE    DOE Joint Genome Institute.
AUTHORS      DOE Joint Genome Institute.
TITLE        Direct Submission
JOURNAL      Submitted (25-JAN-2002) Production Sequencing Facility, DOE Joint
COMMENT      Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
-----
Project Information
Center Project Name: 632820
Center clone name: CITB-H1_2013L15
-----
Summary Statistics
Consensus quality: 124488 bases at least Q40
Consensus quality: 128031 bases at least Q30
Consensus quality: 128642 bases at least Q20
Estimated insert size: 135000; agarose-fp estimation
Estimated insert size: 129829; sum-of-contigs estimation
Quality coverage: 7.66 in Q20 bases; agarose-fp estimation
Quality coverage: 7.97 in Q20 bases; sum-of-contigs estimation
* NOTE: This is a 'working draft' sequence. It currently
```

```
* consists of 4 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 4320: contig of 4320 bp in length
* 4321 4420: gap of unknown length
* 4421 23712: contig of 19292 bp in length
* 23713 23812: gap of unknown length
* 23813 48602: contig of 24790 bp in length
* 48603 48702: gap of unknown length
* 48703 130129: contig of 81427 bp in length.
FEATURES             Location/Qualifiers
     source            1..130129
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="5"
                     /clone="CTD-2013L15"
                     /clone_lib="CalTech human BAC library D"
BASE COUNT    35337 a 32397 c 30949 g 31146 t 300 others
ORIGIN
Query Match      38.6%; Score 117; DB 2; Length 130129;
Best Local Similarity 100.0%; Pred. No. 4.9e-52;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 120 agaggcgccacgagcgagcagcgcgctgatctcgagagctcaagatcctcattca 179
|||||
Db 19878 AGAGGCGCCACGGCCAGCAGCGCGCTGATGTCGGAGCTCAAGATCCTCATTTCA 19937
|||||

Qy 180 catcggaaccacacacgtgctcaacctctcctcgggcgctgcacaaagccaggg 236
|||||
Db 19938 CATCGGAACCAACCTCAACGTGCTCAACCTCTCGGGCGGTGCACCAAGCCCGCAGGG 19994
|||||

RESULT 11
AC025336/c
LOCUS      Homo sapiens chromosome 5 clone RP11-451H23 map 5, WORKING DRAFT
DEFINITION AC025336
SEQUENCE, 32 unordered pieces.
ACCESSION AC025336.2 GI:7328761
VERSION
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      human.
ORGANISM    Homo sapiens
REFERENCE    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE        1 (bases 1 to 168347)
AUTHORS      Birren,B., Linton,L., Nusbaum,C. and Lander,E.
JOURNAL      Homo sapiens chromosome 5, clone RP11-451H23
REFERENCE    2 (bases 1 to 168347)
AUTHORS      Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,
Boguslavsky,L., Boukhgalter,B., Brown,A., Burkett,G.,
Campopiano,A., Castile,A., Choepel,Y., Colangelo,M., Collins,S.,
Collamore,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S.,
Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D.,
Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
Klein,J., LaRocque,K., Lamazares,R., Landers,T., Lehoczkv,J.,
Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N.,
McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R.,
Meldrum,J., Meneus,L., Mihova,T., Miranda,C., Mienga,V., Morrow,J.,
Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
O'Neill,D., Oliver,T.M., Oliver,J., Peterson,K., Pierre,N.,
Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,
Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
```


Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J.,
Vassiliev,H., Viel,H., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W,J.,
Young,G., Zainoun,J., Zimmer,A. and Zody,M.
Direct Submission
Submitted (08-MAR-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 25, 2000 this sequence version replaced gi:7210017.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WtBR
Web site: http://www.seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L6686
----- Summary Statistics
Sequencing vector: M13; M7815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 150422 bases at least Q40
Consensus quality: 159524 bases at least Q30
Consensus quality: 163013 bases at least Q20
Insert size: 165247; sum-of-contigs
Quality coverage: 3.6 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 32 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 1389: contig of 1389 bp in length
* 1390 1489: gap of 100 bp
* 1490 3130: contig of 1641 bp in length
* 3131 3230: gap of 100 bp
* 3231 4942: contig of 1712 bp in length
* 4943 5042: gap of 100 bp
* 5043 6981: contig of 1939 bp in length
* 6982 7081: gap of 100 bp
* 7082 8708: contig of 1627 bp in length
* 8709 8808: gap of 100 bp
* 8809 10286: contig of 1478 bp in length
* 10287 10386: gap of 100 bp
* 10387 12212: contig of 1826 bp in length
* 12213 12312: gap of 100 bp
* 12313 14658: contig of 2346 bp in length
* 14659 14758: gap of 100 bp
* 14759 17941: contig of 3183 bp in length
* 17942 18041: gap of 100 bp
* 18042 21297: contig of 3256 bp in length
* 21298 21397: gap of 100 bp
* 21398 24992: contig of 3595 bp in length
* 24993 25092: gap of 100 bp
* 25093 27768: contig of 2676 bp in length
* 27769 27868: gap of 100 bp
* 27869 31188: contig of 3320 bp in length
* 31189 31288: gap of 100 bp
* 31289 33714: contig of 2426 bp in length
* 33715 33814: gap of 100 bp
* 33815 37277: contig of 3463 bp in length
* 37278 37377: gap of 100 bp
* 37378 42302: contig of 4925 bp in length
* 42303 42402: gap of 100 bp
* 42403 47816: contig of 5414 bp in length
* 47817 47916: gap of 100 bp
* 47917 52586: contig of 4670 bp in length
* 52587 52686: gap of 100 bp
* 52687 56567: contig of 3881 bp in length
*

* 56568 56667: gap of 100 bp
* 56668 61557: contig of 4890 bp in length
* 61558 61657: gap of 100 bp
* 61658 66724: contig of 5067 bp in length
* 66725 66824: gap of 100 bp
* 66825 71568: contig of 4744 bp in length
* 71569 71668: gap of 100 bp
* 71669 76578: contig of 4910 bp in length
* 76579 76678: gap of 100 bp
* 76679 83312: contig of 6634 bp in length
* 83313 83412: gap of 100 bp
* 83413 90053: contig of 6641 bp in length
* 90054 90153: gap of 100 bp
* 90154 99426: contig of 9273 bp in length
* 99427 99526: gap of 100 bp
* 99527 108015: contig of 8489 bp in length
* 108016 108115: gap of 100 bp
* 108116 118144: contig of 10029 bp in length
* 118145 118244: gap of 100 bp
* 118245 130468: contig of 12224 bp in length
* 130469 130568: gap of 100 bp
* 130569 142239: contig of 11671 bp in length
* 142240 142339: gap of 100 bp
* 142340 157135: contig of 14796 bp in length
* 157136 157235: gap of 100 bp
* 157236 168347: contig of 11112 bp in length.
----- Location/Qualifiers
1. 168347
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
/map="5"
/clone="Rp11-451H23"
/clone_lib="RPC1-11 Human Male BAC"
1. 1389
/note="assembly_fragment"
1490. 3130
/note="assembly_fragment"
3231. 4942
/note="assembly_fragment"
5043. 6981
/note="assembly_fragment"
7082. 8708
/note="assembly_fragment"
8809. 10286
/note="assembly_fragment"
10387. 12212
/note="assembly_fragment"
12313. 14658
/note="assembly_fragment"
14759. 17941
/note="assembly_fragment"
18042. 21297
/note="assembly_fragment"
21398. 24992
/note="assembly_fragment"
25093. 27768
/note="assembly_fragment"
27869. 31188
/note="assembly_fragment"
31289. 33714
/note="assembly_fragment"
33815. 37277
/note="assembly_fragment"
37378. 42302
/note="assembly_fragment"
42403. 47816
/note="assembly_fragment"
47917. 52586
/note="assembly_fragment"
52687. 56567
/note="assembly_fragment"
56668. 61557

JOURNAL
REFERENCE
2 (bases 1 to 173341)
DOE Joint Genome Institute.
AUTHORS
Direct Submission
TITLE
JOURNAL
Submitted (12-JAN-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Jan 25, 2002 this sequence version replaced gi:18139363.
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov

Project Information
Center Project Name: 1519801
Center clone name: RPCJ-11_586L9

Summary Statistics
Consensus quality: 164442 bases at least Q40
Consensus quality: 167261 bases at least Q30
Consensus quality: 167771 bases at least Q20
Estimated insert size: 186250; agarose-fp estimation
Estimated insert size: 172741; sum-of-contigs estimation
Quality coverage: 10.29 in Q20 bases; agarose-fp estimation
Quality coverage: 11.1 in Q20 bases; sum-of-contigs estimation
NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1
1596: contig of 1596 bp in length
1696: gap of unknown length
1697
3940: contig of 2244 bp in length
3941
4040: gap of unknown length
4041
5104: contig of 1064 bp in length
5105
5204: gap of unknown length
5205
6286: contig of 1082 bp in length
6287
6386: gap of unknown length
6387
20063: contig of 13677 bp in length
20064
20163: gap of unknown length
20164
82401: contig of 62238 bp in length
82402
82501: gap of unknown length
82502
173341: contig of 90840 bp in length.

FEATURES
source
Location/Qualifiers
1..173341
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
/clone="RP11-586L9"
/clone_lib="RPCI human BAC library 11"
BASE COUNT 45837 a 42564 c 41389 g 42871 t 680 others
ORIGIN

Query Match 35.0%; Score 106; DB 2; Length 173341;
Best Local Similarity 100.0%; Pred. No. 4e-46;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 gggagagtcgctagcgccttcgggaagtggtggaagctccgcttcggaatc 75
|||||
Db 97431 GGGAGAGTCGCGCTACGGCGCCTTCGGGAAGGTGGTGGAGGCTCGCTTCGGCATC 97490
|||||

Qy 76 cacaagggcagcagctgtgacacccgtgcccgtgaaatgctgaaag 121
|||||
Db 97491 CACAAGGCACAGCTGTGACACCGTGGCCGTGAANAATGCTGAAG 97536
|||||

RESULT 14
MUSRTKA
LOCUS 5284 bp mRNA linear ROD 09-AUG-1993
DEFINITION Mus musculus receptor tyrosine kinase (FLT4) mRNA, complete cds.

ACCESSION L07296
VERSION L07296.1 GI:293780
KEYWORDS receptor protein tyrosine kinase.
SOURCE Mus musculus (strain C57BL/6J, sub_species domesticus) cDNA to mRNA.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 5284)
Flinnerty,H., Kelleher,K., Morris,G.E., Bean,K., Merberg,D.M.,
Kriz,R., Morris,J.C., Sookdeo,H., Turner,K.J. and Wood,C.R.
Molecular cloning of murine FLT and FLT4
Oncogene 8, 2293-2298 (1993)
93330572 Location/Qualifiers

1..5284
/organism="Mus musculus"
/strain="C57BL/6J"
/sub_species="domesticus"
/db_xref="taxon:10090"
1..5284
/gene="FLT4"
45..4136
/gene="FLT4"
/note="putative"
/codon_start=1
/product="receptor tyrosine kinase"
/protein_id="AAA40077.1"
/db_xref="GI:293781"
/translation="MOPGAALNLRNLCLGLQGLANGYSMTPTLTNITEDSVYIDTG
DSLSISCRGHPLEWTWPGAEVLTTGGKSEDTRVVHDFKHPFINKPDTLLVNRKGMWPCVL
ANNITGYHCYKYIKARIECTAASTVFYFDFKHPFINKPDTLLVNRKGMWPCVL
SIPCLNITLBSQSALHPDGOEVLWDDRGHRYPTOLLRDALYLCCETTQDNFLSN
LFVYHITGNELYDIQLYPKKSMELLGKLYLNCTVWAEFDSGVTFDMDTPGQAEARA
KWPERRSQOHTLESILTIHNVSQNDLGPYCEANNQIQRFESETEIVHKEKPFIS
VEWLKGEVLEATAGDELVLKPLVLAAYPPPEFQYDKRKAATGRHNHPALVKEVTEA
SAGYITLWNSAAGLRQNLSELVNVPPHIIHEKASPSIYSHRNROTLCITAYGV
PQPLSVQWHRPWTCKTFAQRSLRRQQRQDGMPCQCRDMKEVTTQADVNPITSLDSWT
EFVEGKNKTVSKLVDADNYSAMYKCVVNVKVGDERLIYFVTTIPDGFSIESEPE
DPLEGOSVRLSCRADNVTYELRWYRLNLSLHDAQGNPLLLDCKKVHLPATPLEANL
EEAEPGARHATLSLNTIPRAPEDEGDYCEVQDRRQDKCHKKYSVQALEAPRLTQ
NLTDLLVNSDSLEMRCPVAGAHVPSIVWTKDKRLEKESGIDLASNOKLSFORRE
EDAGRYLCVNCNASSAVAGESEKSMIEVILIGTGVIAVFWVLLLLIFC
NMKRAHADIKTGYLSIIDNDGVEPLEEQCEYLSYDASQWEPFRHLRHLVGLHGF
GKVVESAFGIKNGSCDVAVKMLKEGATASRHALMSLKILIHGNHLNVNLLG
ACTKPGPLMVIIEFCYKGNLNFVRKRTFNPAEKSPEORRRFRAMVEGAKADRR
RPGSSORALFTRELKCGSARRAPLVQEAEDLWLSPLTHEDLYCYSFQVARGHEFLAS
KCIHRDLAARNILLSSEDLVKICDFGLARDIYKDPDYVRKGSARLPKWMAPESIFD
KYVTTSDVMSFGVLLWEIFSLGASYPGVQIINEFCORLKDGTMRAPELATPAIRH
IMQSCWSDPKARPAFSDLVEILGDLQGGGQWEEEREMALHSSQSEEDGFMQAST
TALHITADADDSPSMHCHSLAARYNVCYSPFGLARGTKTPGSSRMKTFEELPMTTP
TTYKASMDNOTDSGMVLASEFEFELESRRHPEGSFCSCKPGQOHMDIPRGHPDPQGRRR
RPTQGAQGGKVFYNNEYGVSQCTEGDCPCPSAGSTFFADSS!"

BASE COUNT 1221 a 1533 c 1466 g 1064 t
ORIGIN

Query Match 7.6%; Score 23; DB 10; Length 5284;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 82 ggcagcagctgtgacacccgtggc 104
|||||
Db 2652 GGCAGCAGCTGTGACACCGTGGC 2674
|||||

RESULT 15
AL646088
LOCUS 260266 bp DNA linear HTG 30-JAN-2002
DEFINITION Mus musculus chromosome 11 clone RP23-58E13, *** SEQUENCING IN
PROGRESS ***, in unordered pieces.
ACCESSION AL646088
VERSION AL646088.11 GI:18476932

KEYWORDS HTG: HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE 1 (sites)
JOURNAL Direct Submission
COMMENT Submitted (28-JAN-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquerry@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Feb 1, 2002 this sequence version replaced gi:18151535.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquerry@sanger.ac.uk
----- Project Information
Center project name: BM58E13
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 258539 bases at least Q40
Consensus quality: 258926 bases at least Q30
Consensus quality: 259227 bases at least Q20
Insert size: 259766; sum-of-contigs
Insert size: 225486; 6.3% error; agarose-fp
Quality coverage: 9.68x in Q20 bases; sum-of-contigs Quality
coverage: 11.43x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

FEATURES
source
1..260266
Location/Qualifiers
/organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="11"
/clone="RP23-58E13"
/clone_lib="RPC1-23"
1..8902
misc_feature
/note="assembly_fragment:05530
fragment_chain:1"
9003..87162
misc_feature
/note="assembly_fragment:05707
fragment_chain:1"
87263..123670
misc_feature
/note="assembly_fragment:05852
fragment_chain:1"
123771..188404
misc_feature
/note="assembly_fragment:00429"
188505..214152
misc_feature
/note="assembly_fragment:05868"
214253..260266
/note="assembly_fragment:05872"
BASE COUNT 80139 a 55470 c 56089 g 68066 t 502 others
ORIGIN

Query Match 7.6%; Score 23; DB 2; Length 260266;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 82 ggcagcagctgtgacacgtggc 104
|||||
Db 162194 gccagcagctgtgacacgtggc 162216

RESULT 16
AF402786 4254 bp mRNA linear ROD 11-OCT-2001
LOCUS AF402786
Rattus norvegicus receptor tyrosine kinase VEGFR-3 (Vegfr3) mRNA,
complete cds, alternatively spliced.

DEFINITION Rattus norvegicus receptor tyrosine kinase VEGFR-3kt (Vegfr3) mRNA,
complete cds, alternatively spliced.
ACCESSION AF402786
VERSION AF402786.1 GI:16033529
KEYWORDS
SOURCE Norway rat.
ORGANISM Rattus norvegicus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
TITLE 1 (bases 1 to 4254)
JOURNAL Krishnan,J. and Sleeman,J.P.
COMMENT Characterization of a novel alternatively spliced form of VEGFR-3
Unpublished
REFERENCE 2 (bases 1 to 4254)
AUTHORS Krishnan,J. and Sleeman,J.P.
TITLE Direct Submission
JOURNAL Submitted (25-JUL-2001) Institut fuer Toxikologie und Genetik,
Forschungszentrum Karlsruhe, Postfach 3640, Karlsruhe 76021,
Germany

FEATURES
source
1..4254
Location/Qualifiers
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
1..4254
/gene="Vegfr3"
1..3279
/gene="Vegfr3"
/note="kinase domain truncated form of VEGFR-3;
alternatively spliced"
/codon_start=1
/product="receptor tyrosine kinase VEGFR-3kt"
/protein_id="AAL13270.1"
/db_xref="GI:16033530"
/translation="MQPGAALNRRLMLCLGLLOGLANGYSMTPTLNTEDSYVIDTG
DSLSISCRGQHPLEWTRGAQEVLTGGKDSQEDTVVQDCGTEARPCYKAVLSLAOTH
ANNTGSYCYKYIKARIECTAASYVYFVRDEQPIKPTDLLNRRKDSMWVPCLY
SIPGLNITLRSSQSVLHPDQGEVLMDDRRMRVPTLLRLDRLYLQCEITMGDDQFLSN
PFLVHTGNELYDIOLYPKKSELLVGEKLVNCTVMAEFDSTVDWDPYQKQAEERA
KWPPERSSQHTSELSILTIHNVSQHDLPYVCEANNGIQOFRSTEVVHEKPTIS
SAGVYTLALNSAAGLRQNI SLELVNVPPIIHEKASSPSIYSRISROPTLCTTGV
PQSLQVQWHRPWT PCKTFAORSLRRRQPCQDMKNEVTTQDAVNPESLDTWT
ESVEGKNKTVSLIODANSYKCVFNKQDRLIYFYVTIIPDGFSEISEPSE
DPLEGQSVRLSCRADNYTEHLRHYRLNLSTLHDAQGNPLLLDCKNVLFPATPEANL
EEAPEGARHATLSLNPVPAPEDEGTVCEVQDRRQDQKHKKYLSVQALEAPRLTQ
NLTDLLVNRVTSLEMRCPVAGAHVPSIVMYKDERLLEKESGIDLADSNQRLSTQVRE
EDAGRYLCYCNAGKCVNSASVAVESGDKSMEIVILIGTGVIAVFFVWLLLLIFC
NMRRPAHADIKTGLSLIIMDPGEVPLEQCEYLSYDVQVOWEPFRLHGLRVNLHGF
GKVVESAFGINKGSCDTVAVKMLKEGATASPHRALMSKELKILIHGNHNVNLLIFC
ACTKPNGLMVI VEFCKYGNLSNLFVRKRETFDPAEKSPQRRFRFRAWVEGAKDRR
RLGSTDRALPTRELKMGKSARRAPFVQEAEDLWLSPLTHEDLYCYFSQVARGHEFLAS
RKCIHRDLAARNLLSESDIVKICDFGLANDIYKDPDYVRKKSARLPLTLTGYSMRN
SASG"
BASE COUNT 989 a 1236 c 1224 g 805 t
ORIGIN

Query Match 6.9%; Score 21; DB 10; Length 4254;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 268 tacggcaacctctccaacttc 288
|||||
Db 2794 TACGGCAACCTCTCCAACCTTC 2814

RESULT 17
AF402785 4360 bp mRNA linear ROD 11-OCT-2001
LOCUS AF402785
Rattus norvegicus receptor tyrosine kinase VEGFR-3 (Vegfr3) mRNA,
complete cds, alternatively spliced.

[illegible]

Estimated insert size: 111412; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-fp estimation
Quality coverage: 1.5x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 75 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 5831: contig of 5831 bp in length
* 5832: gap of unknown length
* 5932: contig of 5453 bp in length
* 11384: gap of unknown length
* 11385: contig of 5411 bp in length
* 11485: 16895: contig of 5411 bp in length
* 16896: 16995: gap of unknown length
* 16996: 21784: contig of 4789 bp in length
* 21785: 21884: gap of unknown length
* 21885: 25354: contig of 3470 bp in length
* 25355: 25454: gap of unknown length
* 25455: 29460: contig of 4006 bp in length
* 29461: 29560: gap of unknown length
* 29561: 32307: contig of 2747 bp in length
* 32308: 32407: gap of unknown length
* 32408: 35443: contig of 2936 bp in length
* 35444: 38216: contig of 2773 bp in length
* 38217: 38316: gap of unknown length
* 38317: 41183: contig of 2867 bp in length
* 41184: 41283: gap of unknown length
* 41284: 43959: contig of 2676 bp in length
* 43960: 44059: gap of unknown length
* 44060: 47285: contig of 3226 bp in length
* 47286: 47385: gap of unknown length
* 47386: 50539: contig of 3154 bp in length
* 50540: 50639: gap of unknown length
* 50640: 54276: contig of 3637 bp in length
* 54277: 54376: gap of unknown length
* 54377: 57921: contig of 3544 bp in length
* 57921: 60505: contig of 2485 bp in length
* 60506: 60605: gap of unknown length
* 60606: 62900: contig of 2295 bp in length
* 62901: 63000: gap of unknown length
* 63001: 64914: contig of 1914 bp in length
* 64915: 65014: gap of unknown length
* 65015: 67533: contig of 2519 bp in length
* 67534: 67634: gap of unknown length
* 67634: 70777: contig of 3144 bp in length
* 70778: 70877: gap of unknown length
* 70878: 73509: contig of 2632 bp in length
* 73510: 73609: gap of unknown length
* 73610: 76056: contig of 2447 bp in length
* 76057: 76156: gap of unknown length
* 76157: 78450: contig of 2294 bp in length
* 78451: 78550: gap of unknown length
* 78551: 80050: contig of 1500 bp in length
* 80051: 80150: gap of unknown length
* 80151: 82169: contig of 2019 bp in length
* 82170: 82269: gap of unknown length
* 82270: 83776: contig of 1507 bp in length
* 83777: 83876: gap of unknown length
* 83778: 85747: contig of 1871 bp in length
* 85748: 85847: gap of unknown length
* 85848: 87806: contig of 1959 bp in length
* 87807: 87906: gap of unknown length
* 87907: 89679: contig of 1773 bp in length
* 89680: 89779: gap of unknown length
* 89780: 91266: contig of 1487 bp in length

* 91267: 91366: gap of unknown length
* 91367: 93812: contig of 2446 bp in length
* 93813: 93913: gap of unknown length
* 93913: 95639: contig of 1727 bp in length
* 95640: 95739: gap of unknown length
* 95740: 97396: contig of 1657 bp in length
* 97397: 97496: gap of unknown length
* 97497: 99145: contig of 1649 bp in length
* 99146: 99245: gap of unknown length
* 99246: 100913: contig of 1668 bp in length
* 100914: 101013: gap of unknown length
* 101014: 102955: contig of 1942 bp in length
* 102956: 103055: gap of unknown length
* 103056: 104468: contig of 1413 bp in length
* 104469: 104568: gap of unknown length
* 104569: 106375: contig of 1807 bp in length
* 106376: 106475: gap of unknown length
* 106476: 108691: contig of 2216 bp in length
* 108692: 108791: gap of unknown length
* 108792: 110626: contig of 1835 bp in length
* 110627: 110726: gap of unknown length
* 110727: 111801: contig of 1075 bp in length
* 111802: 111901: gap of unknown length
* 111902: 113358: contig of 1457 bp in length
* 113359: 113458: gap of unknown length
* 113459: 114629: contig of 1171 bp in length
* 114630: 114729: gap of unknown length
* 114730: 116364: contig of 1635 bp in length
* 116365: 116464: gap of unknown length
* 116465: 118200: contig of 1736 bp in length
* 118201: 118300: gap of unknown length
* 118301: 119330: contig of 1230 bp in length
* 119331: 119630: gap of unknown length
* 119631: 121318: contig of 1688 bp in length
* 121319: 121418: gap of unknown length
* 121419: 122620: contig of 1202 bp in length
* 122621: 122720: gap of unknown length
* 122721: 124128: contig of 1408 bp in length
* 124129: 124228: gap of unknown length
* 124229: 126159: contig of 1931 bp in length
* 126160: 126259: gap of unknown length
* 126260: 128394: contig of 2135 bp in length
* 128395: 128494: gap of unknown length
* 128495: 130496: contig of 2002 bp in length
* 130497: 130596: gap of unknown length
* 130597: 132111: contig of 1515 bp in length
* 132112: 132294: contig of 1083 bp in length
* 132295: 133394: gap of unknown length
* 133395: 134851: contig of 1457 bp in length
* 134852: 134951: gap of unknown length
* 134952: 136002: contig of 1051 bp in length
* 136003: 136102: gap of unknown length

Query Match 6.9% Score 21; DB 2; Length 161580;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 268 tacggcaacctctccaaattc 288
|||||
Db 26979 TACGGCACTCTCCAACTC 26959

RESULT 19

AF063657

LOCUS

DEFINITION

mRNA, complete cds.

ACCESSION

AF063657.1

VERSION

GI:3132830

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

4017 bp mRNA linear PRI 11-MAY-2001
endothelial growth factor receptor (FLT1)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE 1 (bases 1 to 4017)
 AUTHORS Herley, M. T., Yu, Y., Whitney, R. G. and Sato, J. D.
 TITLE Characterization of the VEGF binding site on the Flt-1 receptor
 JOURNAL Biochem. Biophys. Res. Commun. 262 (3), 731-738 (1999)
 MEDLINE 99400442
 PUBMED 10471394

REFERENCE 2 (bases 1 to 4017)
 AUTHORS Yu, Y., Whitney, R. G. and Sato, J. D.
 TITLE Direct Submission
 JOURNAL Submitted (06-MAY-1998) Adirondack Biomedical Research Institute, 10 Old Barn Rd., Lake Placid, NY 12946, USA

FEATURES
 source
 1..4017
 Location/Qualifiers

gene
 1..4017
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /cell_type="endothelium"
 /tissue_type="umbilical vein"

CDS
 1..4017
 /gene="FLT1"
 /note="VEGFR: tyrosine kinase"

1..4017
 /codon_start=1
 /product="vascular endothelial growth factor receptor"

protein_id="AAC16449.1"
 /db_xref="GI:3132831"

translation="MVSVDGVLGALLCLLLTGSSGSKLKDPELSKGTQHIMQ
 AGOTLHLCREAAHKSLPWSKESERLSITKACRNGKQFCSTLTLTAAOAHNT
 GFYCKYLAVPTKKKTESAIYIFISDTGRPFVEMYSEIPIHMTGRELVPICRV
 NPLNTITKRPFLDITPDGKRIIDSRKGFISNATYKEIGLTCATVNGHLYKT
 TSLHTROTITIDVOISTPRPKLLRGTLVNLCTATPLNTRVQMTSPYDEKNKRA
 SVRRIDQSNHANIYFSLVITIDKMNKGLYTCRVRSQSPKSVNTSVHIYDKAFI
 TVKRIKQDLTETVACAKSYRLSMKAKAFPSPEVVMKDLGLPAEKSNARYLTRGYSLII
 KLTVEAGNVTIILSIKQSNVFNLTATLIVNKKFOIYEKAVSPDPALYPLGSRQ
 IDTCTAGIPIQPTIKWHPNHNHSEARDFCSNNEESFILDADSNMGRNIESITOR
 MAILEGNKASTLIVADRSIGIYICIASNKVGTGVRNLSFYITDVPNGFVYNLEKM
 PTEGEDLKLSCTVNVKFLYRDVITLLTRVNNRMHYSISKQMAITKHSITLNLTIM
 NVSLQDSQTVACRARNYVTEITLQKKEITRQOEAPYLLRNLSHDHTVALSSSTLLDC
 HANGVPEPQITWKNHNIQOEPGILUGCSSTLFERTVEDEGVYHCKATNOKGSV
 ESSAYLTVOGTSKSNLELITLCTCAATLFWLLTLFLRKMKRSSEIKTDYLSII
 MDPEVPLDQCEPRLPYDASKWEAFERLKLGLRGVAGFQVVOASAFIKYPTPCR
 TVAVMLKCATASEYKALMTPLKILTHIGHHLNVNLLGACTKOGGLMWIVYECKY
 GNLSYLKSRDLFFLNKDAALHMEPKKMEPEGLQGGKPRLDSTVSSEFASGFO
 EDKSLSDVEEEDSDGPKYKEPITMEDLISYFQVARGMEFLSSRKCIRDLAARNILL
 SENNVYICDFGLARDIYKNPDYVRKGDTRLPKLMAPESIFDKIYSTKSDVMSYGLV
 LWEIFSLGGSPYQVQMDYFCRSLRGRMRAPYSTPEIYQIMLDCHHRDPKPRR
 FAELVEKGLDLOANVOQDGKXIPINAILTNGSGTYSTPAFSEDFKESISAPKFN
 SGSSDDVRYVNAFKENSLEKRIKTFEELLNATSMFDYQDGSSTLLASPMKRFRTWD
 SKPKASKLIDLRVTSKSGSLSDVSRPSCFSSCHSGHVSEGRKRRFTYDHAELERKTIAC
 CSPPPDYNVVLVSTPPI"

BASE COUNT 1236 a 915 c 903 g 963 t

ORIGIN

Query Match 6.68; Score 20; DB 9; Length 4017;

Best Local Similarity 100.0%; Pred. No. 12;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 106 GTGAATGCTGAAGAGGG 125

Db 2578 GTGAATGCTGAAGAGGG 2597

RESULT 20

AB065372

LOCUS

DEFINITION

Gallus gallus mRNA for vascular endothelial growth factor

receptor-1, complete cds.

AB065372

AB065372.1

GI:18652860

KEYWORDS

SOURCE
 ORGANISM

Gallus gallus

Gallus gallus

REFERENCE

1 (sites)

Yamauchi, S., Iwata, K. and Shibuya, M.

Soluble Flt-1 (VEGFR-1), a potent natural antiangiogenic molecule

in mammals, is phylogenetically conserved in avians

Unpublished

JOURNAL

REFERENCE

2 (bases 1 to 4272)

Shibuya, M.

Direct Submission

Submitted (11-JUL-2001) Masabumi Shibuya, University of Tokyo,

Institute of Medical Science, 4-6-1 Shirokane-dai, Minato-ku, Tokyo,

108-8639, Japan (E-mail: shibuya@ims.u-tokyo.ac.jp,

Tel: 81-3-5449-5550, Fax: 81-3-5449-5425)

FEATURES

Location/Qualifiers

1..4272

/organism="Gallus gallus"

/db_xref="taxon:9031"

/tissue_lib="whole embryo"

267..4250

/gene="vegfr-1"

267..4250

/note="vegfr-1"

/codon_start=1

/product="vascular endothelial growth factor receptor-1"

protein_id="BAB84690.1"

/db_xref="GI:18652861"

translation="MPRLSLGTVLLGAFLLAGSTSGSKLKVPLSVNGRQHVVOAG
 QTLNLTCEGMLHNSLSEALSKDLNVTYACRNGTQFCSTLTLSRTOANDTGR
 YSCRYPTSPKPKRESIVYFINDTSPNPFVEMHSDIPKIIHMTVGKMIIPCRVTA
 IAVTLKIPRETLIPDGKTIIDNMRGFRPEATYRIFGLSCETIGGHKSTKYLT
 HRETNTIFDKLSTPLVKLLGDSLATNCTVKAATRVQMTHTYFGAAMKRGSVTQ
 RIDOKNREANFYSLIVDKVRDIPDKQYACHVSGSNKLVNTTVIVDKRFINLAR
 RRKTMLEAVAGKSYRLPMKVRDPEVTWLDGLPAEKRCAMVKNYKSLIKDVA
 EEDAGTIIILSRWNLKSLNLTVLKNVKNPQIYENAVSFPDPLNLLSSKOVLT
 TVYGPPTKIPITMMPYPCRNHSTKTRGFCSTGPNLKTGSGNIGRNIQSIERTAIL
 EGKNTASTLVAAKSGSIYSCVSNKVGKAERNVFLVTPVSPGPHISLEKVPLEG
 ENLVSCSANKFMYKDISWILPRTVNTQARKALNKEYSITLTLTRNVSLSHSGTY
 TCRNHIETQESQIILGPGSRMLFIERVEDEGLQCIATNLKGSVESTATVVOG
 TVERNLELITCTCTCAATLFWLLTLFIRKLKRPVYSETKTNHLSIIMDPEVPL
 DEQCELPYDASKWEIARERLKLGLGAGFQVVOASAFIKYPTPCRIVAVKMLK
 EGATASEYKALMTPLKILTHIGHHLNVNLLGACTKOGGLMWIVYECKY
 SKRNFSPPTKDPISLQGLMKDKGIEPVEGKORLASVTSSEFASGFOEDKSLSDA
 EDEDAALYKPLTWEDLISYFQVARGMEFLSSRKCIRDLAARNILLSNNVYK
 ICDFGLARDIYKNPDYVRKGDARLPKLMAPESIFDKIYNTKSDVMSYGLLWEIFSL
 CASPYGVQIDEDFCSKLKEGTRMRAPEQATEEYIQLMDCWRSNPNRPFSELYKR
 LGDLJQASVQOEGKDIPLDITFAESGFPASPDLCKNEKFPVPSNCRSTERYIN
 TFKIPPORIKTFEELPKELVNDYQADSGMVLASEELKRTFTGSKOKWTLFCMK
 GVSRSKESGLSGITKPRSCFSCDQLSESKRRTYTGNTVLEKMKACHSPPPDYSVW
 HYSQPSI"

BASE COUNT 1266 a 1001 c 1083 g 922 t

ORIGIN

Query Match 6.68; Score 20; DB 5; Length 4272;

Best Local Similarity 100.0%; Pred. No. 12;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 34 ggcgccttcgggaagtggt 53

Db 2748 GCGCCTTCGGGAAGTGGT 2767

RESULT 21

HSFLT

LOCUS

DEFINITION

Human flt mRNA for receptor-related tyrosine kinase.

7680 bp mRNA linear PRI 15-NOV-1993

ACCESSION	X51602	QY	106	gtgaaaaatgctgaagaggg	125
VERSION	X51602.1	Db	2827	gtgaaaaatgctgaagaggg	2846
KEYWORDS	flt gene; fms-related tyrosine kinase gene; tyrosine kinase.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	1 (bases 1 to 7680)				
TITLE	Shibuya, M.				
JOURNAL	Submitted (02-JAN-1989) Shibuya M., Institute of Medical Science, University of Tokyo, 4-6-1 Shirokane-dai, Minato-ku, Tokyo 108, Japan				
REFERENCE	2 (bases 1 to 7680)				
AUTHORS	Shibuya, M., Yamaguchi, S., Yamane, A., Ikeda, T., Tojo, A., Matsushima, H. and Sato, M.				
TITLE	Nucleotide sequence and expression of a novel human receptor-type tyrosine kinase gene (flt) closely related to the fms family				
JOURNAL	Oncogene 5 (4), 519-524 (1990)				
MEDLINE	90221591				
REFERENCE	3 (bases 1 to 7680)				
AUTHORS	Han, H.J., Fujiwara, T., Shin, S. and Nakamura, Y.				
TITLE	Dinucleotide repeat polymorphism in the 3' non-coding region of the FLT1 gene				
JOURNAL	Hum. Mol. Genet. 2 (12), 2204 (1993)				
MEDLINE	94154724				
COMMENT	Data kindly reviewed (20-JUL-1990) by Shibuya M.				
FEATURES	Location/Qualifiers				
source	1..7680				
	/organism="Homo sapiens"				
	/db_xref="taxon:9606"				
	/chromosome="13"				
	/map="19q12"				
	/clone="3-7, 3-5"				
	/tissue_type="placenta"				
	250..4266				
	/note="flt gene product (AA 1-1338)"				
	/codon_start=1				
	/protein_id="CAA35946.1"				
	/db_xref="GI:31432"				
	/db_xref="SWISS-PROT:P17948"				
	/translation="MVSYMDTGVLICALLSCLLLTGTSSGSKLKDPELSLKGTHIQM AGOTLHLCRGAAHKWSLPEWVSKESERLSITKSACRNGKQFCSTLTLTNAQNHIT GPYCKYLAVPTSKKTESAIYIPISDTGRPFVEMYSIEPIIHTMGRELVLPCRV TSPNTVTLKFPLOTLPIDGKRILWDSKGFISNATYKEIGLLTCEATVNGHLYKT NVLRHRONTIIDVISTPRPVKLHGTLLVNLCTATTPLNTRVQMTSPYDEKNKRA SVRRIDGNSHANIFYSVLTIDKMONDKGLYTCRVSRGSPFSKSVNTSVHIDKAFI TVKHKQOVLETVAGKRSYRLSMKVAFPSPEVWMLKDLPLATEKSARYLTRYSLII KDVTEDAGNTVILLIKOSNVFKNLATLIVNVKPOLYKAVSFPPDPLPLGSSRO ILTCTAYGIPOPTIKFWHPHCNHNHSEARCFCSNNEESFILDADSNMGNIESTOR MAIIEGKNKMASTLVVADSRISGIYICIASNKVGTGVGNISFYITDPNGFHVNLKEM PEGEDKLSCSTVNVKFLYRDVTWILLRTVNNRTHYSISKQMAITKEHSTLTNTIM NVSLQDSGYACRANVTYGTBEILQKKEITIROEAPYLLRLNSDHTVAISSTTLDG HANGVPEQITWFKNNHRIQOEPGIIILGPGSSTLFLERVTEDEGVYHCKATNGKGS ESSAYLTVOGTSKSNLELITLTCTCVATLFWLLLTLLIKMRSSSEIKTDLSII MDQPVLPDEOCERLPDYASKEHFAERKLKGLSGUGAFKGVQVAAFGVTKKPTCR TVAVKMLGEGATSYKALMTLTKLTHIGHLVNVLNLLAGCTKQGLPLVIVETCKY GNLNSLYSKERDLFFFLKNDAAALHMEPEKMEPGLEQCKPKRLDSVTSSSFASGGQ EDKLSLDEEEDSDGFYKEPTIMEDLISYSFOVARGMEFLSSRKCIRHDLARNILL SENNVVKICDFGLARDIYKNPDYVRKGDTRLPLKMWAPESIFDKLYTSKSDWNSYGLV LWEIFLSGSPYGVONDEDFCSRLRGRMRAREYSTPEIYQIMLDCWHDRKPRR FAELVEKLCDLLQANVQDQKDIPIINALTNGSGFTSYTFAFSEDFKESISAPKRN SGSSDDVRYVNAFKPMSLERIKTFEELLPNATSMFDDYQGDSTLLASPMLKREFTWD SKPKASLKIDLRVTSKSKESGLSDVSRPSFCHSCSGHVSCKRRTFYDHAELERKIIAC CSPPPDYSNVVLYSTPPI"				
BASE COUNT	2279 a 1661 c 1739 g 2001 t				
ORIGIN					
Query Match	6.6%; Score 20; DB 9; Length 7680;				
Best Local Similarity	100.0%; Pred. No. 12;				
Matches	20: Conservative 0; Mismatches 0; Indels 0; Gaps 0;				

SC9C7 31360 bp DNA linear BCT 12-JAN-1999

Streptomyces coelicolor cosmid 9C7.

AL035161

AL035161.1 GI:4154059

acetyltransferase; acyl-CoA dehydrogenase; acyl-peptide hydrolase; aminocyclase; ccr; coenzyme B12-dependent mutase; crotonyl CoA reductase; efflux protein; lyase; meoA; oxidoreductase; peptidase; tetR family; transcriptional regulator.

Streptomyces coelicolor A3(2).

Streptomyces coelicolor A3(2).

Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.

1 (bases 1 to 31360)

Seeger, K.J. and Harris, D.

Unpublished

2 (bases 1 to 31360)

Submitted (08-JAN-1999) Streptomyces coelicolor sequencing project, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk NR4 7UH, UK

3 (bases 1 to 31360)

Redenbach, M., Kieser, H.M., Denapaita, D., Eichner, A., Cullum, J., Kinashi, H. and Hopwood, D.A.

A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome

Mol. Microbiol. 21 (1), 77-96 (1996)

97000351

Notes:

Streptomyces coelicolor sequencing at The Sanger Centre is funded by the BBSRC.

Details of S. coelicolor sequencing at the Sanger Centre are available on the World Wide Web.

(URL: http://www.sanger.ac.uk/Projects/S_coelicolor/) CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary strand).

The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons is given for each CDS.

Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the Frameplot program of Bibb et al., Gene 30:157-66(1984) as implemented at <http://www.nih.go.jp/jun/cgi-bin/frameplot.pl>.

CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gtg, ttg or att) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream initiation codon.

IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions. Cosmid 9C7 lies between 1A1 and 1E6 on the AseI-A genomic restriction d fragment.

Location/Qualifiers

1..31360

/organism="Streptomyces coelicolor A3(2)"

/strain="A3(2)"

FEATURES

source


```

/db_xref="taxon:100226"
/clone="cosmid 9C7"
complement(1..147)
/gene="SC9C7.01c"
complement(1..147)
/gene="SC9C7.01c"
/notes="SC9C7.01c, partial CDS, unknown, len: 49aa;
overlapping extreme N-terminal region of partial CDS,
SC1A11.2c from Streptomyces coelicolor cosmid 1A11."
/codon_start=1
/transl_table=11
/product="hypothetical protein SC9C7.01c"
/protein_id="CAA22713.1"
/db_xref="GI:4154060"
/translation="MTADYATYIAGLPRLVLAGAAVPRDAAGRVLLVEPNYREGMAL
PGGT1"
misc_feature
1..112
/notes="Overlap with SC1A11 Streptomyces coelicolor cosmid
1A11."
332..1474
/gene="SC9C7.02"
332..1474
/gene="SC9C7.02"
/notes="SC9C7.02, conserved hypothetical protein, len:
380aa; similar to many eg. SW:YXAA_BACSU hypothetical
protein from Bacillus subtilis (382 aa) fasta scores: opt:
1045, z-score: 998.9, E(): 0. (46.3% identity in 374 aa
overlap)."
/codon_start=1
/transl_table=11
/product="conserved hypothetical protein"
/protein_id="CAA22714.1"
/db_xref="GI:4154061"
/translation="MDGTRVLVAADKFKGSLTAVEAERVVTAGLRRVVDVLVEALP
VADGGCTVAAAVAGFERREARVAGPLCEEVTAAYALRGCTAVYEMAEASGLQLPE
GVLPDSTYSGELLRAALDAGARTIVFGGGSGLDSDVELVSLASDVNDPLTGPKGAPYVQKGPASPD
DYTDALAHAFKVLERTEGVGARAAEYVAAAPGAGGIGFGAGLLGARGFRPGIEV
MLDVLGFALERADLVITGEGSLDEQTLHGKAPAGVAAAARAAGKEVVAVVAGGRALP
AEVLGRAGIRRAYPLTDPVPOVAKCIADAGPLIVERVASEIARDELA"
complement(1744..2526)
/gene="SC9C7.03c"
complement(1744..2526)
/gene="SC9C7.03c"
/notes="SC9C7.03c, probable integral membrane protein,
possible phosphatidylserine synthase, len: 260aa; similar
to many from prokaryotes (all putative) and eukaryotes eg.
SW:PSS_YEAST phosphatidylserine synthase from
Saccharomyces cerevisiae (275 aa) fasta scores: opt: 187,
z-score: 258.6, E(): 6.8e-07, (35.9% identity in 170 aa
overlap). Contains possible membrane spanning regions."
/codon_start=1
/transl_table=11
/product="putative phosphatidylserine synthase"
/protein_id="CAA22715.1"
/db_xref="GI:4154062"
/translation="MPLSLRLSIADTLTGLNATCGFMAYVTTTGLILPHLMGDSDESG
MARHSAATAVILMLCAAIFDLFDGLVARKLRSSPMGAELDNLSISFLGAPAYFVLV
YGMVADDAVQRYAAVAVVLLAVLRARFSCVTVKDGTFQGMPSFGALTIVSIVL
LELPVATLLAILTGLAWLMSRVKPKRGLAVAMLSKVLISMLGLAGWAFDAPSGQ
LLLTGCGALQLVKGAVIPLFATARNVFRNDRRAARAQLP"
complement(2585..3241)
/gene="SC9C7.04c"
complement(2585..3241)
/gene="SC9C7.04c"
/notes="SC9C7.04c, conserved hypothetical protein, len:
218aa; similar to several hypothetical proteins eg.
TR:O27105 (EMBL:AE000875) Methanobacterium
thermoautotrophicum (223 aa) fasta scores: opt: 405,
z-score: 712.9, E(): 2e-32, (39.2% identity in 212 aa
overlap)."
/codon_start=1
/transl_table=11

```

```

/product="conserved hypothetical protein"
/protein_id="CAA22716.1"
/db_xref="GI:4154063"
/translation="MPHSQTSAPRDSLAGVRLARGASPMILLPTVATAAVSLLRRRSRG
TAKAVAPATALAAGLMFRRDPERITQGRVSPADGVQVSIIMPKDGRTRVAIFMS
PLNVHVNRPAGLTVTSVHPVGGVPAFNKESNNERNVYMHFOTELGDIEMIQIAGA
VARRIVPVPGQTKVQEGERVGLIRFGSRVDLYLPEGVDEVVEVGQKTAVGTRIDRD
"
complement(3412..4617)
/gene="SC9C7.05c"
complement(3412..4617)
/gene="SC9C7.05c"
/notes="SC9C7.05c, possible acyl-CoA dehydrogenase, len:
401aa; similar to many from prokaryotes and eukaryotes
egs. SW:ACDB_BACSU acyl-CoA dehydrogenase from Bacillus
subtilis (379 aa) fasta scores: opt: 520, z-score: 1209.6,
E(): 0, (38.9% identity in 386 aa overlap) and
SW:ACDM_MOUSE acyl-CoA dehydrogenase from Mus musculus
(mouse) (421 aa) fasta scores: opt: 484, z-score: 1178.1,
E(): 0, (40.3% identity in 390 aa overlap). Contains Pfam
match to entry PF00441 Acyl-CoA_dh, Acyl-CoA
dehydrogenase."
/codon_start=1
/transl_table=11
/product="putative acyl-CoA dehydrogenase"
/protein_id="CAA22717.1"
/db_xref="GI:4154064"
/translation="MSRLAQTHGLTDVOREILSTVDFVDKEIIPVATELEHRDEYPO
DIVGLKELGLFLGMLPIPEEYGGGLGESLTYALCVEEIARGMWSGIINTHFIYAYML
KQHTGEQKDFHFLPRMAAGDIRGAFSMSEPALGSDVSAISSKARGEYVNLGQKMW
LTNGQTSLLVALVSKSDGHPGEGTAPHKSMITFLVEKEPGEVGRPGTLTIPGKIDKMG
YKGVDTTELIMDGLRIPANRVLGVTGRTGEGYQMDGVVEVGRVNAARCGVAAORAFEL
GVRVAQQRHTGKQIAQHOAQIOFKLAENATKVEAAHVMYNAARKKDSEGRNDLEACH
AKYLASEYCKVEVEDAFRIHGIGYGFSEYERLKTREAPMLLIGETAEIOMNLIIGRR
LLEERYFOG"
complement(3445..4590)
/gene="SC9C7.05c"
/notes="Pfam match to entry PF00441 Acyl-CoA_dh, Acyl-CoA
dehydrogenase."
complement(4620..5132)
/gene="SC9C7.06c"
complement(4620..5132)
/gene="SC9C7.06c"
/notes="SC9C7.06c, unknown, len: 170aa; similar to
TR:006163 (EMBL:Z95556) from Mycobacterium tuberculosis
(185 aa) fasta scores: opt: 342, z-score: 497.2, E():
2.1e-20, (38.8% identity in 152 aa overlap)."
/codon_start=1
/transl_table=11
/product="hypothetical protein SC9C7.06c"
/protein_id="CAA22718.1"
/db_xref="GI:4154065"
/translation="MQFGTYEEFEVGYATYKHWPGKTVTEYDDHLFCLLTNNHPLHM
DANYAERTDFGKNVYVGNIIYLLGLMSVPDVGKAIANLEISLKHVAPTFHGDTV
YGQTVLTDKNWPKSKNDRGIVHVETGKYQDQTLVCFVFRKVMVPTETTYTKERGGEQ
GRPELKEQGK"
complement(5138..6157)
/gene="SC9C7.07c"
complement(5138..6157)
/gene="SC9C7.07c"
/notes="SC9C7.07c, probable lyase, len: 339aa; similar to

```

Query Match 6.6%; Score 20; DB 1; Length 31360;

Best Local Similarity 100.0%; Pred. No. 10;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 gctcggtacggcgcttcg 43

|||||

Db 30332 GCTCGGCTACGGCGCTTCG 30351

RESULT 23

AC108477


```

T78245 W33296 N66794 D25981 A1087007 AA797250 N77410
T78078 A1183552 AA466871 AA704510 AA333129 W02194 AF034173
AA70471 R34961 AA868396 R36376 R98224 A1117325 AA704529
R32697 AA374195"
complement(14284. .>14835)
/note="match: GSS A0009498 clone 2283M18"
16414. .16503
/note="MER5B repeat: matches 14. .102 of consensus"
16562. .16688
/note="MIR repeat: matches 109. .245 of consensus"
16821. .17150
/note="LTR16A repeat: matches 1. .353 of consensus"
complement(join(17388. .17542,21080. .21170,34884. .35186,
35960. .36221,36534. .36657,39000. .39131,41630. .41787,
44954. .46147))
/genes="dJ524E15.1"
complement(join(<17388. .17542,21080. .21170,34884. .35186,
35960. .36221,36534. .36657,39000. .39131,41630. .41787,
44954. .>46147))
/genes="dJ524E15.1"
match: protein P55201"
/codon_start=3
/evidence=not_experimental
/product="dJ524E15.1 (PEREGRIN (BR140 PROTEIN))"
/protein_id="CAB06488.1"
/db_xref="GI:4107440"
/db_xref="SPTREMBL:O95692"
/translation="LSPOFGAMRKPRKSRQNAEGRSPSPYSILKCSPTRETLTYAQ
AQRIVEVDIGRLHRIISYDPLKLIITEDELTAQDITEGNSKNKSEQPFQPKSKKKS
SKGKKKSCSRHASTSFHLQPSFRWVDSGIQPEAPLPAAYTRYIEKPPEDLDAAEV
EDAFCDDEDLADWVNEKRRVDGHSLSADTELLVDRLKESYLESRSSGAQSLID
EDAPCCDLDECHNSNIIIFCDICNLAVHQCXGVPIPEGWILCRCLQSPSRPVD
CILCPKNGAATQKSDGHWAVCAIWIPEVCFAKTFVLEPIEGIDNIPPAWKLITCY
ICKOKGLGAATQCHKVNCYTAFHVTCQORAGLEFMKIEPMRETSLSNGTITVTKTAYCE
AHSPLKANKICSGLSFORKNPFMRHNYWLLKQARNGVPLIRLHSLHLSQSNADQ
REODETSAVEELKYWGKLRHDLERALLIELRKREKLKREQVKVQQAAMELELMP
FNLLRTTLDLQKEDPAHIFAEPVNLNLEFISKPMDFSTMRRKLSHLYRTLEEF
EDFNLVNCHKNYAKDTIFHRAAVRLDGLGAILRHARROAENIGYDPERGTHLPDG
QHHPREPQVFPVGAAGAAGETGPERHAWQVGPHPSPCPATPGDQSAEAGTAT
TTTATITQODSITQWCAASRPGGSCAGAGLGGARRRWGSLLLPREDRGDLLEPL
VWAKCRGYPSPALIIDPKMPREGLLHNGVPIPVPPDLVLGLGEQKNAEAGEKLEFLVL
FEDNKR".
prim_transcript
complement(17446. .28516)
/genes="dJ524E15.1"
/note="match: 5' EST AA499377 clone Mus musculus 919404"
18059. .18158
/note="L2 repeat: matches 2596. .2690 of consensus"
19182. .19261
/note="40 copies 2 mer aa 71% conserved"
19184. .19255
/note="6 copies 12 mer 72% conserved"
19850. .20026
/note="MER5B repeat: matches 1. .176 of consensus"
complement(<19852. .>20244)
/genes="dJ524E15.1"
/note="match: GSS A0188325"
20238. .20420
/note="L1P1 repeat: matches 5634. .5824 of consensus"
20597. .20731
/note="MIR repeat: matches 13. .166 of consensus"
21202. .21325
/note="L1M1 repeat: matches -345. .-224 of consensus"
21341. .21667
/note="MER58B repeat: matches 1. .341 of consensus"
22240. .22358
/note="FLAN_C repeat: matches 7. .125 of consensus"
22382. .22757
/note="L1ME1 repeat: matches 5417. .5786 of consensus"
23501. .23723
/note="L1ME repeat: matches 5592. .5818 of consensus"
24860. .25162
/note="AluSc repeat: matches 1. .303 of consensus"

```

```

repeat_region 25283. .25335
/note="MER5B repeat: matches 110. .158 of consensus"
25910. .26125
/note="MIR repeat: matches 1. .261 of consensus"
26435. .26499
/note="L2 repeat: matches 2684. .2748 of consensus"
27686. .27982
/note="AluX repeat: matches 1. .299 of consensus"
28457. .29013
/note="match: GSS A0077714 clone 2369P14"
29389. .29687
/note="AluJb repeat: matches 1. .300 of consensus"
complement(<29688. .30045)
/genes="dJ524E15.1"
/genes="match: 5' EST T84329 clone 110390"
29831. .29945
/note="MIR repeat: matches 19. .139 of consensus"
30203. .30395
/note="MIR repeat: matches 11. .218 of consensus"

Query Match 6.3% Score 19 DB 9 Length 80908
Best Local Similarity 100.0% Pred. No. 32
Matches 19 Conservative 0 Mismatches 0 Indels 0 Gaps 0:

Qy 74 tcacaaagggcagcagctg 92
|||||
Db 18064 TCCACAGGCGACGACTG 18082

RESULT 26
AC105566
LOCUS
DEFINITION
AC105566 119916 bp DNA linear HTG 09-JAN-2002
Rattus norvegicus clone CH230-250A15, *** SEQUENCING IN PROGRESS
*** 61 unordered pieces.
AC105566
VERSION
HTG; HTGS_PHASE1
KEYWORDS
Norway rat.
SOURCE
Rattus norvegicus
ORGANISM
Eukaryota; Metazoa
Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
1 (bases 1 to 119916)
AUTHORS
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-Osman,F.R., Allen,C.,
Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbara,J.,
Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J.,
Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C.,
Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F.,
Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R.,
Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C.,
Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C.,
Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O.,
Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H.,
Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C.,
Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J.,
Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T.,
Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S.,
Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Hollaway,C.,
Hollins,B., Homsli,F., Howard,S., Huber,J., Hulyk,S., Hume,J.,
Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S.,
Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J.,
Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C.,
Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W.,
Louiseged,H., Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R.,
Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A.,
Martinez,E., Massey,E., Mawhiney,E., McLeod,M.P., Meador,M.,
Mel,G., Metzker,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K.,
Morgan,M., Morris,S., Moser,M., Neal,D., Newton,J., Newton,N.,
Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokenwo,S.,
Ogih,M., Okwuonu,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B.,
Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L.,
Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojibokan,I., Rolfe,M.,

```

```

Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shooshtari,N.,
Sisson,I., Sodergren,E., Sonaike,T., Sparks,A., Stanley,H.,
Stone,H., Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K.,
Tang,H., Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N.,
Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R.,
Wall,R., Wang,S., Ward-Moore,S., Warren,R., Washington,C.,
Watlington,S., Williams,G., Williamson,A., Wleczyk,R., Wooden,S.,
Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
Weinstock,C. and Gibbs,R.
Direct Submission
Unpublished
2 (bases 1 to 119916)
Worley,K.C.
Direct Submission
Submitted (09-JAN-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Bay Plaza, Houston, TX 77030, USA
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GNFC
Center clone name: CH230-250A15
----- Summary Statistics
Assembly program: Phrap; version 0.990329First call to
findPhrapList
Consensus quality: 85751 bases at least Q40
Consensus quality: 93994 bases at least Q30
Consensus quality: 102334 bases at least Q20
Estimated insert size: 82500; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-fp estimation
Quality coverage: 0.9x in Q20 bases; sum-of-contigs estimation
-----
* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 61 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 5417: contig of 5417 bp in length
* 5418 5517: gap of unknown length
* 5518 9404: contig of 3887 bp in length
* 9405 9504: gap of unknown length
* 9505 12699: contig of 3195 bp in length
* 12700 12799: gap of unknown length
* 12800 16317: contig of 3518 bp in length
* 16318 16417: gap of unknown length
* 16418 19344: contig of 2927 bp in length
* 19345 19444: gap of unknown length
* 19445 22565: contig of 3121 bp in length
* 22566 22665: gap of unknown length
* 22666 24996: contig of 2331 bp in length
* 24997 25096: gap of unknown length
* 25097 27065: contig of 1969 bp in length
* 27066 27165: gap of unknown length
* 27166 29582: contig of 2417 bp in length
* 29583 32613: contig of 2931 bp in length
* 32614 32713: gap of unknown length
* 32714 35399: contig of 2686 bp in length
* 35400 35499: gap of unknown length
* 35500 37557: contig of 2058 bp in length
* 37558 37657: gap of unknown length
* 37658 39153: contig of 1496 bp in length
* 39154 39253: gap of unknown length
* 39254 41229: contig of 1976 bp in length
* 41230 41329: gap of unknown length
*
* 41330 43186: contig of 1857 bp in length
* 43187 43286: gap of unknown length
* 43287 45418: contig of 2132 bp in length
* 45419 45519: gap of unknown length
* 45519 47831: contig of 2313 bp in length
* 47832 47931: gap of unknown length
* 47932 49971: contig of 2040 bp in length
* 49972 50071: gap of unknown length
* 50072 51780: contig of 1709 bp in length
* 51781 51880: gap of unknown length
* 51881 53936: contig of 2056 bp in length
* 53937 54036: gap of unknown length
* 54037 56155: contig of 2119 bp in length
* 56156 56255: gap of unknown length
* 56256 58719: contig of 2464 bp in length
* 58720 58819: gap of unknown length
* 58820 60750: contig of 1931 bp in length
* 60751 60850: gap of unknown length
* 60851 61864: contig of 1014 bp in length
* 61865 61965: gap of unknown length
* 61965 63634: contig of 1670 bp in length
* 63635 63735: gap of unknown length
* 63735 65477: contig of 1643 bp in length
* 65478 66338: contig of 1161 bp in length
* 66339 66739: gap of unknown length
* 66739 67981: contig of 1242 bp in length
* 67981 69889: gap of unknown length
* 69889 71664: contig of 1808 bp in length
* 71665 71765: gap of unknown length
* 71765 73378: contig of 1614 bp in length
* 73379 74629: contig of 1151 bp in length
* 74630 74729: gap of unknown length
* 74730 75903: contig of 1174 bp in length
* 75904 76004: gap of unknown length
* 76004 77279: contig of 1275 bp in length
* 77279 77378: gap of unknown length
* 77379 79018: contig of 1640 bp in length
* 79019 79118: gap of unknown length
* 79119 80715: contig of 1597 bp in length
* 80716 80815: gap of unknown length
* 80816 83063: contig of 2248 bp in length
* 83064 83163: gap of unknown length
* 83164 85404: contig of 2241 bp in length
* 85405 85504: gap of unknown length
* 85505 87875: contig of 2371 bp in length
* 87876 87975: gap of unknown length
* 87976 89148: contig of 1173 bp in length
* 89149 89248: gap of unknown length
* 89249 91394: contig of 2146 bp in length
* 91395 91494: gap of unknown length
* 91495 92792: contig of 1297 bp in length
* 92793 92891: gap of unknown length
* 92892 94174: contig of 1283 bp in length
* 94175 94275: gap of unknown length
* 94276 95295: contig of 1021 bp in length
* 95296 95395: gap of unknown length
* 95396 96788: contig of 1393 bp in length
* 96789 96888: gap of unknown length
* 96889 98468: contig of 1580 bp in length
* 98469 98568: gap of unknown length
* 98569 99706: contig of 1138 bp in length
* 99707 99806: gap of unknown length
* 99807 101157: contig of 1351 bp in length
* 101158 101257: gap of unknown length
* 101258 103154: contig of 1897 bp in length
* 103155 104442: gap of unknown length
* 104443 104542: gap of unknown length
* 104543 105711: contig of 1169 bp in length

```

TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

COMMENT

```

* 105712 105811: gap of unknown length
* 105812 106936: contig of 1125 bp in length
* 106937 107036: gap of unknown length
* 107037 108459: contig of 1423 bp in length
* 108460 108559: gap of unknown length
* 108560 109929: contig of 1370 bp in length
* 109930 110029: gap of unknown length
* 110030 111272: contig of 1243 bp in length
* 111273 111373: gap of unknown length
* 111373 112564: contig of 1192 bp in length
* 112565 112664: gap of unknown length
* 112665 114426: contig of 1762 bp in length

Query Match      6.3%; Score 19; DB 2; Length 119916;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 106 gtgaataactgaagagg 124
    |||||
Db 44969 GTGAAATGCTGAAGAGG 44987

RESULT 27
AC106084
LOCUS      AC106084
DEFINITION Rattus norvegicus clone CH230-121C20, *** SEQUENCING IN PROGRESS
ACCESSION AC106084
VERSION    AC106084.1 GI:18138599
KEYWORDS   HTG: HTGS-PHASE1.
SOURCE     Norway rat.
ORGANISM   Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
            1 (bases 1 to 155825)
            Muzny D.M., Adams C., Adio-Oduola B., Ali-Osman, F.R., Allen, C.,
            Alsbrooks, S.L., Amarantunga, H.C., Are, J.R., Banks, T., Barbaria, J.,
            Benton, J., Bimaga, K., Blankenburg, K., Bonnin, D., Bouck, J.,
            Bowie, S., Brivea, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C.,
            Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F.,
            Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R.,
            Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C.,
            Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C.,
            Davy-Carroll, L., Dederich, R.A., Delaney, K.R., Delgado, O.,
            Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H.,
            Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C.,
            Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J.,
            Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T.,
            Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S.,
            Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C.,
            Hollins, B., Honsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J.,
            Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S.,
            Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J.,
            Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, D.C.,
            Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W.,
            Loulsegad, H., Lozada, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R.,
            Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M.,
            Mei, G., Metzger, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K.,
            Morgan, M., Morris, S., Moser, M., Neal, D., Newton, J., Newton, N.,
            Nguyen, A., Nguyen, S., Nguyen, N., Nickerson, E., Nwokwuo, S.,
            Oguh, M., Okwunonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B.,
            Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L.,
            Quiles, M., Ren, Y., Rivers, M., Rojas, A., Rojibokan, I., Rolfe, M.,
            Ruiz, S., Savory, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N.,
            Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H.,
            Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K.,
            Tang, H., Tansey, J., Taylor, C., Taylor, F., Telford, B., Thomas, N.,
            Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalob, D., Vinson, R.,
            Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C.,
            Watlington, S., Williams, G., Williamson, A., Wleczyk, R., Wooden, S.,

```

```

Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D.,
Weinstock, G., and Gibbs, R.
Direct Submission
Unpublished
2 (bases 1 to 155825)
Worley, K.C.
Direct Submission
Submitted (12-JAN-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GHHP
Center clone name: CH230-121C20
----- Summary Statistics
Assembly program: Phrap; version 0.990329First call to
findPhrapList
Consensus quality: 123657 bases at least Q40
Consensus quality: 132258 bases at least Q30
Consensus quality: 137884 bases at least Q20
Estimated insert size: 107272; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-fp estimation
Quality coverage: 1.4x in Q20 bases; sum-of-contigs estimation
-----
* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 76 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 7184: contig of 7184 bp in length
* 7185 7284: gap of unknown length
* 7285 15297: contig of 8013 bp in length
* 15298 15397: gap of unknown length
* 15398 18433: contig of 3036 bp in length
* 18434 18533: gap of unknown length
* 18534 22113: contig of 3580 bp in length
* 22114 22213: gap of unknown length
* 22214 26752: contig of 4439 bp in length
* 26753 30160: contig of 3408 bp in length
* 30161 32493: contig of 2233 bp in length
* 32494 32593: gap of unknown length
* 32594 36039: contig of 3446 bp in length
* 36040 36139: gap of unknown length
* 36140 39230: contig of 3091 bp in length
* 39231 39331: gap of unknown length
* 39331 42441: contig of 3111 bp in length
* 42442 42541: gap of unknown length
* 42542 44851: contig of 2310 bp in length
* 44852 44951: gap of unknown length
* 44952 47222: contig of 2271 bp in length
* 47223 47322: gap of unknown length
* 47323 49738: contig of 2416 bp in length
* 49739 49838: gap of unknown length
* 49839 53036: contig of 3198 bp in length
* 53037 53136: gap of unknown length
* 53137 55214: contig of 2078 bp in length
* 55215 55314: gap of unknown length
* 55315 57167: contig of 1853 bp in length
* 57168 57267: gap of unknown length
* 57268 60624: contig of 3357 bp in length
* 60625 60724: gap of unknown length
* 60725 63477: contig of 2753 bp in length

```



```
* 63478 63577: gap of unknown length
* 63578 65621: contig of 2044 bp in length
* 65622 65721: gap of unknown length
* 65722 67927: contig of 2206 bp in length
* 67928 68027: gap of unknown length
* 68028 69802: contig of 1775 bp in length
* 69803 69902: gap of unknown length
* 69903 71859: contig of 1957 bp in length
* 71860 71959: gap of unknown length
* 71960 74227: contig of 2268 bp in length
* 74228 74327: gap of unknown length
* 74328 76807: contig of 2480 bp in length
* 76808 76907: gap of unknown length
* 76908 79097: contig of 2190 bp in length
* 79098 79197: gap of unknown length
* 79198 81356: contig of 2159 bp in length
* 81357 81456: gap of unknown length
* 81457 82500: contig of 1044 bp in length
* 82501 82600: gap of unknown length
* 82601 83787: contig of 1187 bp in length
* 83788 83887: gap of unknown length
* 83888 85585: contig of 1698 bp in length
* 85586 85685: gap of unknown length
* 85686 87209: contig of 1524 bp in length
* 87210 87309: gap of unknown length
* 87310 89391: contig of 2082 bp in length
* 89392 89491: gap of unknown length
* 89492 90863: contig of 1372 bp in length
* 90864 90963: gap of unknown length
* 90964 92581: contig of 1618 bp in length
* 92582 92681: gap of unknown length
* 92682 94497: contig of 1816 bp in length
* 94498 94597: gap of unknown length
* 94598 95959: contig of 1362 bp in length
* 95960 96059: gap of unknown length
* 96060 97493: contig of 1434 bp in length
* 97494 97593: gap of unknown length
* 97594 98873: contig of 1280 bp in length
* 98874 98973: gap of unknown length
* 98974 100260: contig of 1287 bp in length
* 100261 100360: gap of unknown length
* 100361 101503: contig of 1143 bp in length
* 101504 101603: gap of unknown length
* 101604 102847: contig of 1244 bp in length
* 102848 102947: gap of unknown length
* 102948 104772: contig of 1825 bp in length
* 104773 104872: gap of unknown length
* 104873 106735: contig of 1863 bp in length
* 106736 106835: gap of unknown length
* 106836 108191: contig of 1356 bp in length
* 108192 108291: gap of unknown length
* 108292 109620: contig of 1329 bp in length
* 109621 109720: gap of unknown length
* 109721 110965: contig of 1245 bp in length
* 110966 111065: gap of unknown length
* 111066 112325: contig of 1260 bp in length
* 112326 112425: gap of unknown length
* 112426 114287: contig of 1862 bp in length
* 114288 114387: gap of unknown length
* 114388 115433: contig of 1046 bp in length
* 115434 115533: gap of unknown length
* 115534 116779: contig of 1246 bp in length
* 116780 116879: gap of unknown length
* 116880 118275: contig of 1396 bp in length
* 118276 118375: gap of unknown length
* 118376 120259: contig of 1884 bp in length
* 120260 120359: gap of unknown length
* 120360 122229: contig of 1870 bp in length
* 122230 122329: gap of unknown length
* 122330 124076: contig of 1747 bp in length
* 124077 124176: gap of unknown length
* 124177 125298: contig of 1122 bp in length
* 125299 125398: gap of unknown length
```

```
* 125399 127106: contig of 1708 bp in length
* 127107 127206: gap of unknown length
* 127207 128266: contig of 1060 bp in length
* 128267 128366: gap of unknown length
* 128367 130055: contig of 1689 bp in length

Query Match
Best Local Similarity 6.3%; Score 19; DB 2; Length 155825;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 268 tacggcaacctctccaact 286
|||||
Db 104433 TACGGCAACCTCTCCAAC 104451
```

```
RESULT 28
AF207872/c
LOCUS AF207872 561 bp DNA linear STS 24-OCT-2000
DEFINITION Ovis aries chromosome 18 clone ODBS565, sequence tagged site.
ACCESSION AF207872
VERSION AF207872.1 GI:7677203
KEYWORDS STS.
SOURCE sheep.
ORGANISM Ovis aries
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Caprinae; Ovis.
REFERENCE 1 (bases 1 to 561)
AUTHORS Fahrenkrug,S.C., Freking,B.A., Rexroad,C.E. III, Leymaster,K.A.,
Kappes,S.M. and Smith,T.P.L.
TITLE Comparative mapping of the ovine c1pg locus
JOURNAL Mamm. Genome 11 (10), 871-876 (2000)
MEDLINE 20458865
PUBMED 11003702
REFERENCE 2 (bases 1 to 561)
AUTHORS Fahrenkrug,S.C.
TITLE Direct Submission
JOURNAL Submitted (23-NOV-1999) Production Systems, USDA Meat Animal
Research Center, PO Box 166, Spur 18D, Clay Center, NE 68933, USA
FEATURES
source
Location/Qualifiers
1..561
/organism="Ovis aries"
/db_xref="taxon:9940"
/chromosome="18"
/clone="ODBS565"
/note="derived from BAC 56R3C11"
```

BASE COUNT 121 a 150 c 159 g 131 t

```
Query Match
Best Local Similarity 5.9%; Score 18; DB 11; Length 561;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 43 ggggaaggtggtggaagcc 60
|||||
Db 218 GGGGAAGGTGGTGAAGCC 201
```

```
RESULT 29
HSA330119/c
LOCUS HSA330119 621 bp DNA linear PRI 01-OCT-2001
DEFINITION Homo sapiens genomic sequence surrounding NotI site, clone
NRI-XE6C.
ACCESSION AJ330119
VERSION AJ330119.1 GI:15874537
KEYWORDS STS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 621)
AUTHORS Kutsenko,A.S., Gizatullin,R.Z., Al-Amin,A.N., Wang,F.,
```


Podawski,R.M., Matushkin,Y.G., Kvasha,S.M., Gyanchandani,A., Muravenko,O.V., Protopopov,A.I., Kashuba,V.I., Kisselev,L.L., Wasserman,W., Wahlestedt,C. and Zabarovsky,E.R.
Analysis of NotI flanking sequences: a new tool for gene discovery and verification of the human genome

JOURNAL Unpublished
REFERENCE 2 (bases 1 to 621)
AUTHORS Zabarovsky,E.R.
TITLE Direct Submission
JOURNAL Submitted (16-MAY-2001) Microbiology and Tumorbiology Centre, Karolinska Institute, Theorells vag, 3, Box 280, Stockholm 171 77, Sweden

FEATURES
source
1..621
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="NRI-XE6C"

BASE COUNT 137 a 198 c 207 g 78 t 1 others
ORIGIN

Query Match 5.9%; Score 18; DB 9; Length 621;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 acggcgcttcgggaagg 49
|||||
Db 98 ACGGCGCTTCGGGAAG 81

RESULT 30
HAUNKTRP/c

LOCUS Human astrovirus type 1 mRNA linear VRL 09-FEB-1999
DEFINITION Human astrovirus type 1 mRNA for non-structural protein.
ACCESSION Z16420
VERSION Z16420.1 GI:59401
KEYWORDS non-structural protein.
SOURCE Human astrovirus type 1.
ORGANISM Human astrovirus type 1
Viruses; ssRNA positive-strand viruses, no DNA stage; Astroviridae; Astrovirus.

REFERENCE 1 (bases 1 to 827)
AUTHORS Willcocks,M.M., Carter,M.J., Silcock,J.G. and Madeley,C.R.
TITLE A dot-blot hybridization procedure for the detection of astrovirus in stool samples
JOURNAL Epidemiol. Infect. 107 (2), 405-410 (1991)
MEDLINE 92037892
REMARK (sites)

REFERENCE 2 (bases 1 to 827)
AUTHORS Willcocks,M.M. and Carter,M.J.
TITLE Sequence analysis of a human Astrovirus
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 827)
AUTHORS Willcocks,M.
TITLE Direct Submission

JOURNAL Submitted (06-OCT-1992) Willcocks M., University of Surrey, School of Biological Sciences, Guildford, Surrey, G42 5XH
FEATURES
source
1..827
/organism="Human astrovirus type 1"
/db_xref="taxon:12456"

transit_peptide 718..726
/function="unknown"
/product="virus non-structural protein"
BASE COUNT 267 a 163 c 204 g 193 t
ORIGIN

Query Match 5.9%; Score 18; DB 14; Length 827;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 165 caagatcctcattcacat 182

Db 79 CAAGATCCTCATTCACAT 62
|||||

RESULT 31
LOCUS RSU62291
DEFINITION Rhodobacter sphaeroides copper containing nitrite reductase (nirK) gene, complete cds.
ACCESSION U62291
VERSION U62291.1 GI:1480719
KEYWORDS
SOURCE Rhodobacter sphaeroides.
ORGANISM Rhodobacter sphaeroides
Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group; Rhodobacter.

REFERENCE 1 (bases 1 to 1307)
AUTHORS Tosques,I.E., Kwiatkowski,A.V., Shi,J. and Shapleigh,J.P.
TITLE Characterization and regulation of the gene encoding nitrite reductase in Rhodobacter sphaeroides
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1307)
AUTHORS Tosques,I.E., Shi,J. and Shapleigh,J.P.
TITLE Direct Submission
JOURNAL Submitted (26-JUN-1996) Microbiology, Cornell University, Wing Hall, Ithaca, NY 14853-8101, USA

FEATURES
source
1..1307
/organism="Rhodobacter sphaeroides"
/strain="2.4.3"
/db_xref="taxon:1063"
56..69
/note="similar to previous Fnr binding sequence"
/bound_moiety="Fnr"
/evidence=not_experimental
136..1260
/gene="nirK"
136..1260
/gene="nirK"
/codon_start=1
/transl_table=11
/product="copper containing nitrite reductase"
/protein_id="AA05767.1"
/db_xref="GI:1480720"

BASE COUNT 237 a 472 c 405 g 193 t
ORIGIN

Query Match 5.9%; Score 18; DB 1; Length 1307;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 122 agggcgccacgcgcgcg 139
|||||

Db 1172 AGGGCGCCACGCACGC 1189

RESULT 32
LOCUS AB025557
DEFINITION Branchiostoma belcheri mRNA for VEGFR-like, partial cds.
ACCESSION AB025557
VERSION AB025557.1 GI:6002454
KEYWORDS VEGFR-like.
SOURCE Branchiostoma belcheri cDNA to mRNA.
ORGANISM Branchiostoma belcheri

REFERENCE AUTHORS TITLE JOURNAL MEDLINE REFERENCE AUTHORS TITLE JOURNAL	Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae; Branchiostoma. 1 (sites) Suga,H., Hoshiyama,D., Kuraku,S., Katoh,K., Kubokawa,K. and Miyata,T. Protein tyrosine kinase cDNAs from amphioxus, hagfish, and lamprey: isoform duplications around the divergence of cyclostomes and gnathostomes J. Mol. Evol. 49 (5), 601-608 (1999) 20020330 2 (bases 1 to 1519) Suga,H. Direct Submission Submitted (31-MAR-1999) Hiroshi Suga, Faculty of Science, Kyoto University, Department of Biophysics, Kitashirakawa-Oiwakecho, Sakyo-ku, Kyoto, Kyoto 606-8502, Japan (E-mail:suga@biophys.kyoto-u.ac.jp, Tel: +81-75-753-4224, Fax: +81-75-753-4223)		62901-6523, USA Location/Qualifiers 1. .2065 /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="11" /cell_line="JEG-3 choriocarcinoma" 51. .1748 /note="NUDR; similar to Homo sapiens suppressin, GenBank Accession Number AF007165; NUDR8 isoform, GenBank Accession Number AF049460, contains altered coding region near amino terminal alanine rich region" /codon_start=1 /product="nuclear DEAF-1 related transcriptional regulator protein" /protein_id="AAC79676.1" /db_xref="GI:3309563" /translation="MEDSDSAKQLGLAEAAVAAAAVAAAAAAGGAEPEPVLRS DEDSEADSAERETPRVTAVVAAEPGHMDGAEALPGDEAAAAAFAEVTVT VANVGAAADNVTTTSVANAASISGHLVSGTALQIGDSLNTKATLIIVHTDGSIVT TCLKGPAAPLTPGQSPPTPLAPGQEGTKYNMDPSYDSELPVRCNIGSTLYKNR LCSGGRGRCIKGGENWYSPTEFEAMAGRASSKDKRSIRYAGRPLOCLIQDILNPHA ASCTCAACDDMTLGGPVLPVYKRRKKENELPTTPVKDKSPKNITLLPATATFTT VTPSQIITSGALTFEDRASTVEATVISESPAQGDVFAGATVQESVQPPCRASHPEP HYPGTQSCQIAPFPEAALPSTHPKIVLTSLPALAVPPPTTKAAPPALVNGLESEP RSMWLEEMVNSLLNTAOLKTLFEQAKHASTYREAAATNOAKIHADAERKQSCVNCG REANLEGTGCHKVNYCTFCQKDKMHOHICGQSAAVTVQADEVHVAESVMEKVTV"	
	FEATURES	source	Location/Qualifiers	
	CDS			
	BASE COUNT	441 a	640 c 656 g 328 t	
REFERENCE AUTHORS TITLE JOURNAL MEDLINE REFERENCE AUTHORS TITLE JOURNAL	Query Match Best Local Similarity 5.9%; Score 18; DB 9; Length 2065; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0; QY 32 acgcgccttcgcggaag 49 DB 18 ACGGCGCCTTCGGGAAG 35 RESULT 34 AF049460 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL MEDLINE REFERENCE AUTHORS TITLE JOURNAL		Homo sapiens nuclear DEAF-1 related transcriptional regulator protein 8 mRNA, complete cds. AF049460.1 GI:3309564 human. Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2329) Curley,P. and Mowen,K.A. Huggenvik,J.I., Michelson,R.J., Collard,M.W., Ziemba,A.J., Gurley,P. and Mowen,K.A. Characterization of a nuclear deformed epidermal autoregulatory factor-1 (DEAF-1)-related (NUDR) transcriptional regulator protein Mol. Endocrinol. 12 (10), 1619-1639 (1998) 98444968 2 (bases 1 to 2329) Huggenvik,J.I., Michelson,R.J., Collard,M.W., Ziemba,A.J., Gurley,P. and Mowen,K.A. Direct Submission Submitted (20-FEB-1998) Physiology, Southern Illinois University School of Medicine, 2053 Life Sciences III, Carbondale, IL 62901-6523, USA	
	FEATURES	source	Location/Qualifiers	
	CDS			
REFERENCE AUTHORS TITLE JOURNAL MEDLINE REFERENCE AUTHORS TITLE JOURNAL	Query Match Best Local Similarity 5.9%; Score 18; DB 3; Length 1519; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0; QY 261 ctgcaagtaaggcaacct 278 DB 214 CTGCAAGTAGCGCAACCT 231 RESULT 33 AF049459 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL MEDLINE REFERENCE AUTHORS TITLE JOURNAL		Homo sapiens nuclear DEAF-1 related transcriptional regulator protein mRNA, complete cds. AF049459.1 GI:3309562 human. Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2065) Huggenvik,J.I., Michelson,R.J., Collard,M.W., Ziemba,A.J., Gurley,P. and Mowen,K.A. Characterization of a nuclear deformed epidermal autoregulatory factor-1 (DEAF-1)-related (NUDR) transcriptional regulator protein Mol. Endocrinol. 12 (10), 1619-1639 (1998) 98444968 2 (bases 1 to 2065) Huggenvik,J.I., Michelson,R.J., Collard,M.W., Ziemba,A.J., Gurley,P. and Mowen,K.A. Direct Submission Submitted (20-FEB-1998) Physiology, Southern Illinois University School of Medicine, 2053 Life Sciences III, Carbondale, IL	
	FEATURES	source	Location/Qualifiers	
	CDS			
	BASE COUNT	395 a	415 c 401 g 308 t	
REFERENCE AUTHORS TITLE JOURNAL MEDLINE REFERENCE AUTHORS TITLE JOURNAL	Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae; Branchiostoma. 1 (sites) Suga,H., Hoshiyama,D., Kuraku,S., Katoh,K., Kubokawa,K. and Miyata,T. Protein tyrosine kinase cDNAs from amphioxus, hagfish, and lamprey: isoform duplications around the divergence of cyclostomes and gnathostomes J. Mol. Evol. 49 (5), 601-608 (1999) 20020330 2 (bases 1 to 1519) Suga,H. Direct Submission Submitted (31-MAR-1999) Hiroshi Suga, Faculty of Science, Kyoto University, Department of Biophysics, Kitashirakawa-Oiwakecho, Sakyo-ku, Kyoto, Kyoto 606-8502, Japan (E-mail:suga@biophys.kyoto-u.ac.jp, Tel: +81-75-753-4224, Fax: +81-75-753-4223)		62901-6523, USA Location/Qualifiers 1. .1519 /organism="Branchiostoma belcheri" /db_xref="taxon:7741" /codon_start=2 /product="VEGFR-like" /protein_id="BAA84747.1" /db_xref="GI:6002455" /translation="QVIEATAGIEKQCVAVVAVMLKDDASSNEVYKALMDLKILI HGOHLNIVNLGACTKDGPIVIVECCYKGLNSYLGRKRKFVSKDQDRSNSSG KCTRVDSPNGKCLRTVSKGLMNYDYTDGDEPLTLEDLVSYQVARGMDYLSAK YCNIRDLARNYLLAKHNVYKICDFGLADVVRNPEYTKMGNAPLVKVMAPESIFDR SYTIQSDVSYGLLWEIFELGSGSPGVQIINEDFDKLRQCFRMRQPKHAPSDLLYOM MLSCNRMEPTPTTDLAESSSOLEATAEOEYLDLSPEIHDDSDGIPNPTPTDS FLPTPADCARQASPPASGNYDNSRPERHSYDVIDEEAVKILMDHPQRAHYHSDA KALVPNSLGVKRGKGGNSKSDNSVSSSHNSGFGHSYDEAPPDYNTVVTVDV"	
	FEATURES	source	Location/Qualifiers	
	CDS			
	BASE COUNT	395 a	415 c 401 g 308 t	

/note="NUDR8; similar to Homo sapiens suppressin, GenBank
Accession Number AF007165; NUDR isoform, GenBank Accession
Number AF049459, contains altered coding region near amino
terminal alanine rich region"
/codon_start=1
/product="nuclear DEAF-1 related transcriptional regulator
protein 8"
/protein_id="AAC79677.1"
/db_xref="GI:3309565"
/translation="MEDSDSAKOLGLADAAAAGGEAEPEPVLSDSEEDADSEAE
ETPRVTAVVAAEPGHMDMGAEALPGDEAAAAAFAEVTITVAVVGAADNVFTT
SVANAASISGHLVSGRTALQIGDSLTKATLIIVHTDGSIVETGLKPAAPLTGP
QSPPTPLAPGQEGKTYNMDPSYDSELVPCRNISGTLKNRGLSGGGRGKIQGE
NMYSPTEFAMAGRASSKDMKRSIRYAGRLQCLIQGILNPHAACTCAACDDMTL
SGPVLFPVYKRRKENELPTTPVKKDSKNTLLPATATFTVTPSGQITTSGLT
FDRASTVEATAVISESPAQGVFAGATVOEASVOPPCRAHPHEPHYCYODSCQIAPF
PEALPSSHPIVLTSALAVPPPTTKAAPALVNGLELSEPRSLWILEEYVNSLL
NTAQLTKLFEQAKHASTYREAATNQAKIHADAERKEQSCVNCGRAMECTGCHKVN
YCSTFCQRKWKDHQICGQSAATVQADEVHVAESVMEKVTV"
BASE COUNT 464 a 739 c 734 g 392 t
ORIGIN

Query Match 5.9%; Score 18; DB 9; Length 2329;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 32 acggcgcccttcgggaag 49
|||||
Db 324 ACGGCGCTTCGGGAAG 341

RESULT 35
AF049461
LOCUS
DEFINITION Pan troglodytes nuclear DEAF-1 related transcriptional regulator
protein mRNA, complete cds.
ACCESSION AF049461
VERSION AF049461.1 GI:3309566
KEYWORDS
SOURCE chimpanzee.
ORGANISM
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
1 (bases 1 to 2405)
Huggenvik,J.I., Michelson,R.J., Collard,M.W., Ziemba,A.J.,
Gurley,P. and Mowen,K.A.
TITLE
Characterization of a nuclear deformed epidermal autoregulatory
factor-1 (DEAF-1)-related (NUDR) transcriptional regulator protein
Mol. Endocrinol. 12 (10), 1619-1639 (1998)
JOURNAL
MEDLINE 98444968
AUTHORS Huggenvik,J.I., Michelson,R.J., Collard,M.W., Ziemba,A.J.,
Gurley,P. and Mowen,K.A.
TITLE Direct Submission
JOURNAL Submitted (20-FEB-1998) Physiology, Southern Illinois University
School of Medicine, 2053 Life Sciences III, Carbondale, IL
62901-6523, USA
FEATURES
Location/Qualifiers
source
1. .2405
/organism="Pan troglodytes"
/db_xref="taxon:9598"
/cell_line="CV-1"
/tissue_type="kidney"
396. .2093
/note="NUDR; similar to Homo sapiens suppressin, GenBank
Accession Number AF007165"
/codon_start=1
/product="nuclear DEAF-1 related transcriptional regulator
protein"
/protein_id="AAC79678.1"
/db_xref="GI:3309567"
/translation="MEDSDSAKOLGLAEAAVAAAAAAGGAEPEPVLRS

DEDESEADSEARETPRVTAVVMAAEPGHMDMGAEALPGDPDEAAAAAFAEVTITVT
VANVGAADNVFTTSVANAASISGHLVSGRTALQIGDSLTKATLIIVHTDGSIVET
TGLKPAAPLTGPQSPPTPLAPGQEGKTYNMDPSYDSELVPCRNISGTLKNR
LGSGRGRCLKQGENMYSPTEFAMAGRASSKDMKRSIRYAGRLQCLIQGILNPH
ASCTCAACDDMTLNSGPVRLFPVYKRRKENELPTTPVKKDSKNTLLPATATFTT
VTPSGQITTSGLTFDRASTVEATAVISESPAQGVFAGATVOEASVOPPCRAHPPEP
HYPCYODSCQIAPFPEALPSSHPIVLTSALAVPPPTTKAAPALVNGLELSEP
RSMWYLEEYVNSLLTTAQLTKLFEQAKHASTYREAANAOKIHADAERKEQSCVNC
REAMNECTGCHKVNYCSTFCQRKWKDHQICGQSAATVQADEVHVAESVMEKVTV"
BASE COUNT 463 a 755 c 774 g 413 t
ORIGIN

Query Match 5.9%; Score 18; DB 9; Length 2405;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 32 acggcgcccttcgggaag 49
|||||
Db 363 ACGGCGCTTCGGGAAG 380

RESULT 36
AF188842
LOCUS
DEFINITION Gallus gallus platelet-derived growth factor receptor alpha
(PDGFR-a) mRNA, complete cds.
ACCESSION AF188842
VERSION AF188842.1 GI:6014686
KEYWORDS
SOURCE chicken.
ORGANISM
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 3614)
Alaliotis,P.
TITLE Platelet-derived growth factor A modulates limb chondrogenesis both
in vivo and in vitro
Mech. Dev. 94 (1-2), 13-24 (2000)
JOURNAL 20302546
MEDLINE 2 (bases 1 to 3614)
REFERENCE Alaliotis,P. and Mercola,M.K.
AUTHORS
TITLE Direct Submission
JOURNAL Submitted (22-SEP-1999) MRC-LMCB, University College London, Gower
Street, London WC1E 6BT, UK
FEATURES
Location/Qualifiers
source
1. .3614
/organism="Gallus gallus"
/db_xref="taxon:9031"
1. .3614
/gene="PDGFR-a"
16. .3279
/gene="PDGFR-a"
/note="receptor tyrosine kinase"
/codon_start=1
/product="platelet-derived growth factor receptor alpha"
/protein_id="AAF01460.1"
/db_xref="GI:6014687"
/translation="MGTPTPTFLILGCLFTGLTLCQLPLPTIPVNRNEMVVLNSN
FTLKCGDSEVSHQYVPTGSHRIDIRHEENNSGLFVTVLEVGNSAAHTGMVVCYN
HTQVEDGEVEGKDIIYVPPDPMPFVPSLPEDQFILVEGDPVIPCRTSDPSAEVTL
VNSLDKPVAFYDSKSGFVGNFLAGPYCTKTMVKGVEFKSDFLIILKRLATSQLPVEI
EALTKYKGTGETIVTVCVFDVFNWLNQNYPGKVEKGLIKLDDIKVPSOKLVYMLT
IPDLVKDGTDECTARHATKEVKNKVVITVHDGFIHLEPQFSPLEAVNLHVEYN
LWLLKNEDEIKRYTFSLLIQVPALIIDLMDHOGSAGROTFRCLAEETPLPOVEWLV
KDIKCSNDSWTLLTNISDIHMEAHLDERNWVESQVTFQKVEETLAVRCVARNDLG
POGHEIYYDDPMOLPYDSRPEPRDGLVILGSGAFGVVEGTAIGLSRSQPMVKY
AVKMLKPTARSSEKQALMSELIMTHLGPHLNIVNLGACTKSGPIYIITEYCFYGD
VNYLHKRNDFLSRHPEKPKDIDFGMPADESTRSYVILSFENTGYEYMDKQADTT
QYVPMLEKREGSKYSIDQRSVYDRPASYKKKLSISESEVKNLLSDDGSEGLSLDLLLSF

```

TYQVARGMEFLASKNCVHRDLAARNVLLAQQKIVKICDFGLARDIMHDSNVYSGKSTF
LPVKHMAPESFDNLYTTLSDVWSIGILLWEIFSLUGGILYPCMMVDSTFYKIKISGYR
MAKPDHATNEVTEINMYKWNNEPEKRPSPFYHLSEIVESLLPCEYKKSYEKIHLDFLKS
DPKPAVTRMGDCDNAYIGVTVYKNEDKIKDRESGFDEQLRSADSGVITPLPDIPDVSED
ELGKNRHSSOTSSESAIETSGSSSTFIKREDETIEDIMDDIDIGIDSSDLVEDSFL"
BASE COUNT      1070 a   735 c   882 g   927 t
ORIGIN

Query Match      5.9%; Score 18; DB 5; Length 3614;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 gccgtgaaataatgctgaaa 120
      |||||
Db 1888 GCCGTGAAAATGCTGAAA 1905

RESULT 37
NEUATPPM/c
LOCUS      NEUATPPM      4784 bp      DNA      linear      PLN 27-APR-1993
DEFINITION Neurospora crassa plasma membrane H+ ATPase gene, complete cds.
ACCESSION J02602
VERSION J02602.1 GI:168764
KEYWORDS H+ ATPase.
SOURCE Neurospora crassa (strain 75-OR23-1A) DNA, clone gNA2.
ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.
REFERENCE 1 (bases 1 to 4784)
AUTHORS Addison,R.
TITLE Primary structure of the Neurospora plasma membrane H+-ATPase
deduced from the gene sequence: Homology to Na+/K+-, Ca2+-, and
K+-ATPases
JOURNAL J. Biol. Chem. 261, 14896-14901 (1986)
MEDLINE 87033715
FEATURES
     source
       1..4784
         /organism="Neurospora crassa"
         /db_xref="taxon:5141"
         <1118..1297
           /note="plasma membrane H+ ATPase"
           /number=1
         join(1118..1297,1356..1562,1687..1820,1885..4079,
              4147..4193)
           /note="plasma membrane H+ ATPase"
           /codon_start=1
           /protein_id="AAA33563.1"
           /db_xref="GI:168765"
           /translation="MADHSASAPALSTNIESGKFDEKAAEAAAYQPKPKVEDDED
IDALIEDSHGDHDAEEEEATPGGRRVYVPEMDLQTDTRVGLTSEEVVQRRKKYGL
NOMKEENHFLLKFLGFVGP IQFMEGAAVLAAGLEDWDFVIGCGLLLLNAAVGVF
QEFQAGSIVDELKKTALAKAVLRDGT LKETEAPVVPDGLQVVEGTIIPADGRIVT
DDAFLOVDSALTGESLAVDKHGDQVFASAVKRGFAVVTATGNTFVGRAALY
NAASGSGHTEVLNGT LILLIVFTLIVVSSYRSNPVQILEFTLITIGV
PVGLPAVYVTTMAGYALAKKKAIVOKLSAIEAGVEILCSDKTGLTKNKLSDHD
PYTVAGVDPEDMLTCLAAARKKKGIDAIDKAPLKSLEYIPRAKSYLSVKYVLQFHP
FDPVSKVAVVSVESPOGERITCVKGAFLFVLKVEEDHP IPEEVDQAYKNKVAEFATR
GFRSLGARRRGGSWEILGIMPCMPDRHDTKYTCVCEAKTGLS IKMLTGDVAGTAR
ETSRQLGLGTNIYNAERLGLGGDMPGSEVDFVEAADGFAEVFPQHKYNVVEILQO
RGYLVAMTQGVNDAPSLKKADTCIAVEGSDAARSADIVFLAPGLGAIIDALKTSR
QIFHRMYAVYVRIALSIHLEIFLGLHIALNLSRLNLELVFFTAIFADVATLAIYDN
APVTSQTVKNLPLKMGMSVLLGVLAGVTWITVTMYAAGENGIVQNGFNDSDEVLV
LQMSLNTDLIFITRANGPEWSSPSQLSGAIFLVDLATCFITWGFHFSHTSIVA
VVRWIFPSFGIFCMGGVYVILQDSVGFNDLHMGKSPKGNQKRSLEDFVVSILQVST
QHEKSO"
       1298..1355
         /note="H+ ATPase cds intron A"
       1356..1562
         /number=2
       1563..1686
         /note="H+ ATPase cds intron B"
       1687..1820

introns
exons
introns
exons

```

```

/number=3
1821..1884
/note="H+ ATPase cds intron C"
1885..4079
/number=4
4080..4146
/note="H+ ATPase cds intron D"
4147..>4193
/note="plasma membrane H+ ATPase"
/number=5
BASE COUNT      943 a   1470 c   1143 g   1228 t
ORIGIN      51 bp upstream of faq1 site.

Query Match      5.9%; Score 18; DB 8; Length 4784;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 200 tggtaaacactctcgggg 217
      |||||
Db 2850 TGGTCAACCTCCTCGGG 2833

RESULT 38
NEUATPASE/c
LOCUS      NEUATPASE      5359 bp      DNA      linear      PLN 12-AUG-1994
DEFINITION N.crassa plasma membrane ATPase gene, complete cds.
ACCESSION M14085 M23211 M23212
VERSION M14085.1 GI:168760
KEYWORDS ATPase.
SOURCE N.crassa (strain 74-OR23-1A) DNA (library of R.Geever and N.Niles),
clones pKH[4,5,14]; cDNA to mRNA (library of M.Sachs and
U.Rajbhandary), clones S1[7,10,18].
ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.
REFERENCE 1 (bases 1 to 5359)
AUTHORS Hager,K.M., Mandala,S.M., Davenport,J.W., Speicher,D.W.,
Benz,E.J.,Jr. and Slayman,C.W.
TITLE Amino acid sequence of the plasma membrane ATPase of Neurospora
crassa: Deduction from genomic and cDNA sequences
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 83, 7693-7697 (1986)
MEDLINE 87017015
REFERENCE 2 (sites)
AUTHORS Aaronson,L.R., Hager,K.M., Davenport,J.W., Mandala,S.M., Chang,A.,
Speicher,D.W. and Slayman,C.W.
TITLE Biosynthesis of the plasma membrane H+-ATPase of Neurospora crassa
JOURNAL J. Biol. Chem. 263, 14552-14558 (1988)
MEDLINE 89008310
COMMENT Draft entry and computer-readable sequence for [1] kindly provided
by K.M.Hager, 05-JAN-1987.
FEATURES
     source
       1..5359
         /organism="Neurospora crassa"
         /db_xref="taxon:5141"
         963..969
           /note="homologue; putative"
           /citation=[2]
       991..997
         /note="homologue; putative"
         /citation=[2]
       1008..1012
         /note="homologue; putative"
         /citation=[2]
       1102..1108
         /note="homologue; putative"
         /citation=[2]
       1120..1124
         /note="homologue; putative"
         /citation=[2]
       1138..1142
         /note="homologue; putative"
         /citation=[2]

```

```
CAAT_signal 1168..1173
              /note="homologue; putative"
              /citation=[2]
              (1191..1199)..1199
              /note="ATPase mRNAs"
              /number=1
prim_transcript 1192..4562
                /note="ATPase mRNA (alt.)"
prim_transcript 1192..4563
                /note="ATPase mRNA (alt.)"
prim_transcript 1192..4564
                /note="ATPase mRNA (alt.)"
prim_transcript 1192..4561
                /note="ATPase mRNA (alt.)"
prim_transcript 1193..4562
                /note="ATPase mRNA (alt.)"
prim_transcript 1193..4561
                /note="ATPase mRNA (alt.)"
prim_transcript 1193..4564
                /note="ATPase mRNA (alt.)"
prim_transcript 1193..4563
                /note="ATPase mRNA (alt.)"
prim_transcript 1194..4564
                /note="ATPase mRNA (alt.)"
prim_transcript 1194..4563
                /note="ATPase mRNA (alt.)"
prim_transcript 1194..4562
                /note="ATPase mRNA (alt.)"
prim_transcript 1195..4564
                /note="ATPase mRNA (alt.)"
prim_transcript 1195..4563
                /note="ATPase mRNA (alt.)"
prim_transcript 1195..4562
                /note="ATPase mRNA (alt.)"
prim_transcript 1195..4561
                /note="ATPase mRNA (alt.)"
prim_transcript 1196..4564
                /note="ATPase mRNA (alt.)"
prim_transcript 1196..4563
                /note="ATPase mRNA (alt.)"
prim_transcript 1196..4562
                /note="ATPase mRNA (alt.)"
prim_transcript 1196..4561
                /note="ATPase mRNA (alt.)"
prim_transcript 1197..4564
                /note="ATPase mRNA (alt.)"
prim_transcript 1197..4563
                /note="ATPase mRNA (alt.)"
prim_transcript 1197..4562
                /note="ATPase mRNA (alt.)"
prim_transcript 1197..4561
                /note="ATPase mRNA (alt.)"
prim_transcript 1198..4564
                /note="ATPase mRNA (alt.)"
prim_transcript 1198..4563
                /note="ATPase mRNA (alt.)"
prim_transcript 1198..4562
                /note="ATPase mRNA (alt.)"
prim_transcript 1198..4561
                /note="ATPase mRNA (alt.)"
prim_transcript 1199..4564
                /note="ATPase mRNA (alt.)"
prim_transcript 1199..4563
                /note="ATPase mRNA (alt.)"
prim_transcript 1199..4562
                /note="ATPase mRNA (alt.)"
prim_transcript 1199..4561
                /note="ATPase mRNA (alt.)"
TATA_signal 1202..1209
              /note="homologue; putative"
              /citation=[2]
```

```
CDS
join(1247..1426,1485..1691,1816..1949,2014..4208,
4276..4322)
/note="plasma membrane ATPase"
/codon_start=1
/protein_id="AAA33561.1"
/db_xref="GI:168761"
/translat="MADHSASGAPALSTNIESGKFDKAAEAAAYOPKPKVEDEDED
IDALIEDSHDGHDAEEBEATPGGRVVPEDMLQTDTRVGLTSEVQRRKYGVL
NOMKEENHFLKFLGFFVGPFOFVMEGAVALAAGLDWDFGVCGLLLNNAVGGV
OEFAQSIVDELAKTLAKAVLRDGTLEIEAPVVPDILQVEEGTIIPADGRIVT
DDAFLQWDQTEALGESLAVONHRGDQVFASAVRGEAFVITAGDNTTFVGRAAALV
NAASGGSGHFEVLNGTIGTILLIIVFTLLIVWSSFSRNPVQILEFTLAITIGV
PYGLPVAVTTTMAVGRAYLAKKAIQKLSAIESLAGVEILCDKDTGTLTKNLSLHD
PVTAVGVDPEDMLTACLAASRRKKGIDAKFLKSLKYIPRAKSVLSKYKVLQFHP
FDPVSKVAVAVESPOGERITCVKGAPLFVLKTVEDDHPPEEVQDAYKKNVAFETR
GFRSLGVARKRGSGSWEILGIMPCMDPPRHDYTKVCEAKTLGLSKMLTGDAVGTA
ETSRQLGLGNTIYNAERLGLGGDDMPGSEVDFVEAADGFAEVFQHKNTNVVEILOO
RGYLVAMTGDVNDAPSLKADTGIAGVSSDAASADIVFLAPGLGAIIDALKTSR
QIPHRVAYVYVYRIALSIHLEIFGLWIAILNRSNLIELVFFAIPADVATLAIYDN
APYSQTPKWNLPKLMGMSVLLGVLAAGTWITVTMYAQGGGIVQNGFNMDEVLF
LOISLTENWLIIFITRANGPFWSSITPSMQLSGAIFLVDILATCFTINGWFEHSDTSIVA
VVRIMFSGFICIMGVYVYLQDSVGFDMHMGKSPKGNQKORSLEDFFVSLQRYST
OHEKSQ"
<1247..1426
/note="plasma membrane ATPase, (EC 3.6.1.35)"
/number=1
1427..1484
/note="ATPase intron A"
1485..1691
/number=2
1692..1815
/note="ATPase intron B"
1816..1949
/number=3
1950..2013
/note="ATPase intron C"
2014..4208
/number=4
4209..4275
/note="ATPase intron D"
4276..(4561,4564)
/note="alternative last exons"
/number=5
4545..4550
/note="homologue; putative"
/citation=[2]
4563..4568
/note="homologue; putative"
/citation=[2]
4648..4653
/note="homologue; putative"
/citation=[2]
BASE COUNT 1095 a 1629 c 1272 g 1363 t
ORIGIN      1 bp upstream of EcoRI site.

Query Match      5.9%  Score 18;  DB 8;  Length 5359;
Best Local Similarity 100.0%;  Pred. No. 1.4e+02;
Matches 18;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy  200  tggtaacctctctcgggg 217
      |||||
Db   2979  TGGTCAACCTCCTCGGGG 2962

RESULT 39
HALCAPNS/c      HALCAPNS      6813 bp  RNA  linear  VRL 27-APR-1995
LOCUS           Human astrovirus type 1 genes for capsid protein and nonstructural
DEFINITION
protein.
ACCESSION      225771
VERSION        225771.1  GI:410445
KEYWORDS       capsid protein; nonstructural protein.
```

LCYQLLAANFAEDHPFKVYVVEHCLSRATAQLRDSGLPARLTEEQHLRIHNRGGPKKCD	86. .2839	exon
/number=1	2824. .4380	exon
/number=2	4373. 6733	CDS
/function="structural"	/citation=[2]	
/codon_start=1	/product="capsid precursor protein"	
/protein_id="CAA81032.1"	/db_xref="GI:410446"	
/db_xref="SPTREMBL:O12792"	/translation="MASKSNKQVTEVNSGRSKSRQSGRDKSKVKITVNSNR	
RARQPGDKRQSSQRYRNIYKQLRKGYTGPKPAICORATATLCTVGSNTSGTSEI	EACILLNPVLVKDATGSTQFGVQALGAQYSMKALKYLVKLTSHWGASAVNCTSVS	
SLNPPTTSTWSGLGARKHLDVTGKNATFFKLKPSDLGGPRDKHMLTWNDAQSD	LPQSEIHTLGRITMSSYKNEQFTGGLFLVELASEMCFYGAANPLNVLNVKSTDNAD	
VTFGSAGSLIMNVPEGSFHTVLAARSTPTTLARAGERTTSDTVQVQVLTAVSAA	ELVTPPENLVLKGMVFKLIAGTRTRTGRSFYVYPSQDALSNNKPAALCTGTPGCM	
RTNPVTTLQFTOMNOPSLGHGEAPAFGRSYPAPGEEFKVVLTFCAPMSPNANKQ	TWVKNPLDAPSGHYNVKIAKDVDHYLTMOGFTSIASVDVYTIDQFSEAPAIQGLQV	
LVNSKKRDAIVAIKQFVTAQTQNNKHQVTSFLVKYVTGFGQVNNYLSFYFRASATGAT	TNLLVGRGTITAGISYTOGGWYLLTNSIVDGASGHYGSEDNTEYLDAPSDQFKEIDTDDIE	
HLIMPPESTQCYEMLTSPRSASGHGYESDNTEYLDAPSDQFKEIDTDDIE	TSDEDEADREFIIDTSEDENETDRVTLTSLTVNQGMTTRATRIARRAFPTLSDR	
IKRGVYMDLLVSGASPGNAWSHACAEARKAAGEINPCTSGSRGHAE"	BASE COUNT 2039 a 1496 c 1559 g 1719 t	
ORIGIN		
Query Match 5.9%; Score 18; DB 14; Length 6813;		
Best Local Similarity 100.0%; Pred. No. 1.4e+02;		
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY 165 caagatccctcattccacat 182		
Db 1664 CAAGATCCTCATTCCACAT 1647		
RESULT 40		
U67544		
LOCUS	10003 bp DNA linear BCT 28-JAN-1998	
DEFINITION	Methanococcus jannaschii section 86 of 150 of the complete genome.	
ACCESSION	U67544 L77117	
VERSION	U67544.1 GI:1591671	
KEYWORDS		
SOURCE	Methanococcus jannaschii.	
ORGANISM	Methanococcus jannaschii	
	Archaea: Euryarchaeota; Methanococci; Methanococcales;	
	Methanococcaceae; Methanococcus.	
REFERENCE	1 (bases 1 to 10003)	
AUTHORS	Bult,C.J., White,O., Olsen,G.J., Zhou,L., Fleischmann,R.D.,	
	Sutton,G.G., Blake,J.A., FitzGerald,L.M., Clayton,R.A.,	
	Gocayne,J.D., Kerlavage,A.R., Dougherty,B.A., Tomb,J., Adams,M.D.,	
	Reich,C.J., Overbeek,R., Kirkness,E.F., Weinstock,K.G.,	
	Merrick,J.M., Glodek,A., Scott,J.D., Geoghegan,N.S., Weidman,J.F.,	
	Fuhrmann,J.L., Nguyen,D.T., Utterback,T., Kelley,J.M.,	
	Peterson,J.D., Sadow,P.W., Hanna,M.C., Cotton,M.D., Hurst,M.A.,	
	Roberts,K.M., Kaine,B.B., Borodovsky,M., Klenk,H.P., Fraser,C.M.,	
	Smith,H.O., Weese,C.R. and Venter,J.C.	
TITLE	Complete genome sequence of the methanogenic archaeon,	
	Methanococcus jannaschii	
JOURNAL	Science 273 (5278), 1058-1073 (1996)	
MEDLINE	96337999	
REFERENCE	2 (bases 1 to 10003)	
AUTHORS	Bult,C.J., White,O., Olsen,G.J., Zhou,L., Fleischmann,R.D.,	
	Sutton,G.G., Blake,J.A., FitzGerald,L.M., Clayton,R.A.,	
	Gocayne,J.D., Kerlavage,A.R., Dougherty,B.A., Tomb,J., F.	
	Adams,M.D., Reich,C.I., Overbeek,R., Kirkness,E.F., Weinstock,K.G.,	
	Merrick,J.M., Glodek,A., Scott,J.D., Geoghegan,N.S., Weidman,J.F.,	
	Fuhrmann,J.L., Nguyen,D.T., Utterback,T., Kelley,J.M.,	

Peterson, J.D., Sadow, P.W., Hanna, M.C., Cotton, M.D., Hurst, M.A., Roberts, K.M., Kaine, B.B., Borodovsky, M., Klenk, H.P., Fraser, C.M., Smith, H.O., Woese, C.R. and Venter, J.C.
 Direct Submission
 Submitted (27-AUG-1996) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA
 On Oct 3, 1996 this sequence version replaced gi:1564047.
 Location/Qualifiers
 1..10003
 /organism="Methanococcus jannaschii"
 /db_xref="taxon:2190"
 complement(59..817)
 /gene="MJ1012"
 complement(59..817)
 /gene="MJ1012"
 /note="similar to PID:633995 percent identity: 68.80;
 identified by sequence similarity; putative"
 /codon_start=1
 /transl_table=11
 /product="phosphate specific transport complex component (pstB)"
 /protein_id="AAB99016.1"
 /db_xref="GI:1591672"
 /translation="MTKVKETKLNWLYGEKQALFDINLPYENKNTALIGPFGCGK
 STFKLRNLNDLPNRIEVEVLGDKNIYDKDQVYELKRRVGMVFPQNPFPMSI
 YDNVAFGRINGIKDKELDKIVEMALKKAALMDVDELRKNAISLQSGQOORLCIA
 RAIAVKEPVLMDPEPTSLADPISLTKIEELMVELAKDQYTIIVVTHNQQAQSRVSDYTA
 FFLMGKLIETFEQTOIFLNPQKKTDDYISGRFC"
 complement(848..1693)
 /gene="MJ1013"
 complement(848..1693)
 /gene="MJ1013"
 /note="similar to GB:L42023 SP:P45190 PID:1007425
 PID:1221519 PID:1205616 percent identity: 36.16;
 identified by sequence similarity; putative"
 /codon_start=1
 /transl_table=11
 /product="phosphate transport system permease protein A (pstA)"
 /protein_id="AAB99017.1"
 /db_xref="GI:1591673"
 /translation="MSPKIKHTIRMKDKIFLFTVGALTLLAILPLFHIISIVKGL
 PIIMERGLTEFTLSSGGIGPAIVGLTLMFTLTLGLPLAFAGAYATEFNSFIG
 RAYKMLQMLEPFTLLVGLVGMGLVPMPTGSALAGALALILTPYVAVTEEAM
 AEPVKYKEGALGCTRAQVIFVKITMKAGKILGITLIGMAKAGETAPLFTAGG
 LYEYVTPNPEPGAIPLLIYTLVQSPSIEDHQMAGALVMLIIFLAIFVPIRYALK
 DDIKL"
 complement(1680..2627)
 /gene="MJ1014"
 complement(1680..2627)
 /gene="MJ1014"
 /note="similar to GB:L42023 SP:P45191 PID:1007427
 PID:1221520 PID:1205617 percent identity: 38.25;
 identified by sequence similarity; putative"
 /codon_start=1
 /transl_table=11
 /product="phosphate transport system permease protein C (pstC)"
 /protein_id="AAB99018.1"
 /db_xref="GI:1591674"
 /translation="MKTWEIKLLRKIDEKIITLPAIFVFFILVILGIFYFNALP
 AIERYGIDLFTWNAKAEPAKEVIGLAAPISYITATVIALPLALPISYIAFVN
 AIAPKRLKPLVISIDMAGLPTIYINGAFILVPLLRDHIMKFLYHFSPLEFDY
 PPLSGYCLSLGLTMTVTPFAAIIIRAYAMIPSYKEGLVALGATRYETTKVLIK
 YIRPAISGLILAFGRALGETAVSLVIGNSFNLYTKLPAGVTISSLIANQFGNAVL
 YEYTSVLVSAGLVLFVIGLVVNIIGIYYLKRREHVS"
 complement(2792..3961)
 /gene="MJ1015"
 complement(2792..3961)
 /gene="MJ1015"
 /note="similar to GB:L10328 SP:P06128 GB:K01992 GB:M24254
 PID:147256 percent identity: 37.79; identified by sequence
 similarity; putative"

/codon_start=1
 /transl_table=11
 /product="periplasmic phosphate-binding protein (psts)"
 /protein_id="AAB99019.1"
 /db_xref="GI:1591675"
 /translation="MNDTQPTKGDVKKILALILGLCLIVPVISTAGCVGGNSQPS
 NNEKPSIIIRTGATFPKYQIQKWIEDYOKTHPNVKIEYEGGSGGQGAFAKGLTD
 IGRDPPVKESMKKFLSTQDQLOPPEIVGAVVTYNIPEIGDKTLKLSRDYLAIDF
 LGKIEYDDEIRINKINPEIADKLHEKIIIVHVRSDASGTTAIFTVLISLISKWAERK
 GAGKTVNPDITNIGRVAGVGVVAIVKSTPTVYATLSVAIEQKLPAALLENKN
 GKFKVNTDETIIKASAVKASIPNPTGEYKEDLKOMLDAPGDNAYPIVATHLLVME
 NKNKHSPEKAKAIKDELTWLTTEGOKPEHLAPGYGLPEDVAKIGLVNAYNMIRE"
 4192..5076
 /gene="MJ1016"
 4192..5076
 /gene="MJ1016"
 /note="hypothetical protein; identified by GeneMark;
 putative"
 /codon_start=1
 /transl_table=11
 /product="M. jannaschii predicted coding region MJ1016"
 /protein_id="AAB99022.1"
 /db_xref="GI:1499857"
 /translation="MEFSEWTKNKRKLNNLEELKRDIIQFEKKNALDEGIVVMASGG
 KDSSTAIALADGLNIEYLIHFYHMSWDVSKMYEKLKSKFDIPVFNITDELLK
 RTGKAGSSICRICKNIMDKDAVDISKEGIRIIMTGDSSALEKVSQVAMVYLRDVG
 VYKNMELTPVPOKYSKGDKEVLEFRPLRLACEDVLIKMDYNIETIERAHEVGDKI
 GFHRECCLOYADENALLNEKLFNELYKYNKIATEYAKKHGPRASIKLPSKKIMVVPK
 KDEYITLIKNALRDVDES"
 5066..5677
 /gene="MJ1017"
 5066..5677
 /gene="MJ1017"
 /note="hypothetical protein; identified by GeneMark;
 putative"
 /codon_start=1
 /transl_table=11
 /product="M. jannaschii predicted coding region MJ1017"
 /protein_id="AAB99023.1"
 /db_xref="GI:1499858"
 /translation="MKVYRVGGITGIFLIFLILLILLIILATVALPIFLILMAIFGG
 YILUKTKISFFRKVYNNIRKKIKIEDTSTNGEVKINFAKRIEIDGKIETNNITL
 LDYDENTKSFAYLLKNIGAEFRDDGIYFKGYKIYPIFKKSYPIEIIISLRYPENIDA
 VVLGLGEYDPKFLYLIKPEFLKDRMSISELKRFEIGDMVLK"
 complement(5684..7258)
 /gene="MJ1018"
 complement(5684..7258)
 /gene="MJ1018"
 /note="similar to GB:L09228 SP:P35136 PID:1146196
 PID:410116 GB:AL009126 percent identity: 42.02; identified
 by sequence similarity; putative"
 /codon_start=1
 /transl_table=11
 /product="phosphoglycerate dehydrogenase (serA)"
 /protein_id="AAB99020.1"
 /db_xref="GI:1591676"
 /translation="MVKILVTDPLHEDATKILEEVEGEVATGLTKEELELEKIDKADV
 LVVRSGTKVTRDVIKAEKLVIGRAGVGDNDVEATEKGIIVVNPADASSISVAE
 LTNGLMLAARNIPQATSLKRGEDRRKRFKGLIYKGLVIGLGRICQGVKRAKA
 FMNIGIDPYIPKEVAESMGVELVDIDNELCKRADFTLHVPLTPTRTHRIIGREQIA
 LMKNAIIVNCARGGLIDKALYKELKEGIRAAALDVFEPEEPKDNPLLTLDNVI
 PHQGSTAEQAAGTIVAEQIKVLRGELAEVNMNPNIPQKLGKLPYMLAEML
 GTRIMOVGLSYNVRVELIYSGELAKETDLIKRAFLKLLPILLAGILNVAIPIAK
 NNNINVESTSEEKYNAIKTAESDKKFSIVGAIINNKPVILEVDGEYVSFTPEG
 VLAIKHIDRPGTIGRVCITLGDYGINIASMQVGRKEPGESVMLNLDHTVPEEVIE
 KIREIPNIDKDAVINL"
 7391..8455
 /gene="MJ1019"
 7391..8455
 /gene="MJ1019"
 /note="similar to GB:M59757 SP:P25993 PID:143389
 GB:AL009126 percent identity: 48.55; identified by
 sequence similarity; putative"


```
/gene="pabAB"
/codon_start=1
/transl_table=11
/product="PABA synthase"
/protein_id="CAC22117.1"
/db_xref="GI:12231159"
/translation="MRTLLVDNYDSFTYNYLFHLYLSRANGREPEVIRNDDPANRPLGLLD
AFDNVLSPGGTGPHRPADEGLCAIAEGRGLPVGLGHLGHQMALAIGARVGRAPPE
RHGTSVVRHDTGCLGCLQPLEVRYHSLAVTELPPELEATWSGEGVLMALRHRT
LPLGVDFHPESICTDGRLLANFRDLTERHGTRHGGRAHGTCLPPAPARETKAT
TCTPRRLRVIAKSLPTWDAEVAFDLSLFTGDPHFDLSDSRPGGELGQLSNMGDASGP
LARTAKADVHGTVTVRADGASSTVESAFLTWLENDLAGLTETPEVLPFAFAGWCC
LGYELKEDCDGAHRSPDPDAVLVFADRALVLDRHTRTYLLALVEDDAEAEARWL
AASATLDVAGREPEPCPEAPVCTGPELHRDRDGLYLKLDVCCQEIAGETIYEV
LTNMAEDTLTPAAVYALRVSPAPFAAFDFGPMVILSSSEPRFLRIDRHGVMES
KPIKGTTPRGATPOEDAALVRALATCEKDRDAENMIVDLVRHDLGRGAEVGSVADPV
FOVETATYHOLVSTVTLARLSDSSPVAARAAFPGGSMTCAPKIRTMQIIDRLEGCP
RGVYSGAIGYFSLGAVDLSIVITVVLSCGLRVYGGVAVIALSDPADEFEEATAVKA
APLRLUDTATFPFGREAGKDLGDPDGDGTGAGKDLVLPG"
20829..21836
/gene="canRA"
/contig="canRA"
/contig_start=1
/transl_table=11
/product="ABC-transporter"
/protein_id="CAC22118.1"
/db_xref="GI:12231160"
/translation="MNGHLPLPAPLPAPGVSAAAGSDLMIEAEGVSKAYGTVTHALDSV
SLAVPRGVGLGHLNGAGKTLVDILTALPTPSGRARVAGYVDADVPVIRRRIGL
TCQFASVDAQSLGVDNVLVLIARLLGARRAARVRARELLELFRLETVADRASSVSGG
LRRRLDLAVSLGAEVFLDPEPTGLDPSRIINLWEIVGLVEGQTVLLTTOYLEE
ADRLADRIAVLSGAEVAGTAPELKVATGVRRTYLLTLETGEDVSAARTALRGAGFAP
VDGEARTVVVPIDATRAEITADITRSLDQAGVASELNFCEPTLDVVLTALDQAAGRT
A"
21970..22776
/gene="canRB"
/contig="canRB"
/contig_start=1
/transl_table=11
/product="ABC-transporter"
/protein_id="CAC22119.1"
/db_xref="GI:12231161"
/translation="MPRAAVPAFCGSSILFTQIRVLTGRSLPAMVTDPGIVLFLGLIOP
VYILVLTQVFSKMGKMPHFPGVSLDYLVLPVLDVNAQSAQSGVGLVEDOKNGI
VARLSLVPHPGALLAARSLVGLRSVQVAVIMALMTVLYGSPNGAAELALSAGL
TLFTISLGMAFIAAGAWLRRRAEPLQNLALIVIFPLMFASAYVVPADVPLWLGAVAS
VNPLTYAIDATRALADVPGLDHAIPVAVICAVIATVAVGMIAAVRGFRRLP"
BASE COUNT 5144 a 14526 c 14888 g 4756 t
ORIGIN

Query Match 5.9%; Score 18; DB 1; Length 39314;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 127 gccacgcagcagcagc 144
IIIIIIIIIIIIIIIIII
Db 33915 GCCACGCCACGCGAGCAC 33932

RESULT 42
AC102135
LOCUS AC102135 71769 bp DNA linear HTG 23-NOV-2001
DEFINITION Mus musculus clone RP23-253J5, LOW-PASS SEQUENCE SAMPLING.
ACCESSION AC102135
VERSION AC102135.1 GI:17061221
KEYWORDS HTG; HTGS_PHASE0.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
```

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS

1 (bases 1 to 71769)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Mus musculus, clone RP23-253J5
Unpublished
2 (bases 1 to 71769)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Boguslavskiy,L., Boukhgalter,B.,
Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
Choepe,I., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,
Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
Hagos,B., Heaford,A., Horton,L., Hulle,W., Iliev,I., Johnson,R.,
Jones,C., Kamat,A., Karatas,A., Kells,C., Labrecque,K.,
Lamarez,R., Landers,T., Lenocksky,J., Levine,R., Liu,G.,
MacLean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C.,
McCarthy,M., McSwan,P., McKernan,K., McPheeters,R., Melorin,J.,
Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C.,
Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D.,
Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schuback,R.,
Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

TITLE
JOURNAL
COMMENT

Direct Submission
Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit,A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L18082
Center clone name: 253_J5

* NOTE: This record contains 87 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

* 1 701: contig of 701 bp in length
* 702 801: gap of 100 bp
* 802 1529: contig of 728 bp in length
* 1530 1629: gap of 100 bp
* 1630 2343: contig of 714 bp in length
* 2344 2443: gap of 100 bp
* 2444 3201: contig of 758 bp in length
* 3202 3301: gap of 100 bp
* 3302 3970: contig of 669 bp in length
* 3971 4070: gap of 100 bp
* 4071 4787: contig of 717 bp in length
* 4788 4887: gap of 100 bp
* 4888 5594: contig of 707 bp in length
* 5595 5694: gap of 100 bp
* 5695 6413: contig of 719 bp in length
* 6414 6513: gap of 100 bp
* 6514 7265: contig of 752 bp in length
* 7266 7365: gap of 100 bp
* 7366 8102: contig of 737 bp in length
* 8103 8202: gap of 100 bp

```
* 8203 8933: contig of 731 bp in length
* 8934 9033: gap of 100 bp
* 9034 9760: contig of 727 bp in length
* 9761 9860: gap of 100 bp
* 9861 10545: contig of 685 bp in length
* 10546 10645: gap of 100 bp
* 10646 11375: contig of 730 bp in length
* 11376 11475: gap of 100 bp
* 11476 12221: contig of 746 bp in length
* 12222 12321: gap of 100 bp
* 12322 13056: contig of 735 bp in length
* 13057 13156: gap of 100 bp
* 13157 13876: contig of 720 bp in length
* 13877 13976: gap of 100 bp
* 13977 14720: contig of 744 bp in length
* 14721 14820: gap of 100 bp
* 14821 15539: contig of 719 bp in length
* 15540 15639: gap of 100 bp
* 15640 16379: contig of 740 bp in length
* 16380 16479: gap of 100 bp
* 16480 17219: contig of 740 bp in length
* 17220 17319: gap of 100 bp
* 17320 18054: contig of 735 bp in length
* 18055 18154: gap of 100 bp
* 18155 18884: contig of 730 bp in length
* 18885 18984: gap of 100 bp
* 18985 19709: contig of 725 bp in length
* 19710 19809: gap of 100 bp
* 19810 20511: contig of 702 bp in length
* 20512 20611: gap of 100 bp
* 20612 21342: contig of 731 bp in length
* 21343 21442: gap of 100 bp
* 21443 22186: contig of 744 bp in length
* 22187 22286: gap of 100 bp
* 22287 22981: contig of 695 bp in length
* 22982 23081: gap of 100 bp
* 23082 23815: contig of 734 bp in length
* 23816 23915: gap of 100 bp
* 23916 24643: contig of 728 bp in length
* 24644 24743: gap of 100 bp
* 24744 25454: contig of 711 bp in length
* 25455 25554: gap of 100 bp
* 25555 26295: contig of 741 bp in length
* 26296 26395: gap of 100 bp
* 26396 27140: contig of 745 bp in length
* 27141 27240: gap of 100 bp
* 27241 27982: contig of 742 bp in length
* 27983 28082: gap of 100 bp
* 28083 28811: contig of 729 bp in length
* 28812 28911: gap of 100 bp
* 28912 29631: contig of 720 bp in length
* 29632 29731: gap of 100 bp
* 29732 30452: contig of 721 bp in length
* 30453 30552: gap of 100 bp
* 30553 31286: contig of 734 bp in length
* 31287 31386: gap of 100 bp
* 31387 32106: contig of 720 bp in length
* 32107 32206: gap of 100 bp
* 32207 32941: contig of 735 bp in length
* 32942 33041: gap of 100 bp
* 33042 33780: contig of 739 bp in length
* 33781 33880: gap of 100 bp
* 33881 34629: contig of 749 bp in length
* 34630 34729: gap of 100 bp
* 34730 35477: contig of 748 bp in length
* 35478 35577: gap of 100 bp
* 35578 36309: contig of 732 bp in length
* 36310 36409: gap of 100 bp
* 36410 37112: contig of 703 bp in length
* 37113 37212: gap of 100 bp
* 37213 37940: contig of 728 bp in length
* 37941 38040: gap of 100 bp
* 38041 38741: contig of 701 bp in length
```

```
* 38742 38841: gap of 100 bp
* 38842 39549: contig of 708 bp in length
* 39550 39649: gap of 100 bp
* 39650 40336: contig of 687 bp in length
* 40337 40436: gap of 100 bp
* 40437 41137: contig of 701 bp in length
* 41138 41237: gap of 100 bp
* 41238 41971: contig of 734 bp in length
* 41972 42071: gap of 100 bp
* 42072 42787: contig of 716 bp in length
* 42788 42887: gap of 100 bp
* 42888 43615: contig of 728 bp in length
* 43616 43715: gap of 100 bp
* 43716 44446: contig of 731 bp in length
* 44447 44546: gap of 100 bp
* 44547 45294: contig of 748 bp in length
* 45295 45394: gap of 100 bp
* 45395 46114: contig of 720 bp in length
* 46115 46214: gap of 100 bp
* 46215 46944: contig of 730 bp in length
* 46945 47044: gap of 100 bp
* 47045 47781: contig of 737 bp in length
* 47782 47881: gap of 100 bp
* 47882 48604: contig of 723 bp in length
* 48605 48704: gap of 100 bp
* 48705 49432: contig of 728 bp in length
* 49433 49532: gap of 100 bp
* 49533 50250: contig of 718 bp in length
* 50251 50350: gap of 100 bp
* 50351 51079: contig of 729 bp in length
* 51080 51179: gap of 100 bp
* 51180 51920: contig of 741 bp in length
* 51921 52020: gap of 100 bp
* 52021 52750: contig of 730 bp in length
* 52751 52850: gap of 100 bp
* 52851 53581: contig of 731 bp in length
* 53582 53681: gap of 100 bp
* 53682 54413: contig of 732 bp in length
* 54414 54513: gap of 100 bp
* 54514 55213: contig of 700 bp in length
* 55214 55313: gap of 100 bp
* 55314 56064: contig of 751 bp in length
* 56065 56164: gap of 100 bp
* 56165 56894: contig of 730 bp in length
* 56895 56994: gap of 100 bp
```

Query Match 5.9%; Score 18; DB 2; Length 71769;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 177 tcacatcggaaccacct 194

|||||

Db 36239 TCACATCGGCAACCACT 36256

RESULT 43

AC060793/c 74586 bp DNA linear HTG 20-APR-2000

LOCUS Homo sapiens chromosome 2 clone -2012A7 map 2, LOW-PASS SEQUENCE

DEFINITION

AC060793

VERSION AC060793.1 GI:7622457

KEYWORDS HTG; HTGS_PHASE0.

SOURCE human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 74586)

Birren,B., Linton,L., Nusbaum,C. and Lander,E.

Unpublished

REFERENCE 2 (bases 1 to 74586)

Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,

Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F.,
 Boguslavsky, L., Boukhalter, B., Brown, A., Burkett, G.,
 Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S.,
 Collymore, A., Cooke, P., DeArelano, K., Dewar, K., Diaz, J.S.,
 Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D.,
 Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,
 Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L.,
 Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,
 Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczkzy, J.,
 Levine, R., Liu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N.,
 McArthur, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R.,
 Meldrum, J., Menues, L., Mihova, T., Miranda, C., Mienga, V., Morrow, J.,
 Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,
 O'Neill, D., Oliver, T.M., Oliver, J., Peterson, K., Plier, N.,
 Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,
 Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,
 Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
 Testaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J.,
 Vassiliev, H., Vieler, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,
 Young, G., Zainoun, J., Zimmer, A. and Zody, M.

TITLE

JOURNAL

COMMENT

Submitted (20-APR-2000) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: http://www.seq.wi.mit.edu

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L9522

Center clone name: 2012_A_7

* NOTE: This record contains 94 individual
 * sequencing reads that have not been assembled into
 * contigs. Runs of N are used to separate the reads
 * and the order in which they appear is completely
 * arbitrary. Low-pass sequence sampling is useful for
 * identifying clones that may be gene-rich and allows
 * overlap relationships among clones to be deduced.
 * However, it should not be assumed that this clone
 * will be sequenced to completion. In the event that
 * the record is updated, the accession number will
 * be preserved.

1 671: contig of 671 bp in length
 * 672 771: gap of 100 bp
 * 772 1477: contig of 706 bp in length
 * 1478 1577: gap of 100 bp
 * 1578 2278: contig of 701 bp in length
 * 2279 2378: gap of 100 bp
 * 2379 3059: contig of 681 bp in length
 * 3060 3159: gap of 100 bp
 * 3160 3846: contig of 687 bp in length
 * 3847 3946: gap of 100 bp
 * 3947 4639: contig of 693 bp in length
 * 4640 4739: gap of 100 bp
 * 4740 5429: contig of 690 bp in length
 * 5430 5529: gap of 100 bp
 * 5530 6229: contig of 700 bp in length
 * 6230 6329: gap of 100 bp
 * 6330 7022: contig of 693 bp in length
 * 7023 7122: gap of 100 bp
 * 7123 7817: contig of 695 bp in length
 * 7818 7917: gap of 100 bp
 * 7918 8596: contig of 679 bp in length
 * 8597 8696: gap of 100 bp
 * 8697 9406: contig of 710 bp in length
 * 9407 9506: gap of 100 bp
 * 9507 10199: contig of 693 bp in length
 * 10200 10299: gap of 100 bp
 * 10300 10987: contig of 688 bp in length

* 10988 11087: gap of 100 bp
 * 11088 11778: contig of 691 bp in length
 * 11779 11878: gap of 100 bp
 * 11879 12585: contig of 707 bp in length
 * 12586 12685: gap of 100 bp
 * 12686 13384: contig of 699 bp in length
 * 13385 13484: gap of 100 bp
 * 13485 14191: contig of 707 bp in length
 * 14192 14291: gap of 100 bp
 * 14292 15000: contig of 709 bp in length
 * 15001 15100: gap of 100 bp
 * 15101 15787: contig of 687 bp in length
 * 15788 15887: gap of 100 bp
 * 15888 16572: contig of 685 bp in length
 * 16573 16672: gap of 100 bp
 * 16673 17368: contig of 696 bp in length
 * 17369 17468: gap of 100 bp
 * 17469 18171: contig of 703 bp in length
 * 18172 18271: gap of 100 bp
 * 18272 18948: contig of 677 bp in length
 * 18949 19048: gap of 100 bp
 * 19049 19738: contig of 690 bp in length
 * 19739 19838: gap of 100 bp
 * 19839 20545: contig of 707 bp in length
 * 20546 20645: gap of 100 bp
 * 20646 21327: contig of 682 bp in length
 * 21328 21427: gap of 100 bp
 * 21428 22121: contig of 694 bp in length
 * 22122 22221: gap of 100 bp
 * 22222 22927: contig of 706 bp in length
 * 22928 23027: gap of 100 bp
 * 23028 23725: contig of 698 bp in length
 * 23726 23825: gap of 100 bp
 * 23826 24513: contig of 688 bp in length
 * 24514 24613: gap of 100 bp
 * 24614 25307: contig of 694 bp in length
 * 25308 25407: gap of 100 bp
 * 25408 26138: contig of 731 bp in length
 * 26139 26238: gap of 100 bp
 * 26239 26924: contig of 686 bp in length
 * 26925 27024: gap of 100 bp
 * 27025 27718: contig of 694 bp in length
 * 27719 27818: gap of 100 bp
 * 27819 28524: contig of 706 bp in length
 * 28525 28624: gap of 100 bp
 * 28625 29319: contig of 695 bp in length
 * 29320 29419: gap of 100 bp
 * 29420 30108: contig of 689 bp in length
 * 30109 30208: gap of 100 bp
 * 30209 30904: contig of 696 bp in length
 * 30905 31004: gap of 100 bp
 * 31005 31693: contig of 689 bp in length
 * 31694 31793: gap of 100 bp
 * 31794 32509: contig of 716 bp in length
 * 32510 32609: gap of 100 bp
 * 32610 33280: contig of 671 bp in length
 * 33281 33380: gap of 100 bp
 * 33381 34080: contig of 700 bp in length
 * 34081 34180: gap of 100 bp
 * 34181 34878: contig of 698 bp in length
 * 34879 34978: gap of 100 bp
 * 34979 35665: contig of 687 bp in length
 * 35666 35765: gap of 100 bp
 * 35766 36470: contig of 705 bp in length
 * 36471 36570: gap of 100 bp
 * 36571 37268: contig of 698 bp in length
 * 37269 37368: gap of 100 bp
 * 37369 38060: contig of 692 bp in length
 * 38061 38160: gap of 100 bp
 * 38161 38848: contig of 688 bp in length
 * 38849 38948: gap of 100 bp
 * 38949 39627: contig of 679 bp in length
 * 39628 39727: gap of 100 bp

39728 40420: contig of 693 bp in length
* 40421 40520: gap of 100 bp
* 40521 41224: contig of 704 bp in length
* 41225 41324: gap of 100 bp
* 41325 42023: contig of 699 bp in length
* 42024 42123: gap of 100 bp
* 42124 42817: contig of 694 bp in length
* 42818 42917: gap of 100 bp
* 42918 43605: contig of 688 bp in length
* 43606 43705: gap of 100 bp
* 43706 44382: contig of 677 bp in length
* 44383 44482: gap of 100 bp
* 44483 45194: contig of 712 bp in length
* 45195 45294: gap of 100 bp
* 45295 45973: contig of 679 bp in length
* 45974 46073: gap of 100 bp
* 46074 46777: contig of 704 bp in length
* 46778 46877: gap of 100 bp
* 46878 47579: contig of 702 bp in length
* 47580 47679: gap of 100 bp
* 47680 48371: contig of 692 bp in length
* 48372 48471: gap of 100 bp
* 48472 49173: contig of 702 bp in length
* 49174 49273: gap of 100 bp
* 49274 49966: contig of 693 bp in length
* 49967 50066: gap of 100 bp
* 50067 50762: contig of 696 bp in length
* 50763 50862: gap of 100 bp
* 50863 51550: contig of 688 bp in length
* 51551 51650: gap of 100 bp
* 51651 52351: contig of 701 bp in length
* 52352 52451: gap of 100 bp
* 52452 53143: contig of 692 bp in length
* 53144 53243: gap of 100 bp
* 53244 53932: contig of 689 bp in length
* 53933 54032: gap of 100 bp
* 54033 54748: contig of 716 bp in length
* 54749 54848: gap of 100 bp

Query Match 5.9% Score 18; DB 2; Length 74586;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 255 ggagttctgcaagtacgg 272
|||||
DB 3179 GGAGTTCTGCAAGTACGG 3162

RESULT 44

NCBI
LOCUS Neurospora crassa DNA linkage group II BAC clone B1D1
DEFINITION Neurospora crassa DNA linkage group II BAC clone B1D1
ACCESSION AL355927
VERSION AL355927.1 GI:7800790
KEYWORDS
SOURCE Neurospora crassa
ORGANISM Neurospora crassa

REFERENCE 1 (sites) Neurospora crassa

2 (bases 1 to 76072) Neurospora crassa

3 (sites) Neurospora crassa

4 (sites) Neurospora crassa

5 (sites) Neurospora crassa

6 (sites) Neurospora crassa

7 (sites) Neurospora crassa

8 (sites) Neurospora crassa

9 (sites) Neurospora crassa

10 (sites) Neurospora crassa

11 (sites) Neurospora crassa

12 (sites) Neurospora crassa

13 (sites) Neurospora crassa

14 (sites) Neurospora crassa

15 (sites) Neurospora crassa

16 (sites) Neurospora crassa

17 (sites) Neurospora crassa

18 (sites) Neurospora crassa

19 (sites) Neurospora crassa

20 (sites) Neurospora crassa

21 (sites) Neurospora crassa

22 (sites) Neurospora crassa

23 (sites) Neurospora crassa

24 (sites) Neurospora crassa

25 (sites) Neurospora crassa

Stock Center, <http://www.fgsc.net>
Sequencing was performed by MWG Biotech AG, Ebersberg, Germany,
<http://www.mwgna.com>
Information on performance of analysis and a more detailed
annotation of this entry and other sequences of linkage groups II
and V can be viewed at: <http://mips.gsf.de/proj/neurospora>.
Location/Qualifiers
1. 76072
/organism="Neurospora crassa"
/db_xref="taxon:5141"
/chromosome="6"
360. 752
/gene="B1D1.010"
Join(360..513.631..752)
/gene="B1D1.010"
/note="contains EST gb:AI329523"
/codon_start=1
/product="putative protein"
/protein_id="CAD11428.1"
/db_xref="GI:16944430"
/translation="MEASGIAQVFAQSPKASVFAEQYLCPPRLRLVMFCFVRME
NGYILAPWQASRSIGPLNSPQTVPLPSRSRLSGTHVSRVATLYCT"
360..513
/gene="B1D1.010"
/number=1
514..630
/gene="B1D1.010"
/number=1
631..752
/gene="B1D1.010"
/number=2
3428..5684
/gene="B1D1.040"
complement(join(3428..4703,4796..4866,5068..5137,
5235..5258,5659..5684))
/gene="B1D1.040"
complement(join(3428..4703,4796..4866,5068..5137,
5235..5258,5659..5684))
/gene="B1D1.040"
/note="similarity to gene:cg4953, drosophila melanogaster,
TREMBL:AE003628.11"
/codon_start=1
/product="conserved hypothetical protein"
/protein_id="CAD11429.1"
/db_xref="GI:16944431"
/translation="MLHRLFSRNSFKMIRRDVSLPACQSPKLKLGPHFKLPNNH
QRPSPHEVKEPHSVSLKRLSRSLVPQPLHPVIPPSPILSPITSPALPQPHL
PPLASLAYSPLGP IKKHGDAHEAGTGERTRDGYNTERTPLSPVNLPPSPGSA
YVGETFSCITCANHNAPPIGEGTGVKKTIRDVK IEAEMQTFSGOTTKLVLGDTGDD
NAGSGSTANADNDNVITGNSAGGDSNNATEKTETETVATLDLLPSTLTQILN
FGLKEETHVLGVTVSYEATETSGTRAFKMYQFICKPQSLIVRTKAGPLSLPPVK
AGNKKRRRWLEAQLENCSEDAILLKLAQAEVORGLKWRDCNWAGIGVGQGESE
MTGEGISQQSDSQSGPPRRPPLQPGSEQLCFIIEKGGEGCDREDEQEGEAEFE
EKNRIDFGYMLAWRTMGNRGSLLTLKLTGTHKVKPR"
360..513
/gene="B1D1.040"
/number=1
complement(4704..4795)
/gene="B1D1.040"
/number=1
complement(4796..4866)
/gene="B1D1.040"
/number=2
complement(4867..5067)
/gene="B1D1.040"
/number=2
complement(5068..5137)
/gene="B1D1.040"
/number=3
complement(5138..5234)
/gene="B1D1.040"
/number=3
complement(5235..5258)
/gene="B1D1.040"

```
/gene="B1D1.040"
/number=4
complement(5259..5658)
/gene="B1D1.040"
/number=4
complement(5659..5684)
/gene="B1D1.040"
/number=5
complement(join(6034..6057,6110..6329,6380..7032,
7086..7250,7312..7364,7429..7450,7632..7849,7911..8127))
/gene="B1D1.050"
complement(join(6034..6057,6110..6329,6380..7032,
7086..7250,7312..7364,7429..7450,7632..7849,7911..8127))
/gene="B1D1.050"
note="similarity to hypothetical protein SPAC30D11.14,
Schizosaccharomyces pombe, PIR:562572"
/codon_start=1
/product="conserved hypothetical protein"
/protein_id="CAB11430.1"
/db_xref="GI:16944432"
/translation="MDAERRAKSRFDQTEPEPKRVSRFDRRSPPARKSDSGRD
RDSPLSKPRDSATPSTPKPAVDPAAPAAAAAARQAOLQARKGIQHVDPVPRVRSAGT
REGSVANINGEMYSIDGDFIKDIEVNDLRNRYLLTKGSTOKMIKDETGAADVTRGSY
YDPKSAKPANPLPLYLHVTSTTKEGLEKRAVAKIEEMKQELPOLVDERPRRRQEQV
ERDEYGRRKPEERIPINLEVPVGNLRAQVVGCGAYVKHQQQTGCKVOIKGRGSG
YTEASTGRESDDMLHVAGPDPKVKVEKAKELCEDLMENYKQYEEFKSRPPRQYNGP
ROYRDREPRGDSYHGRCYNNNNNNHHHGHGHHDHSHSSYTNPSAPGPGP
SVAPPTPTAAATTDYAAQYTAQYTGGAATDPYAAAGADPYAAYGYQAYVOLYQO
WYAAQAGQVTPAAATGVPGAGSASPPPTTEAAPPPPPSSAAPPPPPPCAPP
GMSGGYSAVPPPPGL"
complement(6034..6057)
/gene="B1D1.050"
/number=1
6034..8127
/gene="B1D1.050"
complement(6058..6109)
/gene="B1D1.050"
/number=1
complement(6110..6329)
/gene="B1D1.050"
/number=2
complement(6330..6379)
/gene="B1D1.050"
/number=2
complement(6380..7032)
/gene="B1D1.050"
/number=3
complement(7033..7085)
/gene="B1D1.050"
/number=3
complement(7086..7250)
/gene="B1D1.050"
/number=4
complement(7251..7311)
/gene="B1D1.050"
/number=4
complement(7312..7364)
/gene="B1D1.050"
/number=5
complement(7365..7428)
/gene="B1D1.050"
/number=5
complement(7429..7450)
/gene="B1D1.050"
/number=6
complement(7451..7631)
/gene="B1D1.050"
/number=6
complement(7632..7849)
/gene="B1D1.050"
/number=7
complement(7850..7910)
/gene="B1D1.050"
```

```
exon
exon
gene
CDS
intron
Query Match 5.9%; Score 18; DB 8; Length 76072;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 200 tggccaacctctcctcgagg 217
|||||
Db 43595 TGGTCAACCTCTCGGGG 43612
|||||
RESULT 45
ALI36378/c
LOCUS
DEFINITION Human DNA sequence from clone RP5-870F10 on chromosome
1q42.11-42.3, complete sequence.
ACCESSION ALI36378
VERSION ALI36378.13 GI:16973784
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 84481)
Brown.J.
Direct Submission
Submitted (16-NOV-2001) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk
On Nov 17, 2001 this sequence version replaced gi:16580164.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
```

abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chrl> RP5-870F10 is from the library RPCI-5 constructed by the group of pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm> VECTOR: pCVPAC2

IMPORTANT: This sequence is not the entire insert of clone RP5-870F10. It may be shorter because we sequence overlapping sections only once, except for a short overlap. The true right end of clone RP5-870F10 is at 84481 in this sequence. The true right end of clone RP4-566D2 is at 2000 in this sequence.

FEATURES
source

Location/Qualifiers
1..84481
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
/map="q42.11-42.3"
/clone="RP5-870F10"
/clone_lib="RPCI-5"
BASE COUNT 21334 a 20549 c 21075 g 21523 t
ORIGIN

Query Match 5.9%; Score 18; DB 9; Length 84481;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 ggctgacactggggagag 22
|||||
Db 51196 GGCTGCACCTGGGGAGAG 51179

Search completed: July 15, 2002, 23:25:30
Job time: 24383 sec

TITLE Pediatric Leukemia cDNA Sequencing Project
JOURNAL Unpublished (2000)
COMMENT Contact: Dr. Judith F. Margolin
Texas Children's Cancer Center and Human Genome Sequencing Center
at Baylor College of Medicine
1102 Bates, MC3-3320 Houston, TX 77030, USA
Tel: 832-824-4536
Fax: 832-825-4038
Email: clones@ccc.org
Citation: Carninci, P. and Hayashizaki, Y. High efficiency
full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Seq primer: M13 primer

FEATURES source
1. .348
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="TCBAP6345"
/clone_lib="Pediatric pre-B cell acute lymphoblastic
leukemia Baylor-HGSC project-TCBA"
/sex="male"
/tissue_type="leukopheresis"
/cell_type="pre-B cell"
/dev_stage="pediatric 2 years"
/lab_host="DH10B"
/note="Vector: lambda PSB: Site_1: BamHI; Site_2: EcoRI;
First strand cDNA was primed with an anchored
XhoI-oligo(dT) primer [5'GGAGACTCGAGCGCGGAGGAGG(7)VN
3'; V-A-C-G; N-A-C-G-T] and then dg tailed. Second strand
was primed with a BamHI-dc primer
15'AGAGAGCTCGGATCGCGCGCAATAATAAT(C) 3'].
Double-stranded cDNA was then digested with BamHI and XhoI
and directionally cloned into the BamHI and SalI sites of
lambda PSB vector. Library went through one round of
normalization. Library was constructed by Wei Yu at RIKEN
of Japan (Carninci P, Westover A, Nishiyama Y, Ohsumi T,
Itoh M, Nagasaki S, Sasakini, Okazaki Y, Muramatsu M,
Schneider C, Hayashizaki Y, High efficiency selection of
full-length cDNA by improved biotinylated cap trapper.,
DNA Res 4: 1, 61-6, Feb 28, 1997)"
BASE COUNT 74 a 105 c 107 g 60 t 2 others
ORIGIN

Query Match 5.1%; Score 209; DB 10; Length 348;
Best Local Similarity 100.0%; Pred. No. 1.8e-82;
Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 302 gtgttgctgtgcacgaggtacatgccaacgacacagcagcagctactgtctactacaag 361
|||||
DB 109 GTGTTGCTGCTGCACGAGGTACATGCCAACGACACAGCGAGCTAGCTCTGCTACTACAAG 168
QY 362 tacatcaagcacgcatcagagggaccacgcccgcagctctactgttctgtgagagac 421
|||||
DB 169 TACATCAAGGCACGATCAGGAGGCACCGCGCGCAGCTCCTAGCTGTCTGAGAGAC 228
QY 422 tttagcagccattcatcaacagcctgacacgctcttgggtcaacaggaagcagccatg 481
|||||
DB 229 TTTGACGACCCATTTCATCAACAGCTGACACGCTCTTGGTCAACAGGAGACGCCCATG 288
QY 482 tgggtgccctgtgtgtgtccatccccgg 510
|||||
DB 289 TGGTGCCCTGTCTGTGTGCCATCCCGG 317

RESULT 6
BM172350 598 bp mRNA linear EST 04-DEC-2001
LOCUS imageqc.4_2001/smu279bdf41.x1 NIH_MGC_97 Homo sapiens cDNA clone
DEFINITION IMAGE:4830201 5', mRNA sequence.
ACCESSION BM172350
VERSION BM172350.1 GI:17311913
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS 1 (bases 1 to 598)
Kale, P. I., Harsch, T. J., Folta, P. A., Nelson, D. O., Sanders, C. G. and
Prange, C. K.
TITLE The I.M.A.G.E. Consortium quality control effort: clone
resequencing for verification
JOURNAL Unpublished (2001)
COMMENT Other_ESTs: BG717758
Contact: Prange CK
The I.M.A.G.E. Consortium
Lawrence Livermore National Laboratory
Livermore, CA, USA
Email: help@image.llnl.gov
This read has been verified (found to hit its original self in the
correct orientation), as part of the I.M.A.G.E. Consortium quality
control effort. High quality sequence is defined as having 100 or
more base pairs with a phred quality value of 20 or greater, where
a sliding window of 4 base pairs with a phred quality value of 15
or greater marks the beginning and end of the sequence. For
information on obtaining this clone, please contact
info@image.llnl.gov.

Plate: L1AM10750 row: p column: 10
Seq primer: -21ml3
High quality sequence stop: 598.
FEATURES source
1. .598
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4830201"
/clone_lib="NIH_MGC_97"
/lab_host="DH10B"
/note="Organ: testis; Vector: pBluescriptR (modified
pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtc9ag
); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTVN-3',
size-selected for average insert size 2.2 kb and
normalized to ROT 5. This is a primary library enriched
for full-length clones and constructed using the
Cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NIMH/NHGRI, National
Institutes of Health). Note: this is a NIH_MGC Library."

BASE COUNT 114 a 196 c 197 g 90 t 1 others
ORIGIN
Query Match 5.0%; Score 206; DB 10; Length 598;
Best Local Similarity 99.6%; Pred. No. 4.2e-81;
Matches 256; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ccacgcgacgcccgcgagatgcacgcccgcgcgcgtgtgcctgcgaactggcctcg 60
DB 66 CCACGCGCAGCGCCGCGAGATGCACGCGGCGCGCGCTGTCCCTGCCACTGTGGCTCTG 125
QY 61 cctgggactcctggacgcccgtggtgagtggtactccatgacccccgcaccttgaacat 120
DB 126 CCTGGACTTCTGGACGGCCTGGTGAGTGGCTACTCCATGACCCCCGACCTTGAACAT 185
QY 121 cacggaggagtcacacgtcatcgacacccggtgacagcctgtccatctcctgcaggggaca 180
DB 186 CACGGAGGAGTCACACGTCATCGACACCGGTGACAGCGCTGTCCATCTCTCTCAGGGGACA 245
QY 181 gaccccccctcagtggtgcttggccagagatcaggagcgccagccaccgagagaagga 240
DB 246 GCACCCCTCGAGTGGGCTTGGCCAGGAGCTCAGGAGGCGCCGACGCCACCGGAGACAAGGA 305
QY 241 cagcgaggacacggsgg 257
DB 306 CAGCGAGGACACGGGGG 322

RESULT 7
AA367842

Qy	2721	ttcatatcggaacaccactcaactcagctggtccaacctcttcctggggcgctgcaccaaacgccagg	2780
Db	181	TTCATACGGCAACCACCTCAACGCTGGTCAACCTCCCTCGGGCGGTGCCAACAGCCGCAGG	240
RESULT	8		
A1696515			
LOCUS		555 bp mRNA linear EST 16-DEC-1999	
DEFINITION		tx51f02.xl NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273115 3'	
		similar to gb:X68203 TYROSINE-PROTEIN KINASE RECEPTOR FLTA	
		PRECURSOR (HUMAN); mRNA sequence.	
ACCESSION		A1696515	
VERSION		A1696515.1 GI:4984415	
KEYWORDS		EST.	
SOURCE		human.	
ORGANISM		Homo sapiens	
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
AUTHORS		1 (bases 1 to 555)	
TITLE		NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.	
JOURNAL		National Cancer Institute, Cancer Genome Anatomy Project (CGAP),	
COMMENT		Tumor Gene Index Unpublished (1997) Contact: Robert Strausberg, Ph.D. Email: rcapbs-r@mail.nih.gov Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.lnlni.gov/dbfp/image/image.html Insert length: 675 Std Error: 0.00 Seq primer: -400P from Gibco High quality sequence stop: 320.	
FEATURES		Location/Qualifiers	
source		1..555	
		/organism="Homo sapiens"	
		/db_xref="taxon:9606"	
		/clone="IMAGE:2273115"	
		/clone_lib="NCI_CGAP_Lu24"	
		/tissue_type="carcinoid"	
		/lab_host="DH108"	
		/note="Organ: lung; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI_CGAP_Lu5 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1414920-1417991 and 1520904-1522439). Subtraction by Bento Soares and M. Fatima Bonaldo."	
BASE COUNT		159 a 130 c 148 g 111 t	
ORIGIN		7 others	
Query Match		4.5%; Score 184; DB 9; Length 555;	
Best Local Similarity		100.0%; Pred. No. 2.9e-71;	
Matches 184; Conservative		0; Mismatches 0; Indels 0; Gaps 0;	
Qy	3729	ccgggtgcttgccagagggtcgagaccgttggtctctccagatgaagacatttcagg	3788
Db	1	CCGGGTGCCCTGGCAGAGGGCGTGAGACCGCTGGTTCTCCAGATTGAAGACATTTGAGG	60
Qy	3789	aattccccatgaccccaacgacctacaaggctctgtgacacaccagacagctggga	3848
Db	61	AATTCCCCATGACCCCNACGACCTACAAGGCTCTGTGGACAACACAGACAGTGGGA	120
Qy	3849	tgggtcgtggcctcgaggagttttagcacatagagagcgagcatacacagaagcggct	3908
Db	121	TGTCGTGGCTCGAGGACTTTGACATACAGAGCAGGCTATACACAGAAGAGCGCT	180

Qy 3909 tcag 3912
||||
Db 181 TCAG 184

RESULT 9

AWB72408
LOCUS
DEFINITION
h191g10.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3009378 3' similar to gb:X68203 TYROSINE-PROTEIN KINASE RECEPTOR FLT4
PRECURSORS (HUMAN): mRNA sequence.
AWB72408
ACCESSION
VERSION
KEYWORDS
SOURCE
EST.
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 591)
AUTHORS
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), National Cancer Index
JOURNAL
COMMENT
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL, send email to: info@image.lnl.gov
Info@image.lnl.gov

Seq primer: -40UP from Gibco
High quality sequence stop: 428.
Location/Qualifiers

FEATURES source

1..591
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3009378"
/clone_lib="NCI_CGAP_Lu24"
/tissue_type="carcinoid"
/lab_host="DH10B"
/note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI_CGAP_Lu5 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1414920-1417991 and 1520904-1522439). Subtraction by Bento Soares and M. Fatima Bonaldo."
BASE COUNT 162 a 146 c 166 g 117 t
ORIGIN

Query Match 4.5%; Score 184; DB 9; Length 591;
Best Local Similarity 100.0%; Pred. No. 3e-71;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3729 ccgggtgctgcccagagggtgagaccgctgtgtccctccaggatgaagacatttgagg 3788
Db 1 CCGGGTGCCTGGCCAGAGGGGCTGACACCCGTGTTCTCCAGGATGAAGACATTGAGG 60
Qy 3789 aattccccatgaccccaagacctacaaggctctgtggacacacagacagctggga 3848
Db 61 AATTCCCCATGACCCCAAGACCTACAAGAGGCTCTGTGGACCAACACAGACAGCTGGGA 120
Qy 3849 tggctgtgctcgaggaggtttgagcagatagagcaggcatagacagaagacggct 3908
Db 121 TGGTGTGCTGCGAGGAGTGTGACCATAGACAGACAGGCGCATAGACAAGAAAGCGGCT 180

Qy 3909 tcag 3912
||||
Db 181 TCAG 184

RESULT 10

BE245906
LOCUS
DEFINITION
TCBAP1D3468 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project-TCBA Homo sapiens cDNA clone TCBAP3468, mRNA sequence.
BE245906
ACCESSION
VERSION
KEYWORDS
SOURCE
EST.
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 365)
AUTHORS
Wei,Y., Tsang,Y.T.M., Mei,G., Ku,J.M., Ali-Osman Jr.,F.R., Muzny,D., Bouck,J., Gibbs,R.A. and Margolin,J.F.
TITLE
JOURNAL
COMMENT
Pediatric Leukemia cDNA Sequencing Project Unpublished (2000)
Contact: Dr. Judith F. Margolin
Texas Children's Cancer Center and Human Genome Sequencing Center at Baylor College of Medicine
1102 Bates, MC3-3320 Houston, TX 77030, USA
Tel: 832-824-4536
Fax: 832-825-4038
Email: clones@tccc.org
Citation: Carninci, P. and Hayashizaki, Y. High efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Seq primer: M13 primer.
Location/Qualifiers

FEATURES source

1..365
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="TCBAP3468"
/clone_lib="Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project-TCBA"
/sex="male"
/tissue_type="leukopheresis"
/cell_type="pre-B cell"
/dev_stage="pediatric 2 years"
/lab_host="DH10B"
/note="Vector: lambda PSB; Site_1: BamHI; Site_2: EcoRI; First strand cDNA was primed with an anchored XhoI-oligo(dT) primer [5'GGAGACTCGAGCGCCGAGGAG(T)VN 3'; V=A,C,G; N=A,C,G,T] and then dg tailed. Second strand was primed with a BamHI-dc primer [5'AGAGCTCGGATCGCGCGCGCAATATAAT(C) 3']. Double-stranded cDNA was then digested with BamHI and XhoI and directionally cloned into the BamHI and SalI sites of lambda PSB vector. Library was constructed by Wei Yu at RIKEN of Japan [Carninci P, Westover A, Nishiyama Y, Ohsumi T, Itoh M, Nagaoka S, Sasakini, Okazaki Y, Muramatsu M, Schneider C, Hayashizaki Y, High efficiency selection of full-length cDNA by improved biotinylated cap trapper.. DNA Res 4: 1, 61-6, Feb 28, 1997]."
BASE COUNT 78 a 107 c 112 g 68 t
ORIGIN

Query Match 3.6%; Score 148; DB 10; Length 365;
Best Local Similarity 99.5%; Pred. No. 3.6e-55;
Matches 198; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 343 ctacgtctgctactacaagtcacacagcagcatcagggcaccacgcccagctc 402
Db 149 CTACGCTCTGCTACTACAAGTACATCAAGGCACGCATCGAGGGCCACCGCGCCGCGAGCTC 208
Qy 403 ctacgtgttcgtgagactttgagcagcattcatcatcaacagcctgacagcgtctgtgt 462

```

|||||
Db 209 ATACGTGTCGTGAGAGACTTTGACGACCCATTATCAACAAGCCTGACAGCCTCTTGCT 268
Qy 463 caacaggaagacgcacatgtgggtgccctgtgtgtgtccatccccgcctcaatgtcac 522
|||||
Db 269 CAACAGGAAGACGCATGTGGTGCCTGTCTGTGTGTCCATCCCGGCCTCAATGTCCAC 328
Qy 523 gctgcgtcgcaaaactcg 541
Db 329 GCTGCGCTCGCAAGACTCG 347

RESULT 11
AA223868
LOCUS
DEFINITION
  AA223868 344 bp mRNA linear EST 11-MAR-1998
  cDNA clone IMAGE:551143 5' similar to gb:X68203 TYROSINE-PROTEIN
  KINASE RECEPTOR FLT4 PRECURSOR (HUMAN); mRNA sequence.
ACCESSION
  AA223868
VERSION
  AA223868.1 GI:1844453
KEYWORDS
  EST.
SOURCE
  human.
ORGANISM
  Homo sapiens
REFERENCE
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS
  Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
  Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin
  J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
  White,Y., Wyllie,T., Waterston,R. and Wilson,R.
  WashU-NCI Human EST Project
  Unpublished (1997)
  Contact: Wilson RK
  Washington University School of Medicine
  444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
  Tel: 314 286 1800
  Fax: 314 286 1810
  Email: est@watson.wustl.edu
  This clone is available royalty-free through LLNL; contact the
  IMAGE Consortium (info@image.llnl.gov) for further information.
  Insert Length: 1275 Std Error: 0.00
  Seq primer: -28ml3 rev1 ET from Amersham
  High quality sequence stop: 238.
  Location/Qualifiers
    1..344
      /organism="Homo sapiens"
      /db_xref="GDB:5588193"
      /db_xref="taxon:9606"
      /clone="IMAGE:551143"
      /dev_stage="Ntera-2 neuroepithelial cells"
      /issue_type="neuroepithelial cells"
      /lab_host="SOLR (kanamycin resistant)"
      /note="Organ: brain; Vector: pBluescript SK-; Site:1:
      EcoRI; Site:2: XhoI; Cloned unidirectionally. Primer:
      Oligo dt. Uninduced, exponentially growing neuroepithelial
      cells (Ntera-2/cl.D1). Average insert size: 1.0 kb;
      Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGCAGCAG
      3' -3' adaptor sequence: 5' CTCGACTTTTTTTTTTTT 3'"
BASE COUNT 65 a 92 c 115 g 56 t 6 others
ORIGIN
  Query Match 3.5%; Score 143; DB 9; Length 344;
  Best Local Similarity 100.0%; Pred. No. 6.2e-53;
  Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

|||||
Qy 3257 tggatggccctgaagcatcttcgacaggtgtacaccacgagtgacgtgtgtgcc 3316
|||||
Db 1 TGCATGGCCCTCGAAAGCATCTTCGACAAGGTGTACACACGACGAGTGACGTGTGTC 60
Qy 3317 ttgggggtctctctgggagatctctctctgggggctccccgtacccctggggtgcag 3376
|||||

```

```

Db 61 TTTGGGTGCTTCTCTGGGAGATCTTCTCTCTGGGGCCCTCCCGTACCCCTGGGGTCAG 120
Qy 3377 atcaatgaggagttctgccagcg 3399
|||||
Db 121 ATCAATGAGGAGTTCTGCCAGCG 143

RESULT 12
T28462
LOCUS
DEFINITION
  T28462 411 bp mRNA linear EST 06-SEP-1995
  Kinase receptor FLT4, class III (HT:1601), mRNA sequence.
ACCESSION
  T28462
VERSION
  T28462.1 GI:610560
KEYWORDS
  EST.
SOURCE
  human.
ORGANISM
  Homo sapiens
REFERENCE
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS
  Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult
  C.J., Lee,N., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White
  O., Sutton,G., Blake,J.A., Brandon,R.C., Chiu,M.-W., Clayton,R.A.,
  Cline,R.T., Cotton,M.D., Earle-Hughes,J., Fine,L.D., FitzGerald
  L.M., FitzHugh,W.M., Fritchman,J.L., Geoghagen,N.S.M., Glodek,A.,
  Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinklejr,P.S., Kelley,J.M.,
  Klinek,K.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
  Moreno-Palancas,R.F., McDonald,L.A., Nguyen,D.T., Pellegrino,S.M.,
  Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
  Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
  Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.-J.,
  Dimke,D., Feng,P., Ferrie,A., Fischer,C., Hastings,G.A., He,W.-W.,
  Hu,J.-S., Greene,J.M., Gruber,J., Hudson,P., Kim,A., Kozak,D.L.,
  Kunsch,C., Ji,H., Li,H., Meissner,P.S., Olsen,H., Raymond,L., Wei
  M.R., Wing,J., Xu,C., Yu,G.-L., Ruben,S.M., Dillon,P.J., Fannon
  Venter,J.C.
  Initial Assessment of Human Gene Diversity and Expression Patterns
  Based Upon 83 Million Basepairs of cDNA Sequence
  Nature 377, 3-174 (1995)
  96026280
  Contact: Venter, JC
  The Institute for Genomic Research
  932 Clopper Rd, Gaithersburg, MD 20878
  Tel: 3018699056
  Fax: 3018699423
  Email: tdbinfo@tdb.tigr.org
  For clone availability, additional sequence and expression
  information related to this EST, please contact the TIGR database
  (tdbinfo@tdb.tigr.org)
  Seq primer: M13 Reverse.
  Location/Qualifiers
    source
      1..411
        /organism="Homo sapiens"
        /db_xref="ATCC (inhost):102639"
        /db_xref="taxon:9606"
        /clone.lib="Human kidney"
        /note="Organ: kidney"
BASE COUNT 123 a 87 c 110 g 86 t 5 others
ORIGIN
  Query Match 3.2%; Score 133; DB 10; Length 411;
  Best Local Similarity 100.0%; Pred. No. 1.9e-48;
  Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

|||||
Qy 3780 catttggaattccccatgacccccacgacctacaaggtctgtggacaacacagacag 3839
|||||
Db 1 CATTTGAGGAATTCCTCCATGACCCCAACGACCTACAAAGGCTCTGTGTGACAACACAGAC 60
Qy 3840 acagtggaatgggtgctggcctcgaggaggtttgagcagatagagagcagcagacag 3899
|||||
Db 61 ACATGGGATGGTCTGCTGGCGCTCGGAGGAGTTTGAGCAGATAGAGAGCAGCATAGACAAG 120

```

QY 3900 aaagcggttcag 3912
|||||
Db 121 AAAGCGCTTCAG 133

RESULT 13
AW950116
LOCUS AW950116 546 bp mRNA linear EST 01-JUN-2000
DEFINITION EST362081 MAGE resequences, MAGA Homo sapiens cDNA, mRNA sequence.
ACCESSION AW950116
VERSION AW950116.1 GI:8139652
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 546)
AUTHORS Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C., Holt
I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and
Quackenbush,J.
TITLE Assessment of gene expression patterns in a model of colon tumor
metastasis using a 19,200 element cDNA microarray
JOURNAL Unpublished (2000)
COMMENT The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
Email: johnq@tigr.org
Plate: 9
Seq primer: Reverse.
Location/Qualifiers
1..546
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="MAGE resequences, MAGA"
/note="Vector: pBluescriptSKm"

BASE COUNT 155 a 125 c 151 g 115 t
ORIGIN

Query Match 3.2%; Score 132; DB 9; Length 546;
Best Local Similarity 100.0%; Pred. No. 5.5e-48;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3781 atttgagggaattccccatgaccccaacgacctacaaaggctctgtggacaaccagacaga 3840
|||||
Db 1 ATTTGAGGAATTCCCATGACCCCAACGACCTACAAAGGCTCTGTGGACAACACACAGA 60

QY 3841 cagtggatgtgctggcctcgaggagtttgagcagatagagcagcagcagacaga 3900
|||||
Db 61 CAGTGGATGTGCTGGCCCTCGGAGGAGTTTGAGCAGATAGAGCAGGCATAGACAAGA 120

QY 3901 aaagcggttcag 3912
|||||
Db 121 AAAGCGCTTCAG 132

RESULT 14
AW950567
LOCUS AW950567 587 bp mRNA linear EST 01-JUN-2000
DEFINITION EST362637 MAGE resequences, MAGA Homo sapiens cDNA, mRNA sequence.
ACCESSION AW950567
VERSION AW950567.1 GI:8140223
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 587)
AUTHORS Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C., Holt
I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and

Quackenbush,J.
Assessment of gene expression patterns in a model of colon tumor
metastasis using a 19,200 element cDNA microarray
Unpublished (2000)
Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
Email: johnq@tigr.org
Plate: 16
Seq primer: Reverse.
Location/Qualifiers
1..587
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="MAGE resequences, MAGA"
/note="Vector: pBluescriptSKm"

BASE COUNT 162 a 150 c 155 g 120 t
ORIGIN

Query Match 3.2%; Score 132; DB 9; Length 587;
Best Local Similarity 100.0%; Pred. No. 5.6e-48;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3781 atttgagggaattccccatgaccccaacgacctacaaaggctctgtggacaaccagacaga 3840
|||||
Db 1 ATTTGAGGAATTCCCATGACCCCAACGACCTACAAAGGCTCTGTGGACAACACACAGA 60

QY 3841 cagtggatgtgctggcctcgaggagtttgagcagatagagcagcagcagacaga 3900
|||||
Db 61 CAGTGGATGTGCTGGCCCTCGGAGGAGTTTGAGCAGATAGAGCAGGCATAGACAAGA 120

QY 3901 aaagcggttcag 3912
|||||
Db 121 AAAGCGCTTCAG 132

RESULT 15
AQ801382/c
LOCUS AQ801382 497 bp DNA linear GSS 09-AUG-1999
DEFINITION HS.5394.AL.E12.T7A.RPCI-11 Human Male BAC Library Homo sapiens
genomic clone Plate-970 Col-23 Row-I, DNA sequence.
ACCESSION AQ801382
VERSION AQ801382.1 GI:5718714
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 497)
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380589
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.bufo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.bufo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Plate: 970 row: 1 column: 23

```

Seq primer: T7
Class: BAC ends
High quality sequence stop: 497.
Location/Qualifiers
Source
1..497
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Plate-970 Col=23 Row=I"
/clone_lib="RPCI-11 Human Male BAC Library"
/sex="male"
/note="Vector: pBACE3.6; Site_1: EcoRI; Site_2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor
and partially digested with a combination of EcoRI and
EcoRI Methylase. Size selected DNA was cloned into the
pBACE3.6 vector at EcoRI sites."
BASE COUNT      90 a   147 c   146 g   110 t      4 others
ORIGIN

Query Match      3.1%; Score 127; DB 12; Length 497;
Best Local Similarity 100.0%; Pred. No. 9.4e-46;
Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3985 ttgagcgggggcccgagagccaggtgttttacacagcagtgatggggagctgcgga 4044
|||||
DB 341 TCAGCGGGGGCCCGAGGAGCCAGGTGTTTACAAACAGCGAGTATGGGAGCTGTCCGA 282

QY 4045 gccagcgaggaggaccactgtcccgctgtcccgctgacgttcttcacagacaacag 4104
|||||
DB 281 GCCAAGCGAGGAGGACCACTGCTCCCGCTGCTCCCGCGCTGACTTTCTTCACAGACAACAG 222

QY 4105 ctactaa 4111
DB 221 CTAATAA 215

RESULT 16
AG038807/c
LOCUS
DEFINITION
Pan troglodytes DNA, clone: PTB-015L14.F, genomic survey sequence.
ACCESSION
AG038807
VERSION
AG038807.1 GI:16567532
KEYWORDS
GSS; GSS (genome survey sequence).
SOURCE
Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
BAC Library clone:PTB-015L14.F.
ORGANISM
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
1 (sites)
Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
Unpublished
2 (bases 1 to 702)
Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Japan
1-7-22 Suehiro-cho,Tsrumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimpbes@sc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
clone tracking errors.
PRIMERS
Sequencing: -21M13
LIBRARY
Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI.
Location/Qualifiers
1..702

```

```

/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="PTB-015L14.F"
/sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
BASE COUNT      146 a   223 c   199 g   131 t      3 others
ORIGIN

Query Match      3.0%; Score 122; DB 12; Length 702;
Best Local Similarity 99.4%; Pred. No. 1.7e-43;
Matches 172; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 832 gcaggcagagcgaggtaagtgggtgccgagcagctccacgacagccacacagaact 891
|||||
DB 351 GCAGGCAGAGCGGGGTAAAGTGGGTGCCCGAGCGAGCTCCCGACGACCCACAGAACT 292

QY 892 ctccagcatcctgaccatccacaacgtcagccagcagcagacctggctcgtatgtgtgcaa 951
|||||
DB 291 CTCGAGCATCTGACCATCCACAACGTCAGCCAGCAGCAGCTGGCTCGTATGTGCGA 232

QY 952 ggcacaacacggcctcagcgatttcgggagagcagcgaggctcattgtgcagt 1004
|||||
DB 231 GGCCAACAACGGCATCCAGCGATTTCGGGAGAGCAGCGAGCTCATTTGTCATG 179

RESULT 17
AA368924/c
LOCUS
DEFINITION
EST80250 Placenta I Homo sapiens cDNA similar to similar to
tyrosine kinase, receptor FLT4, class III, mRNA sequence.
ACCESSION
AA368924
VERSION
AA368924.1 GI:2021242
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 344)
Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Feldner,R.A., Bult
,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White
,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A.,
,Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald
,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodak,A.,
,Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr., Kelley,J.M.,
Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
Moreno-Palancas,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.P., Li,Y.,
Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
Dimke,D., Feng,D.-F., Fertle,A., Fischer,C., Hastings,G.A., He,W.W.,
Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L.,
Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H., Raymond,L.,
Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillon,P.J., Fannon
,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and
Venter,J.C.
Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995)
JOURNAL
MEDLINE
96026280
Other_ESTs: THCI92054
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13-21.

```


RESULT 20
AA368926
LOCUS
DEFINITION
Accession
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
COMMENT
FEATURES
BASE COUNT
ORIGIN
Query Match
Best Local Similarity
Matches
QY 1623
Db 1
QY 1683
Db 61

211 bp mRNA linear EST 21-APR-1997
receptor FL14, class III, mRNA sequence.
AA368926.1 GI:2021244
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 211)
Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult
,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Cocayne,J.D., White
,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A.,
Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., FitzGerald
,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodek,A.,
Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr., Kelley,J.M.,
Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W.,
,Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L.,
Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,H., Raymond,L.,
Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon
,M.R., Rosen,C.A., Haseitine,W.A., Fields,C., Fraser,C.M. and
,Venter,J.C.
Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995)
96026280
Other-ESTs: THC85507
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (<http://www.tigr.org/tdb/hgi/hgi.html>)
Seq primer: M13-21.
Location/Qualifiers
1..211
/organism="Homo sapiens"
/db_xref="ATCC (inhost):173626"
/db_xref="taxon:9606"
/clone_lib="Placenta 1"
/tissue_type="placenta"
/dev_stage="fetus"
/note="Organ: Placenta; Vector: pBluescript SK-; site_1:
EcoRI; Site_2: EcoRI"
46 a 71 c 36 t 4 others

1.9%; Score 79; DB 9; Length 211;
Best Local Similarity 100.0%; Pred. No. 2.6e-24;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1623 tgggtctcaacaagggtggccagatgagcggctcatcttctatgtgaccacatcc 1682
|||||
Db 1 TGGTCTCCACACAGGTGGCCAGATGAGCGGCTCATCTTCTATGTGACCACCATCC 60
QY 1683 ccgacgggttcacatcga 1701
|||||
Db 61 CCGACGGCTTCACCATCGA 79

RESULT 21
BG015039/c
LOCUS
DEFINITION
Accession
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
COMMENT
FEATURES
BASE COUNT
ORIGIN
Query Match
Best Local Similarity
Matches
QY 1537
Db 327
QY 1597
Db 267

327 bp mRNA linear EST 24-JAN-2001
QV2-GN0208-221200-579-g06 GN0208 Homo sapiens cDNA, mRNA sequence.
BG015039
BG015039.1 GI:12466844
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 327)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl1-QV2&t2-QV2-GN0208-221200-579-g06&t3-2000-12-22&t4=1>)
Seq primer: puc 18 forward
High quality sequence stop: 218.
Location/Qualifiers
1..327
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="GN0208"
/dev_stage="Adult"
/note="Organ: placenta_normal; Vector: puc18; site_1: SmaI
; Site_2: SmaI; A mini-library was made by cloning
products derived from ORESTES PCR (U.S. Letters Patent
application No. 196,716 - Ludwig Institute for Cancer
Research) profiles into the pUC 18 vector. Reverse
transcription of tissue mRNA and cDNA amplification were
performed under low stringency conditions."
65 a 84 c 99 g 79 t

1.5%; Score 61; DB 10; Length 327;
Best Local Similarity 100.0%; Pred. No. 3.1e-16;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1537 ctggaccagcttctgtgaggggaagaataagactgtgacagctggtgtccagaatgc 1596
|||||
Db 327 CTGGACCGAGTTTGTGGAGGGAAGAATAGACTGTGACGAGCTGTGTGATCCAGAATGC 268
QY 1597 c 1597
Db 267 C 267

RESULT 22
BG717758
LOCUS
DEFINITION
Accession
VERSION

810 bp mRNA linear EST 08-MAY-2001
602698040F1 NTH_MGC_97 Homo sapiens cDNA clone IMAGE:483201 5',
mRNA sequence.
BG717758
BG717758.1 GI:13996945

```
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 810)
JOURNAL NIH-MGC http://mgc.nci.nih.gov/.
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LAM10750 row: p column: 10
High quality sequence start: 8
High quality sequence stop: 240.
FEATURES
Location/Qualifiers
1..810
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4830201"
/clone_lib="NIH_MGC_97"
/lab_host="DH10B"
/notes="Organ: testis; Vector: pBluescriptR (modified
pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag
); Oligo-dT primed using primer 5'-TTTTTTTTTTTNN-3',
size-selected for average insert size 2.2 kb and
normalized to ROT 5. This is a primary library enriched
for full-length clones and constructed using the
Cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NIH/NHGRI, National
Institutes of Health). Note: this is a NIH_MGC Library."
BASE COUNT 163 a 237 c 252 g 158 t
ORIGIN

Query Match 1.3%; Score 52; DB 10; Length 810;
Rest Local Similarity 100.0%; Pred. No. 3.8e-12;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 35 qgcgtgtcctgcgactgtgctctgctggactcctgaacgctggtga 86
|||||
Db 118 GCGCTGTGCTGCGACTGTGCTGCTGCGACTCTGGACGCGCTGGTCA 169

RESULT 23
AA868172/c
LOCUS
DEFINITION
AA868172 610 bp mRNA linear EST 04-JAN-1999
ak38f09.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1408265
3' similar to gb:X68203 TYROSINE-PROTEIN KINASE RECEPTOR FLT4
PRECURSOR (HUMAN); mRNA sequence.
ACCESSION
AA868172
VERSION
AA868172.1 GI:2963617
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 610)
JOURNAL NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
COMMENT Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo
, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1499 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 400
```

```
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1919 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 417.
FEATURES
Location/Qualifiers
1..610
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1408265"
/clone_lib="Soares_testis_NHT"
/sex="male"
/lab_host="DH10B"
/notes="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech Laboratories
, inc., and primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGGAGCGCGCCCAATTTTTTTTTTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization to Cot5, and was
constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT 133 a 155 c 148 g 174 t
ORIGIN

Query Match 1.2%; Score 50; DB 9; Length 610;
Rest Local Similarity 100.0%; Pred. No. 2.9e-11;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3852 tgcctgcctcggaggagctttgagcagatagagcagcagcagacaaga 3901
|||||
Db 586 TGCTGGCTCGGAGGAGTTTGACAGATAGAGCAGCAGCATACACAGAA 537

RESULT 24
A1553743/c
LOCUS
DEFINITION
A1553743 877 bp mRNA linear EST 12-MAY-1999
tn28c09.x1 NCI-CCAP_Brn25 Homo sapiens cDNA clone IMAGE:2168944 3'
similar to gb:X68203 TYROSINE-PROTEIN KINASE RECEPTOR FLT4
PRECURSOR (HUMAN); contains element MER22 repetitive element ;, mRNA
sequence.
ACCESSION
A1553743
VERSION
A1553743.1 GI:4486106
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 877)
JOURNAL NCI/NINDS-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
COMMENT National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTGP), Tumor Gene Index
Unpublished (1998)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1499 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 400
```

```

FEATURES
  source
    POLYA-No.
      Location/Qualifiers
        1. .877
        /organism="Homo sapiens"
        /db_xref="taxon:9606"
        /clone_image="IMAGE:2168944"
        /clone_lib="NCI CGAP Brn25"
        /tissue_type="anaplastic oligodendroglioma"
        /lab_host="DH10B"
        /note="Organ: Brain; Vector: pT7T3D-Pac (Pharmacia) with a
        modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
        strand cDNA was primed with a Not I - oligo(dT) primer [5',
        TGTTCACCAATCTCAAGTCGACGCGCATAGGTTTCTTTTCTTTTCTTTTCTTTT
        T 3']; double-stranded cDNA was ligated to Eco RI
        adaptors (Pharmacia), digested with Not I and cloned into
        the Not I and Eco RI sites of the modified pT7T3 vector.
        Library is normalized, and was constructed by Bento
        Soares and M.Fatima Bonaldo."
        BASE COUNT 152 a 257 c 260 g 202 t 6 others
        ORIGIN

    Query Match
      Best Local Similarity 1.2%; Score 49; DB 9; Length 877;
      Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

    Oy 3579 cccgcgcagctctcagagctcagaagggcagctctcgcaggtgtc 3627
      |||||||
    Db 741 CCCGCGCAGCTCTCAGAGCTCAGAGGCGCAGCTTCTCGCAGGTGTC 693

  RESULT 25
  CNS054KM/c
  LOCUS
  DEFINITION
    Tetraodon nigroviridis genome survey sequence T3 end of clone
    009L17 of library A from Tetraodon nigroviridis, genomic survey
    sequence.
  AL320863
  VERSION
    AL320863.1 GI:9553747
  KEYWORDS
    GSS; genome survey sequence.
  SOURCE
    Tetraodon nigroviridis.
  ORGANISM
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
    Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
    Tetraodontidae; Tetraodon.
    1 (bases 1 to 1091)
    Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
    Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
    Saurin,W. and Weissenbach,J.
    Estimate of human gene number provided by genome-wide analysis
    using Tetraodon nigroviridis DNA sequence
    Nat. Genet. 25 (2), 235-238 (2000)
    20296633
  TITLE
    2 (bases 1 to 1091)
    Crolius,H.R., Jaillon,O., Dasilva,C., Ozouf-Costaz,C., Fizames,C.,
    Fischer,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W.,
    Bernot,A. and Weissenbach,J.
  AUTHORS
    Characterization and repeat analysis of the compact genome of the
    freshwater pufferfish tetraodon nigroviridis
    Genome Res. 10 (7), 939-949 (2000)
    20359837
  TITLE
    3 (bases 1 to 1091)
    Genoscope.
  JOURNAL
    Direct Submission
  MEDLINE
    Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases
  REFERENCE
    This sequence is a single read and was generated as part of a large
    scale clone-end sequencing project of the Tetraodon nigroviridis
    genome. For more information, please take a look at
    http://www.genoscope.cns.fr/Tetraodon.
  FEATURES
    Location/Qualifiers
      1. .1091
      /organism="Tetraodon nigroviridis"

```

```

/db_xref="taxon:99883"
/clone="009L17"
/clone_lib="A"
/note="Genoscope sequence ID : COAA009CF09A1-end : T3"
BASE COUNT 294 a 228 c 294 g 242 t 33 others
ORIGIN

  Query Match
    Best Local Similarity 0.9%; Score 38; DB 12; Length 1091;
    Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

  Oy 2438 gacatcagacggctacgtctccatcatcatcgaccc 2475
    |||||||
  Db 362 GACATCAAGACGGCTACCTCTCCATCATCATGACCC 325

  RESULT 26
  BB647382
  LOCUS
  DEFINITION
    BB647382 RIKEN full-length enriched, 10 days neonate cerebellum Mus
    musculus cDNA clone B930088118 5', mRNA sequence.
  BB647382
  VERSION
    BB647382.1 GI:16481711
  KEYWORDS
    EST.
  SOURCE
    house mouse.
  ORGANISM
    Mus musculus
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
    1 (bases 1 to 570)
    Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Haru,A.,
    Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda
    ,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,
    Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki
    ,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
    Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
    Muramatsu,M. and Hayashizaki,Y.
    RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
    Unpublished (2001)
  TITLE
    RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
  JOURNAL
    Contact: Yoshihide Hayashizaki
  COMMENT
    Laboratory for Genome Exploration Research Group, RIKEN Genomic
    Sciences Center(GSC), Yokohama Institute
    The Institute of Physical and Chemical Research (RIKEN)
    1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
    Tel: 81-45-503-9222
    Fax: 81-45-503-9216
    Email: genome-res@gsr.riken.go.jp,
    URL:http://genome.gsc.riken.go.jp/
    Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
    ,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
    Normalization and subtraction of cap-trapper-selected cDNAs to
    prepare full-length cDNA libraries for rapid discovery of new
    genes. Genome Res. 10 (10), 1617-1630 (2000)
    wagi,K., Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
    Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
    ,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
    Hayashizaki,Y.
    RIKEN integrated sequence analysis (RISA) system--384-format
    sequencing pipeline with 384 multicapillary sequencer. Genome Res.
    10 (11), 1757-1771 (2000)
    Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
    ,Y. and Hayashizaki,Y.
    Computer-based methods for the mouse full-length cDNA
    encyclopedia: real-time sequence clustering for construction of a
    nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
    Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa
    ,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
    Hayashizaki,Y.
    Computational Analysis of Full-Length Mouse cDNAs Compared with
    Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
    Please visit our web site (http://genome.gsc.riken.go.jp) for
    further details.
    e mouse tissues.

```

Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18

```

/clone_lib=-GNUL34
/dep_stage="Adul1t"

```

/note="Organ: placenta_normal; Vector: puc18; Site_1: SmaI
 : Site_2: SmaI; A mini-library was made by cloning
 products derived from ORESTES PCR (U.S. Letters Patent
 application No. 196,716 - Ludwig Institute for Cancer
 Research) profiles into the pUC 18 vector. Reverse
 transcription of tissue mRNA and cDNA amplification were
 performed under low stringency conditions."
 54 a 48 c 64 g 50 t

Query Match 0.7%; Score 29; DB 10; Length 216;
 Best Local Similarity 100.0%; Pred. No. 0.062;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 900 tcttcacatccacagacagcagcagc 928

Db 47 TCCTGACCATCCACACAGCTGACCCAGCAC 19

RESULT 29
 BG815223
 LOCUS
 DEFINITION
 dec02f10.y1 NICHD XGC Emb2 Xenopus laevis cDNA clone IMAGE:4405795
 5' similar to TR:Q91897 091897 FIBROBLAST GROWTH FACTOR RECEPTOR
 PRECURSOR. ; mRNA sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

REFERENCE
 AUTHORS
 Clifton, S., Johnson, S.L., Blumberg, B., Song, J., Hillier, L., Pape, D.,
 Martin, J., Wylie, T., Underwood, K., Theising, B., Bowers, Y., Person
 , B., Gibbons, M., Harvey, N., Ritter, E., Jackson, Y., McCann, R.,
 Waterston, R. and Willson, R.
 Washu Xenopus EST project, 1999
 Unpublished (1999)
 Contact: Sandy Clifton, Ph.D.
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 Library constructed by Life Technologies. DNA Sequencing by:
 Washington University Genome Sequencing Center
 Clone distribution: Xenopus clones from this library are available
 through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov.

FEATURES
 source
 1. .189
 /organism="Xenopus laevis"
 /db_xref="taxon:8355"
 /clone="IMAGE:4405795"
 /clone_lib="NICHD XGC Emb2"
 /tissue_type="embryo, stage 17/19"
 /lab_host="DH10B (phage-resistant)"
 /note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI;
 Cloned unidirectionally. Primer: Oligo dT. Average insert
 size 2.1 kb. Constructed by Life Technologies."
 49 a 48 c 50 g 42 t

Query Match 0.7%; Score 27; DB 10; Length 189;
 Best Local Similarity 100.0%; Pred. No. 0.47;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3112 aaagtgcacacagacagcctggctgc 3138
 |||||

Db 125 AAAGTCATCCACAGACCTGGCTGC 151

RESULT 30

LOCUS

DEFINITION

RG5656884
 df25g11.y1 Wellcome CRC PRN3 St10 5 Xenopus laevis cDNA clone
 IMAGE:3558357 5' similar to TR:Q91897 091897 FIBROBLAST GROWTH
 FACTOR RECEPTOR PRECURSOR. ; mRNA sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

REFERENCE
 AUTHORS
 Clifton, S., Johnson, S.L., Blumberg, B., Song, J., Hillier, L., Pape, D.,
 Martin, J., Wylie, T., Underwood, K., Theising, B., Bowers, Y., Person
 , B., Gibbons, M., Harvey, N., Ritter, E., Jackson, Y., McCann, R.,
 Waterston, R. and Willson, R.
 Washu Xenopus EST project, 1999
 Unpublished (1999)
 Other ESTs: df25g11.x1
 Contact: Sandy Clifton, Ph.D.
 Washu Xenopus EST project, 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 Library constructed by N. Garrett, P. LeMaire, A.M. Zorn, and J.B.
 Gurdon (Wellcome/CRC Institute). DNA Sequencing by: Washington
 University Genome Sequencing Center
 Clone distribution: Xenopus clones from this library are available
 through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov
 Seq primer: -40RP from Gibco
 High quality sequence stop: 506.

FEATURES
 source
 1. .514
 /organism="Xenopus laevis"
 /db_xref="taxon:8355"
 /clone="IMAGE:3558357"
 /clone_lib="Wellcome CRC PRN3 St10 5"
 /tissue_type="embryo, stage 10.5"
 /lab_host="DH10B (phage-resistant)"
 /note="Vector: pBSRN3; Site_1: NotI; Site_2: EcoRI; cDNAs
 were oligo-dT primed and directionally cloned. Staging
 according to Nieuwkoop and Faber. Library was constructed
 by N. Garrett, P. LeMaire, A.M. Zorn, and J.B. Gurdon
 (Wellcome/CRC Institute)."
 148 a 110 c 141 g 114 t 1 others

BASE COUNT
 ORIGIN

Query Match 0.7%; Score 27; DB 10; Length 514;
 Best Local Similarity 100.0%; Pred. No. 0.55;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3112 aaagtgcacacagacagcctggctgc 3138
 |||||

Db 444 AAAGTCATCCACAGACCTGGCTGC 470

RESULT 31

LOCUS

DEFINITION

AA637964
 vr30a02.r1 Barstead mouse myotubes MBLR5 Mus musculus cDNA clone
 IMAGE:1122122 5' similar to gb:M84489 EXTRACELLULAR
 SIGNAL-REGULATED KINASE 2 (HUMAN); gb:X58712 Mouse MAPK mRNA for
 mitogen-activated protein kinase (MOUSE); mRNA sequence.
 AA637964

```

VERSION AA637964.1 GI:2561552
SOURCE EST.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 525)
Geisel S., Kucaba, T., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:611458
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 313.
FEATURES
Source
1..525
/organism="Mus musculus"
/strain="C3H"
/db_xref="taxon:10090"
/clone="IMAGE:112212"
/clone.lib="Barstead mouse myotubes MPLR5"
/cell_line="C2C12"
/lab_host="DH10B"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: EcoRI; Site_2: NotI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5',
TGTTACGAATCTGAAGTGGAGCGCGCCCTTTTCTTTTCTTTTCTTTT
3']; Double-stranded cDNA was ligated to Eco RI adaptors
[AAATCGATCCTTG], digested with Not I and cloned into the
Not I and Eco RI sites of the modified pT73 vector.
Library constructed by Bob Barstead. The C2C12 cell line
(available from ATCC, catalog # CRL-1772) differentiates
rapidly, forming contractile myotubes and producing
characteristic muscle proteins."
BASE COUNT 143 a 125 c 115 g 142 t
ORIGIN

Query Match 0.6%; Score 26; DB 9; Length 525;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3173 aagatctgtgacttggccttgcgcg 3198
|||||
Db 232 AAGATCTGTGACTTTGGCCTTGCCCG 257

RESULT 32
AW911950
LOCUS AW911950 542 bp mRNA linear EST 25-MAY-2000
DEFINITION ur89e03.y1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:3157468 5'
similar to gb:X58712 Mouse MAPK mRNA for mitogen-activated protein
kinase (MOUSE);, mRNA sequence.
ACCESSION AW911950
VERSION AW911950.1 GI:8077468
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 542)

AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
Tumor Gene Index
Unpublished (1997)
Other ESTs: ur89e03.x1
Contact: Robert Strausberg, Ph.D.
Email: cgapsb-remail.nih.gov
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml
MGI:1060224
Seq primer: -40RP from Gibco
High quality sequence stop: 423.
FEATURES
Source
1..542
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:3157468"
/clone.lib="NCI_CGAP_Mam6"
/sex="female, virgin"
/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_host="DH10B"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH"
BASE COUNT 150 a 133 c 113 g 145 t
ORIGIN

Query Match 0.6%; Score 26; DB 9; Length 542;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3173 aagatctgtgacttggccttgcgcg 3198
|||||
Db 98 AAGATCTGTGACTTTGGCCTTGCCCG 123

RESULT 33
AZ645762/c
LOCUS AZ645762 589 bp DNA linear GSS 14-DEC-2000
DEFINITION Jm0511E24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0511E24 F, DNA sequence.
ACCESSION AZ645762
VERSION AZ645762.1 GI:11775570
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 589)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellly
, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A.
and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

```

Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0511 row: E column: 24
 Seq primer: CTTTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 589.

FEATURES

source
 Location/Qualifiers
 1. .589
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUCG140511E24"
 /clone_lib="Mouse 10Kb plasmid UUCG1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PWD42 (g114732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT 133 a 149 c 161 g 146 t
 ORIGIN

Query Match 0.6% Score 26; DB 12; Length 589;
 Best Local Similarity 100.0%; Pred. No. 1.6;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 34

LOCUS BG518797 748 bp mRNA linear EST 02-APR-2001
 DEFINITION 602578390F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3491663 5',
 mRNA sequence.

ACCESSION BG518797
 VERSION BG518797.1 GI:13514016

KEYWORDS EST.

SOURCE house mouse.

ORGANISM

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 1 (bases 1 to 748)
 NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.
 CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM8536 row: c column: 24

High quality sequence stop: 735.

FEATURES

source
 Location/Qualifiers
 1. .748
 /organism="Mus musculus"
 /strain="CZECH II (feral)"
 /db_xref="taxon:10090"
 /clone="IMAGE:3491663"
 /clone_lib="NCI_CGAP_Lu29"
 /tissue_type="spontaneous tumor, metastatic to mammary."
 Stem cell origin.
 /lab_host="DH10B"
 /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI;
 Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
 Library constructed by Life Technologies. Investigator
 providing samples: Gilbert Smith, NIH"

BASE COUNT 215 a 180 c 156 g 197 t
 ORIGIN

Query Match 0.6% Score 26; DB 10; Length 748;
 Best Local Similarity 100.0%; Pred. No. 1.6;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3173 aagatctgacattgacctgcccgcg 3198
 |||||||||||||||||||||||||

Db 185 AAGATCTGTGACTTTGGCCTTGCCCG 210

RESULT 35

LOCUS B1112246

DEFINITION 602899921F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:5029733 5',
 mRNA sequence.

ACCESSION B1112246

VERSION B1112246.1 GI:14563147

KEYWORDS EST.

SOURCE house mouse.

ORGANISM

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 1 (bases 1 to 763)
 NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM1083 row: j column: 06

High quality sequence stop: 761.

Location/Qualifiers

FEATURES

source

1. .763
 /organism="Mus musculus"
 /strain="C57/B6"
 /db_xref="taxon:10090"
 /clone="IMAGE:5029733"
 /clone_lib="NCI_CGAP_Mam5"
 /tissue_type="tumor, gross tissue"
 /dev_stage="7 months"
 /lab_host="DH10B"

/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
 Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
 Library constructed by Life Technologies. Investigators
 providing samples: Lothar Hennighausen/Robin Humphreys,
 NIH"

BASE COUNT 222 a 179 c 159 g 203 t

ORIGIN

Query Match 0.6%; Score 26; DB 10; Length 763;
 Best Local Similarity 100.0%; Pred. No. 1.6;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3173 aagatctgtgactttggccttgcccg 3198
 |||||
 Db 200 AAGATCTGTGACTTTGGCCTTGCCCG 225

RESULT 36
 B1158214
 LOCUS
 DEFINITION 789 bp mRNA linear EST 05-JUL-2001
 602920679F1 NIH_CGAP_Mam3 Mus musculus cDNA clone IMAGE:5060946 5',
 mRNA sequence.
 B1158214
 B1158214.1 GI:14618215
 EST.
 B1158214
 SOURCE house mouse.
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NIH-MGC http://mgc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs@email.nih.gov
 Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Place: LLNL1164 row: n column: 19
 High quality sequence start: 3
 High quality sequence stop: 672.
 Location/Qualifiers
 1..789
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 /clone="IMAGE:5060946"
 /clone_lib="NIH_CGAP_Mam3"
 /tissue_type="tumor, gross tissue"
 /lab_host="DH10B"
 /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert 2 kb. Library constructed by Life
 Technologies, catalog #12017-018. Investigators providing
 samples: Lothar Hennighausen/Chu-Xia Deng, NIH Reference
 for transgenic model: Xu et al., Nature Genetics 22, 37-43
 (1999). Note: this is a NCI_CGAP Library."

BASE COUNT 221 a 187 c 176 g 205 t

ORIGIN

Query Match 0.6%; Score 26; DB 10; Length 789;
 Best Local Similarity 100.0%; Pred. No. 1.6;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3173 aagatctgtgactttggccttgcccg 3198
 |||||
 Db 33 AAGATCTGTGACTTTGGCCTTGCCCG 58

RESULT 37
 A1746873
 LOCUS
 DEFINITION 827 bp mRNA linear EST 22-JUN-1999
 ul08e07.y1 Sugano mouse embryo mewa Mus musculus cDNA clone
 IMAGE:2076228 5', similar to gb:X58712 Mouse MAPK mRNA for
 mitogen-activated protein kinase (MOUSE);, mRNA sequence.
 A1746873

ACCESSION

VERSION A1746873.1 GI:5125137
 KEYWORDS house mouse.
 SOURCE Mus musculus
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 827)
 AUTHORS Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
 Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person
 ,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter
 ,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
 Waterston,R. and Wilson,R.
 TITLE The WashU-NCI Mouse EST Project 1999
 JOURNAL Unpublished (1999)
 COMMENT Other_ESTs: ul08e07.x1
 Contact: Marra M/WashU-NCI Mouse EST Project 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:994664
 Seq primer: custom primer used
 High quality sequence stop: 510.
 Location/Qualifiers
 1..827
 /organism="Mus musculus"
 /strain="C57BL"
 /db_xref="taxon:10090"
 /clone="IMAGE:2076228"
 /clone_lib="Sugano mouse embryo mewa"
 /dev_stage="embryo, 14 dpc"
 /lab_host="DH10B"
 /note="Vector: pME18S-FL3; Site_1: DraIII (CACTGTGTG);
 Site_2: DraIII (CACCATGTG); 1st strand cDNA was primed
 with an oligo(dT) primer [ATGCGCCCTTTTCTTTTTTTTTTTT];
 double-stranded cDNA was ligated to a draIII adaptor
 [TGTGGCCTACTGG], digested and cloned into distinct draIII
 sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site
 CACCATGTG). XhoI should be used to isolate the cDNA
 insert. Size selection was performed to exclude fragments
 <1.5kb. Library constructed by Dr. Sumio Sugano
 (University of Tokyo Institute of Medical Science).
 Custom primers for sequencing: 5' end primer
 CTTTGTGCTTAAAGCTGCG and 3' end primer
 CGACCTGCAGCTCAGCACA."

BASE COUNT 199 a 226 c 223 g 179 t

ORIGIN

Query Match 0.6%; Score 26; DB 9; Length 827;
 Best Local Similarity 100.0%; Pred. No. 1.6;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3173 aagatctgtgactttggccttgcccg 3198
 |||||
 Db 698 AAGATCTGTGACTTTGGCCTTGCCCG 723

RESULT 38
 BE279830
 LOCUS
 DEFINITION 846 bp mRNA linear EST 13-JUL-2000
 601157156F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3140604 5',
 mRNA sequence.
 BE279830
 BE279830.1 GI:9154825
 EST.
 BE279830
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.


```

REFERENCE
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM108 row: p column: 13
High quality sequence stop: 85.
Location/Qualifiers
FEATURES
source
1..846
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3140604"
/clone_lib="NIH_MGC_21"
/tissue_type="choriocarcinoma"
/lab_host="DH10B (phage-resistant)"
/Note="Organ: placenta; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
```

BASE COUNT 149 a 263 c 200 g 233 t 1 others

ORIGIN

```

Query Match 0.6% Score 26; DB 10; Length 846;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3479 ggagaccacccaagcgagacctgcatt 3504
|||||
Db 32 CGAGACCCCAAGCGAGACCTGCATT 57

RESULT 39
BG870441
LOCUS BG870441.1 GI:14220981
DEFINITION BG870441.1 NCI_CGAP_SC2 Mus musculus cDNA clone IMAGE:4922505 5',
mRNA sequence.
ACCESSION BG870441
VERSION BG870441.1 GI:14220981
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 869)
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4922605"
/clone_lib="NCI_CGAP_SC2"
/lab_host="DH10B (TI phage-resistant)"
/Note="Organ: salivary gland; Vector: pCMV-SPORT6; Site_1:
NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo
dT. Average insert size 1.3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
```

BASE COUNT 149 a 263 c 200 g 233 t 1 others

ORIGIN

```

Query Match 0.6% Score 26; DB 10; Length 846;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3479 ggagaccacccaagcgagacctgcatt 3504
|||||
Db 32 CGAGACCCCAAGCGAGACCTGCATT 57

RESULT 39
BG870441
LOCUS BG870441.1 GI:14220981
DEFINITION BG870441.1 NCI_CGAP_SC2 Mus musculus cDNA clone IMAGE:4922505 5',
mRNA sequence.
ACCESSION BG870441
VERSION BG870441.1 GI:14220981
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 869)
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4922605"
/clone_lib="NCI_CGAP_SC2"
/lab_host="DH10B (TI phage-resistant)"
/Note="Organ: salivary gland; Vector: pCMV-SPORT6; Site_1:
NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo
dT. Average insert size 1.3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
```

BASE COUNT 149 a 263 c 200 g 233 t 1 others

ORIGIN

```

Query Match 0.6% Score 26; DB 10; Length 876;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3173 aagatctgtgactttggccttgccc 3198
|||||
Db 482 AAGATCTGTGACTTTGGCCTTGCCCG 507

RESULT 40
BG923284
LOCUS BG923284.1 GI:14303760
DEFINITION BG923284.1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:4954067 5',
mRNA sequence.
ACCESSION BG923284
VERSION BG923284.1 GI:14303760
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 876)
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4954067"
/clone_lib="NCI_CGAP_Mam6"
/sex="female, virgin"
/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_host="DH10B"
/Note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH"
```

BASE COUNT 219 a 250 c 224 g 183 t

ORIGIN

```

Query Match 0.6% Score 26; DB 10; Length 876;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3173 aagatctgtgactttggccttgccc 3198
```

```

Db      583  AAGATCTGTGACTTTGGCCTTGCCCG 608
|||||
RESULT  41
LOCUS   BF780935
DEFINITION 602105450F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:4223556
5', mRNA sequence.
ACCESSION BF780935
VERSION   BF780935.1 GI:12085968
KEYWORDS  EST.
SOURCE    house mouse.
ORGANISM  Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 916)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL   National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT   Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9812 row: c column: 13
High quality sequence stop: 677.
FEATURES             source
Location/Qualifiers
1. 916
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4223556"
/lab_host="NCI_CGAP_Kid14"
/notes="Organ: kidney; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library. 1"
BASE COUNT  238 a  228 c  215 g  235 t
ORIGIN
Query Match      0.6%; Score 26; DB 10; Length 916;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  3173  aagatctgtgactttggccttgcccg 3198
|||||
Db      158  AAGATCTGTGACTTTGGCCTTGCCCG 183
|||||
RESULT  42
LOCUS   BF140383
DEFINITION 601787893F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4015703 5',
mRNA sequence.
ACCESSION BF140383
VERSION   BF140383.1 GI:10979423
KEYWORDS  EST.
SOURCE    house mouse.
ORGANISM  Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1002)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL   National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT   Unpublished (1999)
Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9812 row: c column: 13
High quality sequence stop: 677.
FEATURES             source
Location/Qualifiers
1. 916
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4223556"
/lab_host="NCI_CGAP_Kid14"
/notes="Organ: kidney; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library. 1"
BASE COUNT  238 a  228 c  215 g  235 t
ORIGIN
Query Match      0.6%; Score 26; DB 10; Length 916;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  3173  aagatctgtgactttggccttgcccg 3198
|||||
Db      158  AAGATCTGTGACTTTGGCCTTGCCCG 183
|||||
RESULT  42
LOCUS   BF140383
DEFINITION 601787893F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4015703 5',
mRNA sequence.
ACCESSION BF140383
VERSION   BF140383.1 GI:10979423
KEYWORDS  EST.
SOURCE    house mouse.
ORGANISM  Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1002)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL   National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT   Unpublished (1999)
Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9261 row: n column: 24
High quality sequence start: 3
High quality sequence stop: 556.
FEATURES             source
Location/Qualifiers
1. 1002
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:4015703"
/clone_lib="NCI_CGAP_Lu30"
/tissue_type="tumor, metastatic to mammary"
/lab_host="DH10B"
/notes="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; transgenic model WNT-1, expression driven by
MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo
dT. Library constructed by Life Technologies.
Investigator providing samples: Gilbert Smith, NIH"
BASE COUNT  287 a  245 c  231 g  239 t
ORIGIN
Query Match      0.6%; Score 26; DB 10; Length 1002;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  3173  aagatctgtgactttggccttgcccg 3198
|||||
Db      79  AAGATCTGTGACTTTGGCCTTGCCCG 104
|||||
RESULT  43
LOCUS   BF320636
DEFINITION BF320636.y1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:3672947 5',
similar to SW:MK01_MOUSE P27703 MITOGEN-ACTIVATED PROTEIN KINASE 1
; mRNA sequence.
ACCESSION BF320636
VERSION   BF320636.1 GI:11269633
KEYWORDS  EST.
SOURCE    house mouse.
ORGANISM  Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 722)
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
JOURNAL   National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
COMMENT   Unpublished (1997)
Other_Ests: uz55b06.x1
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml
MGI:1433715
High quality sequence stop: 460.
FEATURES             source
Location/Qualifiers
1. 722
/organism="Mus musculus"
/strain="FVB/N"

```

/db_xref="taxon:10090"
/clone="IMAGE:3672947"
/clone_lib="NCI_CCAP_Mam6"
/sex="female, virgin"
/tissue_type="infiltrating ductal carcinoma"
/dev_stages="5 months"
/lab_host="DH10B"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sali;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH"
168 a 201 c 196 g 154 t 3 others

BASE COUNT
ORIGIN

Query Match 0.6%; Score 25; DB 10; Length 722;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3174 agatctgtgaacttgcccttgcccg 3198
|||||
Db 685 ACATCTGCACTTGGCCTTGCCCG 709

RESULT 44

LOCUS R86582 233 bp mRNA linear EST 17-AUG-1995
DEFINITION RABEST157T Rabbit Osteoclast, Dennis Sakai Oryctolagus cuniculus
CDNA clone PRABOC157 5' similar to c-fms, mRNA sequence.

ACCESSION R86582
VERSION R86582.1 GI:947236
KEYWORDS EST,
SOURCE rabbit,
Oryctolagus cuniculus

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

REFERENCE 1 (bases 1 to 233)
AUTHORS Sakai, D., Tong, H.-S. and Minkin, C.
TITLE Osteoclast Molecular Phenotyping by Random cDNA Sequencing
JOURNAL Bone 17 (2), 111-119 (1995)
MEDLINE 96021365
COMMENT Other_ESTs: RABEST035T, RABEST040T, RABEST075T
Contact: Sakai D

Basic Sciences
University of Southern California
USC School of Dentistry, 925 West 34th Street, DEN-4220, Los
Angeles, CA 90089-0641
Tel: 2137405563
Fax: 2137407560
Email: sakai@molbio.usc.edu
Seq primer: T7 promoter.

FEATURES Location/Qualifiers

SOURCE

1..233
/organism="Oryctolagus cuniculus"
/strain="New Zealand White"
/db_xref="taxon:9986"
/clone="PRABOC157"
/clone_lib="Rabbit Osteoclast, Dennis Sakai"
/lab_host="E. coli DH12S"
/note="Vector: pSPORT1; Site_1: Sali; Site_2: NotI; Poly(A
) + RNA was purified from a 97% pure population of
osteoclasts prepared from the long bones of 10 day old
rabbits. First strand cDNA was synthesized by priming
with an oligo(dT)-NotI anchor-primer and second strand
cDNA was synthesized by replacement synthesis as described
by Gubler and Hoffman (Gene 25:283, 1983). Following the
addition of Sali adapters and NotI digestion, the cDNA was
cloned between the Sali (50) and NotI (30) sites of the
pSPORT1 (BRL) plasmid vector."

BASE COUNT
ORIGIN

53 a 61 c 79 g 40 t

Query Match 0.6%; Score 24; DB 10; Length 233;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2578 cggcgcttcgggaaggtggtggga 2601
|||||
Db 75 CGGCGCTTCGGGAAGGTGTTGGA 98

RESULT 45

LOCUS AQ939636 234 bp DNA linear GSS 23-AUG-2000
DEFINITION NR3-110R Human NotI clones Homo sapiens genomic, DNA sequence.

ACCESSION AQ939636
VERSION AQ939636.1 GI:7216014
KEYWORDS GSS.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 234)
AUTHORS Zabarovsky, E.R., Gizatullin, R., Podowski, R.M., Zabarovska, V.V., Xie
, L., Muravenko, O.V., Kozyrev, S., Petrenko, L., Skobeleva, N., Li, J.,
Protopopov, A., Kashuba, V., Ernberg, I., Winberg, G. and Wahlstedt, C.
TITLE NotI clones in the analysis of the human genome
JOURNAL Nucleic Acids Res. 28 (7), 1635-1639 (2000)
MEDLINE 20175728
COMMENT Contact: Podowski RM
Center for Genomics Research
Karolinska Institute
17177 Stockholm, Sweden
Tel: +46-8-728-6372
Fax: +46-8-337983
Email: Raf.Podowski@cgr.ki.se
Class: NotI site.

FEATURES source

1..234
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Human NotI clones"
BASE COUNT 42 a 71 c 75 g 38 t
ORIGIN

Query Match 0.6%; Score 24; DB 12; Length 234;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 560 caggaggtggtgtgggatgacgg 583
|||||
Db 93 CAGGAGGTGTTGGGATGACCGG 116

Search completed: July 15, 2002, 20:07:24
Job time: 14482 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 15, 2002, 20:07:42 ; Search time 808.35 seconds
(without alignments)
8655.626 Million cell updates/sec

Title: US-09-375-248-1
Perfect score: 4111
Sequence: 1 ccacgcgcagcggcgagga.....tcacagacaacagtactaa 4111

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1163369 seqs, 850982142 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2326738

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Pending_Patents_NA_New.*
1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq.*
2: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq.*
3: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq.*
4: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq.*
5: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq.*
6: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq.*
7: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3912	95.2	4416	5	US-09-053-375B-132 Sequence 132, App
2	3912	95.2	4416	5	US-09-442-384B-447 Sequence 447, App
3	420	10.2	420	5	US-09-970-088-9 Sequence 9, Appli
4	223	5.4	463	5	US-09-918-995-21977 Sequence 21977, A
5	145	3.5	477	5	US-09-918-995-23705 Sequence 23705, A
6	127	3.1	770	6	US-10-027-632-20120 Sequence 20120, A
7	123	3.0	671	6	US-10-027-632-144519 Sequence 144519, A
8	123	3.0	671	6	US-10-027-632-144520 Sequence 144520, A
9	96	2.3	476	5	US-09-539-331D-34177 Sequence 34177, A
10	56	1.4	420	5	US-09-970-088-7 Sequence 7, Appli
11	54	1.3	420	5	US-09-970-088-10 Sequence 10, Appli
12	50	1.2	610	5	US-09-919-002-6998 Sequence 6998, App
13	36	0.9	475	5	US-09-918-995-19650 Sequence 19650, A
14	32	0.8	420	5	US-09-970-088-8 Sequence 8, Appli
15	23	0.6	23	5	US-09-704-167A-7 Sequence 7, Appli
16	23	0.6	476	5	US-09-539-331D-34177 Sequence 34177, A
17	23	0.6	6373	6	US-10-027-400-1 Sequence 1, Appli
18	23	0.6	6378	5	US-09-053-375B-419 Sequence 419, App
19	22	0.5	22	5	US-09-704-167A-8 Sequence 8, Appli
20	22	0.5	501	6	US-10-116-712-166 Sequence 166, App
21	22	0.5	517	6	US-10-099-926-644 Sequence 644, App
22	22	0.5	1078	6	US-10-143-883-83 Sequence 83, Appli
23	22	0.5	4479	5	US-09-053-375B-724 Sequence 724, App
24	21	0.5	471	5	US-09-918-995-31410 Sequence 31410, A
25	21	0.5	523	7	US-60-382-445-1176 Sequence 1176, Ap
26	21	0.5	583	6	US-10-027-632-104255, Sequence 104255,

27	21	0.5	583	6	US-10-027-632-325232	Sequence 325232,
c 28	21	0.5	598	7	US-60-377-240-5245	Sequence 6245, Ap
29	21	0.5	641	7	US-60-377-240-1586	Sequence 1386, A
c 30	21	0.5	674	6	US-10-155-881-17468	Sequence 17468, A
c 31	21	0.5	744	6	US-10-027-632-15064	Sequence 15064, A
c 32	21	0.5	997	6	US-10-027-632-30946	Sequence 30946, A
33	21	0.5	2574	6	US-10-045-428A-2	Sequence 2, Appli
34	21	0.5	3314	6	US-10-172-118-1257	Sequence 1257, Ap
35	21	0.5	5470	5	US-09-053-375B-733	Sequence 733, App
c 36	20	0.5	226	5	US-09-540-210B-10654	Sequence 10654, A
c 37	20	0.5	356	5	US-09-721-544-17764	Sequence 17764, A
c 38	20	0.5	366	5	US-09-721-544-17950	Sequence 17950, A
c 39	20	0.5	456	7	US-60-382-445-2302	Sequence 2302, Ap
40	20	0.5	461	5	US-09-721-544-7766	Sequence 7766, Ap
41	20	0.5	462	5	US-09-918-995-24204	Sequence 24204, A
42	20	0.5	484	5	US-09-721-544-7765	Sequence 7765, Ap
43	20	0.5	518	5	US-09-918-995-37258	Sequence 37258, A
c 44	20	0.5	575	7	US-60-377-240-3743	Sequence 3743, Ap
45	20	0.5	627	6	US-10-027-632-142575	Sequence 142575,

ALIGNMENTS

RESULT 1
US-09-053-375B-132
; Sequence 132, Application US/09053375B
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Bibilashvili, Robert
; TITLE OF INVENTION: Nucleic Acid Arrays
; FILE REFERENCE: CLON-006
; CURRENT APPLICATION NUMBER: US/09/053,375B
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 1543
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 132
; LENGTH: 4416
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 4243
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 4243
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 4243
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 4243
; OTHER INFORMATION: n = A,T,C or G
US-09-053-375B-132

Query Match	95.2%	Score 3912;	DB 5;	Length 4416;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 3912;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;
Qy	1	ccacgcgcagcggcgagatgcagcgggcccgcgcgtgtgcctgcactgtggtctcg	60	
Db	1	ccacgcgcagcggcgagatgcagcgggcccgcgcgtgtgcctgcactgtggtctcg	60	
Qy	61	cctgggaactcctggcgcgcctggtgagtggtactactatgaccccccgacctgaaacat	120	
Db	61	cctgggaactcctggcgcgcctggtgagtggtactactatgaccccccgacctgaaacat	120	
Qy	121	cacgcagagatcacacgcatcatcgacacgcggtgacagcgtgccatctctctcagcagggaca	180	
Db	121	cacgcagagatcacacgcatcatcgacacgcggtgacagcgtgccatctctcagcagggaca	180	
Qy	181	gcacccccctcagtggtgtgtgccaggagctcagagggccagccaccgcagagacaagga	240	

Db	181	gcacccctcgagtggggtggccaggagctcaggaggcgccagccacgcgagacaagg	241
Qy	241	cagcagagacacgggggtgggtcgagagctcgaggggcacagacgcagagccctactcgaa	300
Db	241	cagcagagacacgggggtgggtcgagagctcgaggggcacagacgcagagccctactcgaa	300
Qy	301	gggtgtgctgtgcacgaggtacatgccaacgacacaggcagctacgttgtctactacaa	360
Db	301	gggtgtgctgtgcacgaggtacatgccaacgacacaggcagctacgttgtctactacaa	360
Qy	361	gtacatcaagcagcagctcaggggcacacgcgcgcagctctcagttctcgtgagaga	420
Db	361	gtacatcaagcagcagctcaggggcacacgcgcgcagctctcagttctcgtgagaga	420
Qy	421	ctttgagcagccattcatcaacaagctgcacgctcttggtcaacagaaagacgccaat	480
Db	421	ctttgagcagccattcatcaacaagctgcacgctcttggtcaacagaaagacgccaat	480
Qy	481	tggggtgcccctgtgtgtgtccatccccggcctcaatgtcacgctgcgtcgcaagctc	540
Db	481	tggggtgcccctgtgtgtgtccatccccggcctcaatgtcacgctgcgtcgcaagctc	540
Qy	541	ggtgctgtgccaacagggcaggaggtggtgtggatgacggcgggggcatgctcgtctc	600
Db	541	ggtgctgtgccaacagggcaggaggtggtgtggatgacggcgggggcatgctcgtctc	600
Qy	601	cacgccaactgctgcacgatgccctgtacctgcagtcgagacacacactggggagaccaa	660
Db	601	cacgccaactgctgcacgatgccctgtacctgcagtcgagacacacactggggagaccaa	660
Qy	661	cttcctttccaaccccttcctggtgcacatcacaggcaacgagctctatgacatccagct	720
Db	661	cttcctttccaaccccttcctggtgcacatcacaggcaacgagctctatgacatccagct	720
Qy	721	gttaccacagaagtcgctgagagctggtgtagggggagaagcttggcttgaactgcacct	780
Db	721	gttaccacagaagtcgctgagagctggtgtagggggagaagcttggcttgaactgcacct	780
Qy	781	gtgggctgagctttaaactcaggtgtcacctttgaactgggaactaccagagaaagcagga	840
Db	781	gtgggctgagctttaaactcaggtgtcacctttgaactgggaactaccagagaaagcagga	840
Qy	841	gcggggtaagtggtgcccgcagcgcgtcccagcagaccacacagaactctccagcat	900
Db	841	gcggggtaagtggtgcccgcagcgcgtcccagcagaccacacagaactctccagcat	900
Qy	901	ccgtgaccatccacaacgctcagccagcacagacgtgggtcgatgtgtgcaaggccaacaa	960
Db	901	ccgtgaccatccacaacgctcagccagcacagacgtgggtcgatgtgtgcaaggccaacaa	960
Qy	961	cggcatccagcgatttcgggagagcagcagagttcatgtgcatgaaatcccttcacag	1020
Db	961	cggcatccagcgatttcgggagagcagcagagttcatgtgcatgaaatcccttcacag	1020
Qy	1021	cgtcgagtggtctaaaggaccatcctggggccacgcgcagcagagcgtggtagagct	1080
Db	1021	cgtcgagtggtctaaaggaccatcctggggccacgcgcagcagagcgtggtagagct	1080
Qy	1081	gcccggtgaagctggcagcgtaccccccccgagttccagtggtacaaagatggaagggc	1140
Db	1081	gcccggtgaagctggcagcgtaccccccccgagttccagtggtacaaagatggaagggc	1140
Qy	1141	actgtccggggccacagtcacatgccctgggtgctcaaggaggtgcacagggccagcac	1200
Db	1141	actgtccggggccacagtcacatgccctgggtgctcaaggaggtgcacagggccagcac	1200
Qy	1201	aggcactacacccctgcctctggaactccgctgtggtcgtgagcgcaacatcacgct	1260
Db	1201	aggcactacacccctgcctctggaactccgctgtggtcgtgagcgcaacatcacgct	1260
Qy	1261	ggagctgggtggaatgtccccccacatatatgaaaggaggtcctctccccagcat	1320
Db	1261	ggagctgggtggaatgtccccccacatatatgaaaggaggtcctctccccagcat	1320

QY	1321	ctactcggtcaacg	ccg	ccaggccctcaactgcagcgctacgagcggtgcgccccctgcctct	1380
Db	1321	ctactcggtcaacg	ccg	ccaggccctcaactgcagcgctacgagcggtgcgccccctgcctct	1380
QY	1381	cagcatccagtgagc	agccctgacacccctgacacccctgcaagatggtttgccagcgtaagtct	1440	
Db	1381	cagcatccagtgagc	agccctgacacccctgacacccctgcaagatggtttgccagcgtaagtct	1440	
QY	1441	ccggcgccgagcag	caagacctcatgccacagtgcgctgacttgagggcggtgacccac	1500	
Db	1441	ccggcgccgagcag	caagacctcatgccacagtgcgctgacttgagggcggtgacccac	1500	
QY	1501	gcaggatgcggtga	accccatcgagagcctggacacctggaccagtttgtgaggagaaa	1560	
Db	1501	gcaggatgcggtga	accccatcgagagcctggacacctggaccagtttgtgaggagaaa	1560	
QY	1561	gaataagactgtga	gcaagctggtgatccagaatgccaacgtgctccatgtacaagtgtg	1620	
Db	1561	gaataagactgtga	gcaagctggtgatccagaatgccaacgtgctccatgtacaagtgtg	1620	
QY	1621	tgtgtgtctccaag	gtggccaggatgagcgtctcatctacttcttatgtgaccaccat	1680	
Db	1621	tgtgtgtctccaag	gtggccaggatgagcgtctcatctacttcttatgtgaccaccat	1680	
QY	1681	ccccacggcttcac	catcgaaatccaaacccatccgagagctactagagggccagccggt	1740	
Db	1681	ccccacggcttcac	catcgaaatccaaacccatccgagagctactagagggccagccggt	1740	
QY	1741	gctctgagctgcga	gcagctacaagtacagacatctgcgtggttaccgcctcaa	1800	
Db	1741	gctctgagctgcga	gcagctacaagtacagacatctgcgtggttaccgcctcaa	1800	
QY	1801	cctgtccacgctgc	acgctgcagcgaggaacccctctctcgtcgactgcgaagacgtgcga	1860	
Db	1801	cctgtccacgctgc	acgctgcagcgaggaacccctctctcgtcgactgcgaagacgtgcga	1860	
QY	1861	tctgttcgccacct	ctctggcgccagcctggagagaggttgaccctggggcgcgccacgc	1920	
Db	1861	tctgttcgccacct	ctctggcgccagcctggagagaggttgaccctggggcgcgccacgc	1920	
QY	1921	caagctcagcgtga	tatcccccgctgcgcgcgcagacgagggccactatgtgtgcga	1980	
Db	1921	caagctcagcgtga	tatcccccgctgcgcgcgcagacgagggccactatgtgtgcga	1980	
QY	1981	agtgcaagacccgc	gcagccatgacagcactgccacaagaatcacttcggtgcagcg	2040	
Db	1981	agtgcaagacccgc	gcagccatgacagcactgccacaagaatcacttcggtgcagcg	2040	
QY	2041	cctggaaagccctc	gggttcacggaacttgaccacccctcctggtgaaacgtgagcgactc	2100	
Db	2041	cctggaaagccctc	gggttcacggaacttgaccacccctcctggtgaaacgtgagcgactc	2100	
QY	2101	gctggagatcagtg	ctgtgtgcccagacgcagcccgccagcatcgttgtgtacaaaga	2160	
Db	2101	gctggagatcagtg	ctgtgtgcccagacgcagcccgccagcatcgttgtgtgtacaaaga	2160	
QY	2161	cgagaggtgctgag	gaaagtctggagtcgacttggcgactccaaacgaagctgag	2220	
Db	2161	cgagaggtgctgag	gaaagtctggagtcgacttggcgactccaaacgaagctgag	2220	
QY	2221	catccacgctgcg	cgagagagatgcggagacgtatctgtcagcggtgtgaaacgcaa	2280	
Db	2221	catccacgctgcg	cgagagagatgcggagacgtatctgtcagcggtgtgaaacgcaa	2280	
QY	2281	gggctgcgtcaact	ctctcccgccagcgtggccgttggaagctccgaggaataagggcgagcat	2340	
Db	2281	gggctgcgtcaact	ctctcccgccagcgtggccgttggaagctccgaggaataagggcgagcat	2340	
QY	2341	ggagatcgtgatct	gtggttaccggcgctcatcgtgtgtcttcttgtgggtctctctct	2400	
Db	2341	ggagatcgtgatct	gtggttaccggcgctcatcgtgtgtcttcttgtgggtctctctct	2400	

QY 121 cagcgagagatcaacgtctatcgacacccggtgacagcctgtccatctctctgacgggagca 180
|||||
Db 121 cagcgagagatcaacgtctatcgacacccggtgacagcctgtccatctctctgacgggagca 180
QY 181 gcacccctcagtgggcttgccagagctcaggagcgccagcgccacccgagacaagga 240
|||||
Db 181 gcacccctcagtgggcttgccagagctcaggagcgccagcgccacccgagacaagga 240
QY 241 cagcgagagacacgggggtgctgcgagactgctgaggggcacagacgcccactactgcaa 300
|||||
Db 241 cagcgagagacacgggggtgctgcgagactgctgaggggcacagacgcccactactgcaa 300
QY 301 ggtgttctgtctgcagaggtacatgcccaacgacacagcagctactgtctgactacaa 360
|||||
Db 301 ggtgttctgtctgcagaggtacatgcccaacgacacagcagctactgtctgactacaa 360
QY 361 gtacataaaggcagcatcgaggggacccacggccgcagctctactcgttctgtgagaga 420
|||||
Db 361 gtacataaaggcagcatcgaggggacccacggccgcagctctactcgttctgtgagaga 420
QY 421 ctttgagcagcattcatcaaaagcctgacacgctcttggtcaacagaaaggacccat 480
|||||
Db 421 ctttgagcagcattcatcaaaagcctgacacgctcttggtcaacagaaaggacccat 480
QY 481 gtgggtgcctgtctgtgtccatccccggcctcaatgtcaacgctcgctcgcaagctc 540
|||||
Db 481 gtgggtgcctgtctgtgtccatccccggcctcaatgtcaacgctcgctcgcaagctc 540
QY 541 ggtgtctgagcagacggcgagaggtggtgtgggtagaccggcggggcatgctgtgtc 600
|||||
Db 541 ggtgtctgagcagacggcgagaggtggtgtgggtagaccggcggggcatgctgtgtc 600
QY 601 cagcgcaactgtgcagatgcccctgtacctgtcagtcagagacacactggggagaccagga 660
|||||
Db 601 cagcgcaactgtgcagatgcccctgtacctgtcagtcagagacacactggggagaccagga 660
QY 661 ctctcttccaaacccctctctggtgcacatcacaggcaacgagctcta tgacatccagct 720
|||||
Db 661 ctctcttccaaacccctctctggtgcacatcacaggcaacgagctcta tgacatccagct 720
QY 721 gttgccagaagtcgtgagactgctggtgagggagaaagctgg tectgaaactgcacct 780
|||||
Db 721 gttgccagaagtcgtgagactgctggtgagggagaaagctgg tectgaaactgcacct 780
QY 781 gtgggtgagtttaactcaggtgtcacctttgactgggactaccaggaagcaggcaga 840
|||||
Db 781 gtgggtgagtttaactcaggtgtcacctttgactgggactaccaggaagcaggcaga 840
QY 841 gcggggtaagtgggtgcccagcgacgctcccagcagacccacacagaactctccagcat 900
|||||
Db 841 gcggggtaagtgggtgcccagcgacgctcccagcagacccacacagaactctccagcat 900
QY 901 cctgaccatccacaacgtcagcagcagcagacgtggctgtagtg tgcgaaggccaacaa 960
|||||
Db 901 cctgaccatccacaacgtcagcagcagcagcagctggctgtagtg tgcgaaggccaacaa 960
QY 961 cggatccagcagatttcgggagagcacgaggtcatgtgcatgaaatcccttcatcag 1020
|||||
Db 961 cggatccagcagatttcgggagagcacgaggtcatgtgcatgaaatcccttcatcag 1020
QY 1021 cgtcagtggtgtcaaaaggaccatctctgagggccacggcagagacgagctggtgaaact 1080
|||||
Db 1021 cgtcagtggtgtcaaaaggaccatctctgagggccacggcagagacgagctggtgaaact 1080
QY 1081 gccgtgaaactgagcagcgtacccccggcccgagttccagtggttacaaggatggaaaggc 1140
|||||
Db 1081 gccgtgaaactgagcagcgtacccccggcccgagttccagtggttacaaggatggaaaggc 1140
QY 1141 actgtccggggccacagttccacatgccctggtgctcaaggaggtgacagagggccagcac 1200
|||||
Db 1141 actgtccggggccacagttccacatgccctggtgctcaaggaggtgacagagggccagcac 1200
QY 1201 agggacctacacccctgcctctgtggaactcgctgtggtcctgagggcgcaacatcagcct 1260
|||||

Db 1201 aggcacctacacccctgcctgtggaactccgctgtggtcctgagggcgcaacatcagcct 1260
|||||
QY 1261 ggaactggtgggtgaaatgtgtccccccagatacatagaaaggaggtcctctccccagcat 1320
|||||
Db 1261 ggaactggtgggtgaaatgtgtccccccagatacatagaaaggaggtcctctccccagcat 1320
QY 1321 ctactcgctcagcagccgagggccctcactgcacggcctcaggggtgcccctgcctct 1380
|||||
Db 1321 ctactcgctcagcagccgagggccctcactgcacggcctcaggggtgcccctgcctct 1380
QY 1381 caggatccagtggcactggcgcccttggaacccctggacacccctgcaagatggtgcccagcgtagttct 1440
|||||
Db 1381 caggatccagtggcactggcgcccttggaacccctggaacccctgcaagatggtgcccagcgtagttct 1440
QY 1441 ccggcgggcgagcagcagacactcatgcccacagtgcggtgactggaaggcggtgaccac 1500
|||||
Db 1441 ccggcgggcgagcagcagacactcatgcccacagtgcggtgactggaaggcggtgaccac 1500
QY 1501 gcaggatgcccgtgaaccccatcgagagcctggacacccctggacccgagtttgtgaggggaaa 1560
|||||
Db 1501 gcaggatgcccgtgaaccccatcgagagcctggacacccctggacccgagtttgtgaggggaaa 1560
QY 1561 gaataagactgtgagcaagctggtgatccagaatgccaaacgtgctctgccatgtacaaagt 1620
|||||
Db 1561 gaataagactgtgagcaagctggtgatccagaatgccaaacgtgctctgccatgtacaaagt 1620
QY 1621 tgtgtgtctccaaagggtgggcccaggtgagcgggtcatctacttctatgtgaccacacat 1680
|||||
Db 1621 tgtgtgtctccaaagggtgggcccaggtgagcgggtcatctacttctatgtgaccacacat 1680
QY 1681 ccccgacgggttcacatcgaatccaaagcctccgagagctactagaggggcccagccggt 1740
|||||
Db 1681 ccccgacgggttcacatcgaatccaaagcctccgagagctactagaggggcccagccggt 1740
QY 1741 gctctgagctgcccagcgacagctacaagtacagacatctgcgactgcaagaacgtgca 1800
|||||
Db 1741 gctctgagctgcccagcgacagctacaagtacagacatctgcgactgcaagaacgtgca 1800
QY 1801 cctgtccacgtgcaagtcgacggcagggaaacccgcttctgctcgactgcaagaacgtgca 1860
|||||
Db 1801 cctgtccacgtgcaagtcgacggcagggaaacccgcttctgctcgactgcaagaacgtgca 1860
QY 1861 tctgttccacccctctgcccgcagcctgagagagtgccacctggggcgccacgc 1920
|||||
Db 1861 tctgttccacccctctgcccgcagcctgagagagtgccacctggggcgccacgc 1920
QY 1921 caagtcagctgagta tcccccgctgcgcccgcagcacgagggccacatgtgtgcga 1980
|||||
Db 1921 caagtcagctgagta tcccccgctgcgcccgcagcacgagggccacatgtgtgcga 1980
QY 1981 agtgcaagaccggcgagccatgacaagcactgccaagaagtacctgttcggtgcaggc 2040
|||||
Db 1981 agtgcaagaccggcgagccatgacaagcactgccaagaagtacctgttcggtgcaggc 2040
QY 2041 cctggaaacccctcggtctcagcagaaacttgaccgacccctggtgaaactgagcagact 2100
|||||
Db 2041 cctggaaacccctcggtctcagcagaaacttgaccgacccctggtgaaactgagcagact 2100
QY 2101 gctggagatgagtgctgtggcgagcgccagcgcagcccagcatcggtgtgtacaaga 2160
|||||
Db 2101 gctggagatgagtgctgtggcgagcgccagcgcagcccagcatcggtgtgtacaaga 2160
QY 2161 cgagaggtgctggagaaaagtctggagtcgacttggcgactcccaacagagagctgag 2220
|||||
Db 2161 cgagaggtgctggagaaaagtctggagtcgacttggcgactcccaacagagagctgag 2220
QY 2221 catccagcgtgcgcgagagaggtgcgggacgcta tctgtgcagcgtgtgcaacgcaa 2280
|||||
Db 2221 catccagcgtgcgcgagagaggtgcgggacgcta tctgtgcagcgtgtgcaacgcaa 2280
QY 2281 gggctgcgtcaactctccgcccagcgtggccgtggaaaggctcccgagagataaggcgagcat 2340
|||||


```
QY 2231 gtgcgcgaggagatgcgggacgcctatctgtgcaagctgtgtcaacgcgaagggtgcgtc 2290
|||||
Db 121 gtgcgcgaggagatgcgggacgcctatctgtgcaagctgtgtcaacgcgaagggtgcgtc 180
|||||
QY 2291 aactcctccgcagcgtgcgcgtgaaagctccagagataaaggcagcagatgagatcgtg 2350
|||||
Db 181 aactcctccgcagcgtgcgcgtgaaagctccagagataaaggcagcagatgagatcgtg 240
|||||
QY 2351 atcctgtgcgttacgcggcgtcatcgtctcttcttctgtggctcctcctcctcatcttc 2410
|||||
Db 241 a'cctgtgcgttacgcggcgtcatcgtctcttcttctgtggctcctcctcctcatcttc 300
|||||
QY 2411 tgaacatgaggagccgcccacgcagacatcaagacggcgtacctgtccatcatcatg 2470
|||||
Db 301 tgaacatgaggagccgcccacgcagacatcaagacggcgtacctgtccatcatcatg 360
|||||
QY 2471 gaccccgggaggtgcctctgagagcaatgcgaatcctgtcctacgatgccagccag 2530
|||||
Db 361 gaccccgggaggtgcctctgagagcaatgcgaatcctgtcctacgatgccagccag 420
|||||
RESULT 4
US-09-918-995-21977
; Sequence 21977, Application US/09918995
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21977
; LENGTH: 463
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-995-21977

Query Match 5.4%; Score 223; DB 5; Length 463;
Best Local Similarity 100.0%; Pred. No. 4e-98;
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3605 gagggcagcttctcagaggtgtccaccatggccctacacatgcgccaggtgacgctgag 3664
|||||
Db 45 gagggcagcttctcagaggtgtccaccatggccctacacatgcgccaggtgacgctgag 104
|||||
QY 3665 gacagccgcgaagcctgcagccacagcctggtgcccaggtattacaactgggtgtcc 3724
|||||
Db 105 gacagccgcgaagcctgcagccacagcctggtgcccaggtattacaactgggtgtcc 164
|||||
QY 3725 ttcccgggtgcctggccagagggtgagaccgtggttctcctcagatgaagacattt 3784
|||||
Db 165 ttcccgggtgcctggccagagggtgagaccgtggttctcctcagatgaagacattt 224
|||||
QY 3785 gaggaattccccatgacccccacacctacaaagctctgtgg 3827
|||||
Db 225 gaggaattccccatgacccccacacctacaaagctctgtgg 267
|||||

RESULT 5
US-09-918-995-23705
; Sequence 23705, Application US/09918995
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
```

```
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23705
; LENGTH: 477
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; LOCATION: (1)-(477)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-23705

Query Match 3.5%; Score 145; DB 5; Length 477;
Best Local Similarity 100.0%; Pred. No. 4.3e-60;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3768 ccaggatgaagacatttgaggaaattccccatgaccccaacgacctacaaaggctctgtg 3827
|||||
Db 40 ccaggatgaagacatttgaggaaattccccatgaccccaacgacctacaaaggctctgtg 99
|||||
QY 3828 acaaccagacagacagtggagatggtgctgcctcgaggaggtttgacagatagagaca 3887
|||||
Db 100 acaaccagacagacagtggagatggtgctgcctcgaggaggtttgacagatagagaca 159
|||||
QY 3888 ggcatagacaagaagcggtcttcag 3912
|||||
Db 160 ggcatagacaagaagcggtcttcag 184
|||||

RESULT 6
US-10-027-632-20120
; Sequence 20120, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20120
; LENGTH: 770
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-20120

Query Match 3.1%; Score 127; DB 6; Length 770;
Best Local Similarity 100.0%; Pred. No. 2.5e-51;
Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1441 ccggcgcgagcagcagaacacctcatgcacagtcgcgtgactgagggcggtgaccac 1500
|||||
Db 379 ccggcgcgagcagcagaacacctcatgcacagtcgcgtgactgagggcggtgaccac 438
|||||
```

QY 1501 gcagagtcgctgaacccatcgagagcctggacacctggaccgagtttctgtggauggaaa 1560
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
439 gcagagtcgctggaacccatcgagagcctggacacctggaccgagtttctgtggauggaaa 498
QY 1561 gaataag 1567
Db |||||||
499 gaataag 505

RESULT 7
US-10-027-632-144519/c
; Sequence 144519, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 144519
; LENGTH: 671
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-144519

Query Match 3.0%; Score 123; DB 6; Length 671;
Best Local Similarity 100.0%; Pred. No. 2.3e-49;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3585 gcagctctcagagctcagaagaggcgagcttctgcaggggtgtccaccatgcccctacaca 3644
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
123 GCAGCTCTCAGAGCTCAGAAGAGGGCAGCTTCTCGCAGGTGTCCACCATGGCCCTACACA 64
QY 3645 tcgcccaggctgacgctgagagcagccgcgaagcctgcagcgccacagcctggccgcca 3704
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
63 TCGCCAGGCTGACGCTGAGGACAGCCGCCAAGCCCTGCAGCGCCACAGGCTGGCCGCCCA 4
QY 3705 ggt 3707
Db |||
3 GGT 1

RESULT 8
US-10-027-632-144520/c
; Sequence 144520, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676

; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 144520
; LENGTH: 671
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-144520

Query Match 3.0%; Score 123; DB 6; Length 671;
Best Local Similarity 100.0%; Pred. No. 2.3e-49;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3585 gcagctctcagagctcagaagaggcgagcttctgcaggggtgtccaccatgcccctacaca 3644
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
123 GCAGCTCTCAGAGCTCAGAAGAGGGCAGCTTCTCGCAGGTGTCCACCATGGCCCTACACA 64
QY 3645 tcgcccaggctgacgctgagagcagccgcgaagcctgcagcgccacagcctggccgcca 3704
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
63 TCGCCAGGCTGACGCTGAGGACAGCCGCCAAGCCCTGCAGCGCCACAGGCTGGCCGCCCA 4

QY 3705 ggt 3707
Db |||
3 GGT 1
RESULT 9
US-09-539-331D-34177
; Sequence 34177, Application US/09539331D
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Deleageane, Angelo M.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Mullany, Sara J.
; APPLICANT: Naughton, Rebecca E.
; TITLE OF INVENTION: POLYNUCLEOTIDES OF CARDIOVASCULAR SYSTEM TISSUE
; FILE REFERENCE: PD-1022 CIP
; CURRENT APPLICATION NUMBER: US/09/539,331D
; CURRENT FILING DATE: 2000-03-30
; PRIOR APPLICATION removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 40961
; SOFTWARE: PERL Program
; SEQ ID NO 34177
; LENGTH: 476
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: hu01173578
US-09-539-331D-34177

Query Match 2.3%; Score 96; DB 5; Length 476;
Best Local Similarity 100.0%; Pred. No. 3.4e-36;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3085 cacagagtgaggttctctgctcccgaaagtgcatccacagagacctggtgctcgaa 3144
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
24 cacagagtgaggttctctgctcccgaaagtgcatccacagagacctggtgctcgaa 83
QY 3145 cattctgctcggaagcgacgtggtgaagatctg 3180

```
Db 84 cattctgtcggaaagcagcgtggtgaagtctg 119
|||||
RESULT 10
US-09-970-088-7
; Sequence 7, Application US/09970088
; GENERAL INFORMATION:
; APPLICANT: GRAVEREAUX, EDWIN C.
; APPLICANT: SILVER, MARCY
; APPLICANT: ISNER, JEFFREY M.
; APPLICANT: YOON, YOUNG-SUP
; TITLE OF INVENTION: USE OF LYMPHANGIOGENIC AGENTS TO TREAT LYMPHATIC
; TITLE OF INVENTION: DISORDERS
; FILE REFERENCE: 71417/55062
; CURRENT APPLICATION NUMBER: US/09/970,088
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/237,171
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 7
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Oryctolagus cuniculus
US-09-970-088-7

Query Match 1.4%; Score 56; DB 5; Length 420;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2252 cactatctgtgcagcgtgtgcaacgccaaggctgcgtcaactctctccgcagcgt 2307
|||||
Db 142 cactatctgtgcagcgtgtgcaacgccaaggctgcgtcaactctctccgcagcgt 197
|||||

RESULT 11
US-09-970-088-10
; Sequence 10, Application US/09970088
; GENERAL INFORMATION:
; APPLICANT: GRAVEREAUX, EDWIN C.
; APPLICANT: SILVER, MARCY
; APPLICANT: ISNER, JEFFREY M.
; APPLICANT: YOON, YOUNG-SUP
; TITLE OF INVENTION: USE OF LYMPHANGIOGENIC AGENTS TO TREAT LYMPHATIC
; TITLE OF INVENTION: DISORDERS
; FILE REFERENCE: 71417/55062
; CURRENT APPLICATION NUMBER: US/09/970,088
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/237,171
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 10
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Mus sp.
US-09-970-088-10

Query Match 1.3%; Score 54; DB 5; Length 420;
Best Local Similarity 100.0%; Pred. No. 1e-15;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2435 gcagacatcaagcgggctacctgtccatcatcatgaccctggggagggtgcct 2488
|||||
Db 325 gcagacatcaagcgggctacctgtccatcatcatgaccctggggagggtgcct 378
|||||

RESULT 12
US-09-919-002-6998/c
; Sequence 6998, Application US/09919002
```

```
; GENERAL INFORMATION:
; APPLICANT: Leshkowitz, Dena
; APPLICANT: Liu, Jin
; TITLE OF INVENTION: NOVEL CONTIGS OBTAINED FROM VARIOUS CDNA
; TITLE OF INVENTION: LIBRARIES
; FILE REFERENCE: 20411-752CON1
; CURRENT APPLICATION NUMBER: US/09/919,002
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: APPLICATION NUMBER: 09/359,922
; PRIOR FILING DATE: FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: APPLICATION NUMBER: US 09/034,341
; PRIOR FILING DATE: FILING DATE: 1998-02-13
; NUMBER OF SEQ ID NOS: 13203
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6998
; LENGTH: 610
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(610)
; OTHER INFORMATION: n = A,T,C or G
US-09-919-002-6998

Query Match 1.2%; Score 50; DB 5; Length 610;
Best Local Similarity 100.0%; Pred. No. 9.1e-14;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3852 tgcctgacctcagcagaggtttgagcagatagagcagcagcagcatagacaagaa 3901
|||||
Db 586 TGCTGGCCTCGGAGGAGTTTGAGCAGATAGAGCAGCAGCATAGACAAGAA 537
|||||

RESULT 13
US-09-918-995-19650
; Sequence 19650, Application US/09918995
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19650
; LENGTH: 475
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(475)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-19650

Query Match 0.9%; Score 36; DB 5; Length 475;
Best Local Similarity 100.0%; Pred. No. 6.2e-07;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3877 gatagagcagcagcatagacaagaagcggcttcag 3912
|||||
Db 140 gatagagcagcagcatagacaagaagcggcttcag 175
|||||

RESULT 14
US-09-970-088-8
; Sequence 8, Application US/09970088
; GENERAL INFORMATION:
; APPLICANT: GRAVEREAUX, EDWIN C.
```

; APPLICANT: SILVER, MARCY
; APPLICANT: ISNER, JEFFREY M.
; APPLICANT: YOON, YOUNG-SUP
; TITLE OF INVENTION: USE OF LYMPHANGIOGENIC AGENTS TO TREAT LYMPHATIC
; FILE REFERENCE: 71417/55062
; CURRENT APPLICATION NUMBER: US/09/970,088
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/237,171
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Bos sp.
US-09-970-088-8

Query Match 0.8%; Score 32; DB 5; Length 420;
Best Local Similarity 100.0%; Pred. No. 5.5e-05;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2457 tgcctcatcatcatgaccgccggggagggtgcct 2488
|||||
DB 347 tgcctcatcatcatgaccgccggggagggtgcct 378

RESULT 15
US-09-704-167A-7
; Sequence 7, Application US/09704167A
; GENERAL INFORMATION:
; APPLICANT: Havemann, Klaus
; TITLE OF INVENTION: Production and Use of Endothelial-like Cells
; FILE REFERENCE: BPD-100
; CURRENT APPLICATION NUMBER: US/09/704,167A
; CURRENT FILING DATE: 2000-11-01
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; OTHER INFORMATION: VEGFR-3 5'-primer for RT-PCR, VEGFR-3 GenBank accession no. NM002
; OTHER INFORMATION: 020
US-09-704-167A-7

Query Match 0.6%; Score 23; DB 5; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2794 gatcgtgaggtctcgaagtacg 2816
|||||
DB 1 gatcgtgaggtctcgaagtacg 23

RESULT 16
US-09-539-331D-34177/c
; Sequence 34177, Application US/09539331D
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Delegeane, Angelo M.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Mullahy, Sara J.
; APPLICANT: Naughton, Rebecca E.
; TITLE OF INVENTION: POLYNUCLEOTIDES OF CARDIOVASCULAR SYSTEM TISSUE
; FILE REFERENCE: PD-1022 CIP
; CURRENT APPLICATION NUMBER: US/09/539,331D
; CURRENT FILING DATE: 2000-03-30

; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 40961
; SOFTWARE: PERL Program
; SEQ ID NO 34177
; LENGTH: 476
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: hu01173578
US-09-539-331D-34177

Query Match 0.6%; Score 23; DB 5; Length 476;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3063 tctgtcacagcttcacaggtggcc 3085
|||||
DB 27 TCTGCTACAGCTTCCAGGTGCC 5

RESULT 17
US-10-027-400-1
; Sequence 1, Application US/10027400
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, Lewis T.
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market, Steuart Street Tower, 20th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/027,400
; FILING DATE: 19-Dec-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,917
; FILING DATE: 05-JUN-1995
; APPLICATION NUMBER: US 07/151,414
; FILING DATE: 02-FEB-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.
; REGISTRATION NUMBER: 29,684
; REFERENCE/DOCKET NUMBER: 2307K-267-2-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/326-2400
; TELEFAX: 415/326-2422
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6373 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 129..3398
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-027-400-1

Query Match 0.6%; Score 23; DB 6; Length 6373;

Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3170 gtgaagatctgtgactttggcct 3192
|||||
Db 2622 GTGAGATCTGTGACTTTGGCCT 2644

RESULT 18

US-09-053-375B-419
; Sequence 419, Application US/09053375B
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; TITLE OF INVENTION: Bibilashvili, Robert
; FILE REFERENCE: Nucleic Acid Arrays
; CURRENT APPLICATION NUMBER: CLON-006
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 1543
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 419
; LENGTH: 6378
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-053-375B-419

Query Match 0.6%; Score 23; DB 5; Length 6378;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3170 gtgaagatctgtgactttggcct 3192
|||||
Db 2633 gtgaagatctgtgactttggcct 2655

RESULT 19

US-09-704-167A-8/c
; Sequence 8, Application US/09704167A
; GENERAL INFORMATION:
; APPLICANT: Havemann, Klaus
; TITLE OF INVENTION: Production and Use of Endothelial-like Cells
; FILE REFERENCE: BPD-100
; CURRENT APPLICATION NUMBER: US/09/704,167A
; CURRENT FILING DATE: 2000-11-01
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; OTHER INFORMATION: VEGFR-3 3'-primer for RT-PCR, VEGFR-3 GenBank accession no. NM002480
US-09-704-167A-8

Query Match 0.5%; Score 22; DB 5; Length 22;
Best Local Similarity 100.0%; Pred. No. 4.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3160 aagcgacgtgtgaagatctgt 3181
|||||
Db 22 AAGCGACGTGTGAAGATCTGT 1

RESULT 20

US-10-116-712-166/c
; Sequence 166, Application US/10116712
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Switzer, Ann

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.568
; CURRENT APPLICATION NUMBER: US/10/116,712
; CURRENT FILING DATE: 2002-04-07
; NUMBER OF SEQ ID NOS: 670
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 166
; LENGTH: 501
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; LOCATION: 488
; OTHER INFORMATION: n = A,T,C or G
US-10-116-712-166

Query Match 0.5%; Score 22; DB 6; Length 501;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2391 tctctctctctctctctctctg 2412
|||||
Db 377 TCCTCCTCCTCCTCATCTCTG 356

RESULT 21

US-10-099-926-644
; Sequence 644, Application US/10099926
; GENERAL INFORMATION:
; APPLICANT: King, Gordon E.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secrist, Heather
; APPLICANT: Jiang, Yuqiu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.547C2
; CURRENT APPLICATION NUMBER: US/10/099,926
; CURRENT FILING DATE: 2002-03-17
; NUMBER OF SEQ ID NOS: 1982
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 644
; LENGTH: 517
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-099-926-644

Query Match 0.5%; Score 22; DB 6; Length 517;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2391 tctctctctctctctctctctg 2412
|||||
Db 209 tcctctctctctctctctctctg 230

RESULT 22

US-10-143-883-83/c
; Sequence 83, Application US/10143883
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PM029C1N
; CURRENT APPLICATION NUMBER: US/10/143,883
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 09/758,459
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628

; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 406
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 83
; LENGTH: 1078
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (106)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1047)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-143-883-83

Query Match 0.5%; Score 22; DB 6; Length 1078;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2391 tcctctctctctctctctctg 2412
|||||
DB 764 TCCTCTCTCTCTCACTCTG 743

RESULT 23
US-09-053-375B-724
; Sequence 724, Application US/09053375B
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Bibilashvili, Robert
; TITLE OF INVENTION: Nucleic Acid Arrays
; FILE REFERENCE: CLON-006
; CURRENT APPLICATION NUMBER: US/09/053,375B
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 1543
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 724
; LENGTH: 4479
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-053-375B-724

Query Match 0.5%; Score 22; DB 5; Length 4479;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3126 gagactggtctgctcggaacat 3147
|||||
DB 2309 gagactggtctgctcggaacat 2330

RESULT 24
US-09-918-995-31410/c
; Sequence 31410, Application US/09918995
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 31410
; LENGTH: 471
; TYPE: DNA
; ORGANISM: Homo sapiens

; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(471)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-31410

Query Match 0.5%; Score 21; DB 5; Length 471;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2379 tcttcttctgggtctctctcc 2399
|||||
DB 120 TCTTCTTCTGGTCTCTCTCC 100

RESULT 25
US-60-382-445-1176/c
; Sequence 1176, Application US/60382445
; GENERAL INFORMATION:
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Gaiger, Alexander
; APPLICANT: Gordon, Brian
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.573P1
; CURRENT APPLICATION NUMBER: US/60/382,445
; CURRENT FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 2900
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1176
; LENGTH: 523
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-382-445-1176

Query Match 0.5%; Score 21; DB 7; Length 523;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2379 tcttcttctgggtctctctcc 2399
|||||
DB 23 TCTTCTTCTGGTCTCTCTCC 3

RESULT 26
US-10-027-632-104255
; Sequence 104255, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 104255
; LENGTH: 583
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-104255

Query Match 0.5%; Score 21; DB 6; Length 583;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2391 tctctctctctctctctctct 2411
|||||
Db 300 tctctctctctctctctctct 320

RESULT 27

US-10-027-632-325232
; Sequence 325232, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 325232
; LENGTH: 583
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-325232

Query Match 0.5%; Score 21; DB 6; Length 583;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2391 tctctctctctctctctctct 2411
|||||
Db 300 tctctctctctctctctctct 320

RESULT 28

US-60-377-240-6245/c
; Sequence 6245, Application US/60377240
; GENERAL INFORMATION:
; APPLICANT: Diggans, James C.
; APPLICANT: Porter, Mark
; APPLICANT: Wei, Tao
; TITLE OF INVENTION: Canine Gene Microarrays for Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5116-PR
; CURRENT APPLICATION NUMBER: US/60/377,240
; CURRENT FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 11109
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 6245
; LENGTH: 598
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(598)
; OTHER INFORMATION: n = a or c or g or t
US-60-377-240-6245

Query Match 0.5%; Score 21; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2391 tctctctctctctctctctct 2411
|||||
Db 143 TCCTCTCTCTCTCTCTCTCTCT 123

RESULT 29

US-60-377-240-1586
; Sequence 1586, Application US/60377240
; GENERAL INFORMATION:
; APPLICANT: Diggans, James C.
; APPLICANT: Porter, Mark
; APPLICANT: Wei, Tao
; TITLE OF INVENTION: Canine Gene Microarrays for Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5116-PR
; CURRENT APPLICATION NUMBER: US/60/377,240
; CURRENT FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 11109
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1586
; LENGTH: 641
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(641)
; OTHER INFORMATION: n = a or c or g or t
US-60-377-240-1586

Query Match 0.5%; Score 21; DB 7; Length 641;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2478 gggaggtgcctctggaggagc 2498
|||||
Db 154 gggaggtgcctctggaggagc 174

RESULT 30

US-10-155-881-17468/c
; Sequence 17468, Application US/10155881
; GENERAL INFORMATION:
; APPLICANT: Dotson, Stanton B.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; APPLICANT: Lutfiyva, Linda L.
; APPLICANT: McIninch, James
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; FILE REFERENCE: 38-21(15300)J
; CURRENT APPLICATION NUMBER: US/10/155,881
; CURRENT FILING DATE: 2002-05-22

; NUMBER OF SEQ ID NOS: 37595
; SEQ ID NO 17468
; LENGTH: 674
; TYPE: DNA
; ORGANISM: Glycine max
US-10-155-881-17468

Query Match 0.5%; Score 21; DB 6; Length 674;

Best Local Similarity 100.0%; Pred. No. 12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2391 tctctctctctctctctctct 2411

|||||

Db 194 TCCTCTCTCTCTCTCTCTCT 174

RESULT 31

US-10-027-632-15064/c

; Sequence 15064, Application US/10027632

; GENERAL INFORMATION:

; APPLICANT: Wang, David G.

; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

; FILE REFERENCE: 108827.129

; CURRENT APPLICATION NUMBER: US/10/027,632

; CURRENT FILING DATE: 2002-04-30

; PRIOR APPLICATION NUMBER: US 60/218,006

; PRIOR FILING DATE: 2000-07-12

; PRIOR APPLICATION NUMBER: US 60/198,676

; PRIOR FILING DATE: 2000-04-20

; PRIOR APPLICATION NUMBER: US 60/193,483

; PRIOR FILING DATE: 2000-03-29

; PRIOR APPLICATION NUMBER: US 60/185,218

; PRIOR FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: US 60/167,363

; PRIOR FILING DATE: 1999-11-23

; PRIOR APPLICATION NUMBER: US 60/156,358

; PRIOR FILING DATE: 1999-09-28

; PRIOR APPLICATION NUMBER: US 60/146,002

; PRIOR FILING DATE: 1999-08-09

; NUMBER OF SEQ ID NOS: 325720

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 15064

; LENGTH: 744

; TYPE: DNA

; ORGANISM: Human

US-10-027-632-15064

Query Match 0.5%; Score 21; DB 6; Length 744;

Best Local Similarity 100.0%; Pred. No. 12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3079 ggtggccagaggatgagtt 3099

|||||

Db 275 GGTGGCCAGAGGATGAGTT 255

RESULT 32

US-10-027-632-30946/c

; Sequence 30946, Application US/10027632

; GENERAL INFORMATION:

; APPLICANT: Wang, David G.

; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

; FILE REFERENCE: 108827.129

; CURRENT APPLICATION NUMBER: US/10/027,632

; CURRENT FILING DATE: 2002-04-30

; PRIOR APPLICATION NUMBER: US 60/218,006

; PRIOR FILING DATE: 2000-07-12

; PRIOR APPLICATION NUMBER: US 60/198,676

; PRIOR FILING DATE: 2000-04-20

; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30946
; LENGTH: 997
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-30946

Query Match 0.5%; Score 21; DB 6; Length 997;

Best Local Similarity 100.0%; Pred. No. 12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3079 ggtggccagaggatgagtt 3099

|||||

Db 604 GGTGGCCAGAGGATGAGTT 584

RESULT 33

US-10-045-428A-2

; Sequence 2, Application US/10045428A

; GENERAL INFORMATION:

; APPLICANT: Mano, Hiroyuki

; APPLICANT: Sakata, Tsuneki

; APPLICANT: Hasegawa, Mamoru

; APPLICANT: Tabata, Toshiaki

; TITLE OF INVENTION: Promoter

; FILE REFERENCE: 50026/011003

; CURRENT APPLICATION NUMBER: US/10/045,428A

; CURRENT FILING DATE: 2002-04-15

; PRIOR APPLICATION NUMBER: 09/735,103

; PRIOR FILING DATE: 2000-12-12

; PRIOR APPLICATION NUMBER: 09/142,529

; PRIOR FILING DATE: 1999-08-12

; PRIOR APPLICATION NUMBER: PCT/JP97/00741

; PRIOR FILING DATE: 1997-03-10

; PRIOR APPLICATION NUMBER: JP 8/54294

; PRIOR FILING DATE: 1996-03-12

; NUMBER OF SEQ ID NOS: 16

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 2574

; TYPE: DNA

; ORGANISM: Mus musculus

US-10-045-428A-2

Query Match 0.5%; Score 21; DB 6; Length 2574;

Best Local Similarity 100.0%; Pred. No. 12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3118 catccacagagcctgctgc 3138

|||||

Db 1566 catccacagagcctgctgc 1586

RESULT 34

US-10-172-118-1257

; Sequence 1257, Application US/10172118

; GENERAL INFORMATION:

; APPLICANT: Dai, Hongyue

; APPLICANT: He, Yudong

; APPLICANT: Linsley, Peter

```

; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 1257
; LENGTH: 3314
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NM_006235
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-1257

Query Match          0.5%; Score 21; DB 6; Length 3314;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 661 cttcctttccaccctctctc 681
      |||||||
Db 1516 cttcctttccaccctctctc 1536

RESULT 35
US-09-053-375B-733
; Sequence 733, Application US/09053375B
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Bibilashvili, Robert
; TITLE OF INVENTION: Nucleic Acid Arrays
; FILE REFERENCE: CLON-006
; CURRENT APPLICATION NUMBER: US/09/053,375B
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 1543
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 733
; LENGTH: 5470
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-053-375B-733

Query Match          0.5%; Score 21; DB 5; Length 5470;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 382 ccagacagacagtggtggtggt 3852
      |||||||
Db 4047 ccagacagacagtggtggtggt 4057

RESULT 36
US-09-540-210B-10654/c
; Sequence 10654, Application US/09540210B
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Delegeane, Angelo M.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Mullahy, Sara J.
; APPLICANT: Naughton, Rebecca E.
; TITLE OF INVENTION: POLYNUCLEOTIDES OF URINARY TRACT TISSUE
; FILE REFERENCE: PD-1037 CIP
; CURRENT APPLICATION NUMBER: US/09/540,210B
; CURRENT FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: 08/972,899
; PRIOR FILING DATE: November 18, 1997
; PRIOR APPLICATION NUMBER: 08/395,244
; PRIOR FILING DATE: February 27, 1995
; PRIOR APPLICATION NUMBER: 08/722,922
; PRIOR FILING DATE: September 27, 1996
; PRIOR APPLICATION NUMBER: 60/005,526
; PRIOR FILING DATE: September 29, 1995
; PRIOR APPLICATION NUMBER: 08/824,029
; PRIOR FILING DATE: March 25, 1997
; PRIOR APPLICATION NUMBER: 60/014,010
; PRIOR FILING DATE: March 25, 1996
; PRIOR APPLICATION NUMBER: 08/826,847
; PRIOR FILING DATE: April 10, 1997
; PRIOR APPLICATION NUMBER: 60/015,533
; PRIOR FILING DATE: April 10, 1996
; PRIOR APPLICATION NUMBER: 08/903,555
; PRIOR FILING DATE: July 31, 1997
; PRIOR APPLICATION NUMBER: 60/023,308
; PRIOR FILING DATE: July 31, 1996
; PRIOR APPLICATION NUMBER: 08/862,178
; PRIOR FILING DATE: May 22, 1997
; PRIOR APPLICATION NUMBER: 60/018,217
; PRIOR FILING DATE: May 23, 1996
; PRIOR APPLICATION NUMBER: 08/881,589
; PRIOR FILING DATE: June 24, 1997
; PRIOR APPLICATION NUMBER: 60/021,275
; PRIOR FILING DATE: June 25, 1996
; PRIOR APPLICATION NUMBER: 08/903,802
; PRIOR FILING DATE: July 31, 1997
; PRIOR APPLICATION NUMBER: 60/023,308
; PRIOR FILING DATE: July 31, 1996
; PRIOR APPLICATION NUMBER: 08/905,881
; PRIOR FILING DATE: August 1, 1997
; PRIOR APPLICATION NUMBER: 60/025,204
; PRIOR FILING DATE: August 1, 1996
; PRIOR APPLICATION NUMBER: 08/903,471
; PRIOR FILING DATE: July 30, 1997
; PRIOR APPLICATION NUMBER: 60/025,478
; PRIOR FILING DATE: July 31, 1996
; PRIOR APPLICATION NUMBER: 08/903,556
; PRIOR FILING DATE: July 31, 1997
; PRIOR APPLICATION NUMBER: 60/025,217
; PRIOR FILING DATE: August 22, 1996
; PRIOR APPLICATION NUMBER: 08/937,142
; PRIOR FILING DATE: September 23, 1997
; PRIOR APPLICATION NUMBER: 60/026,598
; PRIOR FILING DATE: September 24, 1996
; PRIOR APPLICATION NUMBER: 08/960,746
; PRIOR FILING DATE: October 29, 1997
; PRIOR APPLICATION NUMBER: 60/030,144
; PRIOR FILING DATE: October 30, 1996
; PRIOR APPLICATION NUMBER: 08/826,847
; PRIOR FILING DATE: April 10, 1997
; PRIOR APPLICATION NUMBER: 60/015,533
; PRIOR FILING DATE: April 10, 1996
; PRIOR APPLICATION NUMBER: 08/755,524
; PRIOR FILING DATE: November 22, 1996
; PRIOR APPLICATION NUMBER: 60/007,495
; PRIOR FILING DATE: November 22, 1995
; PRIOR APPLICATION NUMBER: 09/021,031
; PRIOR FILING DATE: February 10, 1998
; PRIOR APPLICATION NUMBER: 60/039,325
; PRIOR FILING DATE: February 13, 1997
; PRIOR APPLICATION NUMBER: 09/035,172
; PRIOR FILING DATE: March 4, 1998
; PRIOR APPLICATION NUMBER: 60/040,431
; PRIOR FILING DATE: March 5, 1997
; PRIOR APPLICATION NUMBER: 09/041,894
; PRIOR FILING DATE: March 12, 1998
; PRIOR APPLICATION NUMBER: 60/040,199
; PRIOR FILING DATE: March 14, 1997
; PRIOR APPLICATION NUMBER: 09/050,817
```

; PRIOR FILING DATE: March 30, 1998
; PRIOR APPLICATION NUMBER: 60/043,792
; PRIOR FILING DATE: April 11, 1997
; PRIOR APPLICATION NUMBER: 09/074,999
; PRIOR FILING DATE: May 8, 1998
; PRIOR APPLICATION NUMBER: 60/048,431
; PRIOR FILING DATE: May 29, 1997
; PRIOR APPLICATION NUMBER: 09/107,592
; PRIOR FILING DATE: June 30, 1998
; PRIOR APPLICATION NUMBER: 60/052,751
; PRIOR FILING DATE: July 1, 1997
; PRIOR APPLICATION NUMBER: 09/094,079
; PRIOR FILING DATE: June 9, 1998
; PRIOR APPLICATION NUMBER: 60/049,975
; PRIOR FILING DATE: June 13, 1997
; NUMBER OF SEQ ID NOS: 35654
; SOFTWARE: PERL Program
; SEQ ID NO 10654
; LENGTH: 226
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: hu00301736
US-09-540-210B-10654

Query Match 0.5%; Score 20; DB 5; Length 226;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1303 ggcctctctccccagcatct 1322
|||||
Db 207 GGCCTCTCTCCCCAGCATCT 188

RESULT 37
US-09-721-544-17764/c
; Sequence 17764, Application US/09721544
; GENERAL INFORMATION:
; APPLICANT: Arterburn, Matthew
; APPLICANT: Asghari, Vida
; APPLICANT: Damavandi, Simin
; APPLICANT: Dickson, Mark
; APPLICANT: Drake, Jim
; APPLICANT: Drmanac, Radoje
; APPLICANT: Engleman, Brandy
; APPLICANT: Faulkner, Brandy
; APPLICANT: Garcia, Veronica
; APPLICANT: Giedt, Gretchen
; APPLICANT: Hunter, Kelly
; APPLICANT: Jones, Aaron
; APPLICANT: Jones, Lee
; APPLICANT: Kita, David
; APPLICANT: Labat, Ivan
; APPLICANT: Laroya, Mimi
; APPLICANT: Lomelli, Michelle
; APPLICANT: Nguyen, Phuong
; APPLICANT: Nogra, Margie
; APPLICANT: Palencia, Servando
; APPLICANT: Raisi, Fariba
; APPLICANT: Smith, Benjamin
; APPLICANT: Tkach, Joe
; APPLICANT: Tran, Lien
; APPLICANT: Verna, Ron
; APPLICANT: Yang, Fei
; APPLICANT: Yim, Kenneth
; TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
; FILE REFERENCE: 728CIP
; CURRENT APPLICATION NUMBER: US/09/721,544
; CURRENT FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: 09/515,128
; PRIOR FILING DATE: 1998-02-13
; NUMBER OF SEQ ID NOS: 24489
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17950
; LENGTH: 366
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-721-544-17950

Query Match 0.5%; Score 20; DB 5; Length 366;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 09/034,341
; PRIOR FILING DATE: 1998-02-13
; NUMBER OF SEQ ID NOS: 24489
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17764
; LENGTH: 356
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-721-544-17764

Query Match 0.5%; Score 20; DB 5; Length 356;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1303 ggcctctctccccagcatct 1322
|||||
Db 211 GGCCTCTCTCCCCAGCATCT 192

RESULT 38
US-09-721-544-17950
; Sequence 17950, Application US/09721544
; GENERAL INFORMATION:
; APPLICANT: Arterburn, Matthew
; APPLICANT: Asghari, Vida
; APPLICANT: Damavandi, Simin
; APPLICANT: Dickson, Mark
; APPLICANT: Drake, Jim
; APPLICANT: Drmanac, Radoje
; APPLICANT: Engleman, Carrie
; APPLICANT: Faulkner, Brandy
; APPLICANT: Garcia, Veronica
; APPLICANT: Giedt, Gretchen
; APPLICANT: Hunter, Kelly
; APPLICANT: Jones, Aaron
; APPLICANT: Jones, Lee
; APPLICANT: Kita, David
; APPLICANT: Labat, Ivan
; APPLICANT: Laroya, Mimi
; APPLICANT: Lomelli, Michelle
; APPLICANT: Nguyen, Phuong
; APPLICANT: Nogra, Margie
; APPLICANT: Palencia, Servando
; APPLICANT: Raisi, Fariba
; APPLICANT: Smith, Benjamin
; APPLICANT: Tkach, Joe
; APPLICANT: Tran, Lien
; APPLICANT: Verna, Ron
; APPLICANT: Yang, Fei
; APPLICANT: Yim, Kenneth
; TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
; FILE REFERENCE: 728CIP
; CURRENT APPLICATION NUMBER: US/09/721,544
; CURRENT FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: 09/515,128
; PRIOR FILING DATE: 1998-02-13
; NUMBER OF SEQ ID NOS: 24489
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17950
; LENGTH: 366
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-721-544-17950

Query Match 0.5%; Score 20; DB 5; Length 366;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3173 aagatctgtgactttggcct 3192
|||||
Db 73 aagatctgtgactttggcct 92

RESULT 39
US-60-382-2302/c
; Sequence 2302, Application US/60382445
; GENERAL INFORMATION:
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Gaiger, Alexander
; APPLICANT: Gordon, Brian
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.573P1
; CURRENT APPLICATION NUMBER: US/60/382.445
; CURRENT FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 2900
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2302
; LENGTH: 456
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-382-445-2302

Query Match 0.5%; Score 20; DB 7; Length 456;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2391 tctctctctctcatcttc 2410
|||||
Db 141 TCCTCTCTCTCATCTTC 122

RESULT 40
US-09-721-544-7766
; Sequence 7766, Application US/09721544
; GENERAL INFORMATION:
; APPLICANT: Arterburn, Matthew
; APPLICANT: Asghari, Vida
; APPLICANT: Damavandi, Simin
; APPLICANT: Dickson, Mark
; APPLICANT: Drake, Jim
; APPLICANT: Drmanac, Radoje
; APPLICANT: Engleman, Carrie
; APPLICANT: Faulkner, Brandy
; APPLICANT: Garcia, Veronica
; APPLICANT: Giedt, Gretchen
; APPLICANT: Hunter, Kelly
; APPLICANT: Jones, Aaron
; APPLICANT: Jones, Lee
; APPLICANT: Klita, David
; APPLICANT: Labat, Ivan
; APPLICANT: Laroya, Mimi
; APPLICANT: Lomelli, Michelle
; APPLICANT: Nguyen, Phuong
; APPLICANT: Nogra, Margie
; APPLICANT: Palencia, Servando
; APPLICANT: Raisi, Fariba
; APPLICANT: Smith, Benjamin
; APPLICANT: Tkach, Joe
; APPLICANT: Tran, Lien
; APPLICANT: Verna, Ron
; APPLICANT: Yang, Fei
; APPLICANT: Yim, Kenneth
; TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
; FILE REFERENCE: 728QIP
; CURRENT APPLICATION NUMBER: US/09/721,544
; CURRENT FILING DATE: 2000-11-21

; PRIOR APPLICATION NUMBER: 09/515,128
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 09/034,341
; PRIOR FILING DATE: 1998-02-13
; NUMBER OF SEQ ID NOS: 24489
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7766
; LENGTH: 461
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(461)
; OTHER INFORMATION: n = A,T,C or G
US-09-721-544-7766

Query Match 0.5%; Score 20; DB 5; Length 461;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3173 aagatctgtgactttggcct 3192
|||||
Db 170 aagatctgtgactttggcct 189

RESULT 41
US-09-918-995-24204
; Sequence 24204, Application US/09918995
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 24204
; LENGTH: 462
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(462)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-24204

Query Match 0.5%; Score 20; DB 5; Length 462;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3173 aagatctgtgactttggcct 3192
|||||
Db 91 aagatctgtgactttggcct 110

RESULT 42
US-09-721-544-7765
; Sequence 7765, Application US/09721544
; GENERAL INFORMATION:
; APPLICANT: Arterburn, Matthew
; APPLICANT: Asghari, Vida
; APPLICANT: Damavandi, Simin
; APPLICANT: Dickson, Mark
; APPLICANT: Drake, Jim
; APPLICANT: Drmanac, Radoje
; APPLICANT: Engleman, Carrie
; APPLICANT: Faulkner, Brandy
; APPLICANT: Garcia, Veronica

```
; APPLICANT: Giedt, Gretchen
; APPLICANT: Hunter, Kelly
; APPLICANT: Jessen, Aaron
; APPLICANT: Jones, Lee
; APPLICANT: Kita, David
; APPLICANT: Labat, Ivan
; APPLICANT: Laroya, Mimi
; APPLICANT: Lomelli, Michelle
; APPLICANT: Nguyen, Phuong
; APPLICANT: Nogra, Margie
; APPLICANT: Palencia, Servando
; APPLICANT: Raisi, Fariba
; APPLICANT: Smith, Benjamin
; APPLICANT: Tkach, Joe
; APPLICANT: Tran, Lien
; APPLICANT: Verna, Ron
; APPLICANT: Yang, Fel
; APPLICANT: Yim, Kenneth
; TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
; TITLE OF INVENTION: From a cDNA Library of Fetal Liver-Spleen
; FILE REFERENCE: 728CIP
; CURRENT APPLICATION NUMBER: US/09/721,544
; CURRENT FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: 09/515,128
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 09/034,341
; PRIOR FILING DATE: 1998-02-13
; NUMBER OF SEQ ID NOS: 24489
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7765
; LENGTH: 484
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(484)
; OTHER INFORMATION: n = A,T,C or G
US-09-721-544-7765
```

```
Query Match 0.5%; Score 20; DB 5; Length 484;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 3173 aagatctgtgacttggcct 3192
|||||
Db 200 aagatctgtgacttggcct 219
```

```
RESULT 43
US-09-918-995-37258
; Sequence 37258, Application US/09918995
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS cDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38034
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 37258
; LENGTH: 518
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(518)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-37258
```

```
Query Match 0.5%; Score 20; DB 5; Length 518;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 2391 tcctctctctctcatcttc 2410
|||||
Db 314 tcctctctctctcatcttc 333
```

```
RESULT 44
US-60-377-240-3743/c
; Sequence 3743, Application US/60377240
; GENERAL INFORMATION:
; APPLICANT: Digheans, James C.
; APPLICANT: Porter, Mark
; APPLICANT: Wei, Tao
; TITLE OF INVENTION: Canine Gene Microarrays for Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5116-PR
; CURRENT APPLICATION NUMBER: US/60/377,240
; CURRENT FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 11109
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3743
; LENGTH: 575
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; OTHER INFORMATION:
; NAME/KEY: misc_feature
; LOCATION: (1)...(575)
; OTHER INFORMATION: n = a or c or g or t
US-60-377-240-3743
```

```
Query Match 0.5%; Score 20; DB 7; Length 575;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 2391 tcctctctctctcatcttc 2410
|||||
Db 418 TCCTCCTCCTCCTCATCTTC 399
```

```
RESULT 45
US-10-027-632-142575
; Sequence 142575, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
```

; SEQ ID NO 142575
; LENGTH: 627
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-142575

Query Match 0.5%; Score 20; DB 6; Length 627;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2391 tctctctctctctcttc 2410
|||||
Db 596 tctctctctctctcttc 615

Search completed: July 16, 2002, 02:56:38
Job time: 24536 sec

**ORIGINAL
COPY**

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 15, 2002, 18:09:07 ; Search time 12941.8 Seconds
(without alignments)
6872.393 Million cell updates/sec

Title: us-09-375-248-1
Perfect score: 4111
Sequence: 1 ccacgcgagcgccggcgaga.....tcacagacaacagctactaa 4111

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 21979536 seqs, 10817449327 residues

Word size : 0
Total number of hits satisfying chosen parameters: 43959072

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Pending_Patents_NA_Main:*

1: /cgn2_6/ptodata/2/pna/PCTUS_COMB.seq:*

2: /cgn2_6/ptodata/2/pna/US06_COMB.seq:*

3: /cgn2_6/ptodata/2/pna/US07_COMB.seq:*

4: /cgn2_6/ptodata/2/pna/US080_COMB.seq:*

5: /cgn2_6/ptodata/2/pna/US081_COMB.seq:*

6: /cgn2_6/ptodata/2/pna/US082_COMB.seq:*

7: /cgn2_6/ptodata/2/pna/US083_COMB.seq:*

8: /cgn2_6/ptodata/2/pna/US084_COMB.seq:*

9: /cgn2_6/ptodata/2/pna/US085_COMB.seq:*

10: /cgn2_6/ptodata/2/pna/US086_COMB.seq:*

11: /cgn2_6/ptodata/2/pna/US087_COMB.seq:*

12: /cgn2_6/ptodata/2/pna/US088_COMB.seq:*

13: /cgn2_6/ptodata/2/pna/US089_COMB.seq:*

14: /cgn2_6/ptodata/2/pna/US090_COMB.seq:*

15: /cgn2_6/ptodata/2/pna/US091_COMB.seq:*

16: /cgn2_6/ptodata/2/pna/US092_COMB.seq:*

17: /cgn2_6/ptodata/2/pna/US093_COMB.seq:*

18: /cgn2_6/ptodata/2/pna/US094_COMB.seq:*

19: /cgn2_6/ptodata/2/pna/US095A_COMB.seq:*

20: /cgn2_6/ptodata/2/pna/US095B_COMB.seq:*

21: /cgn2_6/ptodata/2/pna/US095C_COMB.seq:*

22: /cgn2_6/ptodata/2/pna/US095D_COMB.seq:*

23: /cgn2_6/ptodata/2/pna/US096A_COMB.seq:*

24: /cgn2_6/ptodata/2/pna/US096B_COMB.seq:*

25: /cgn2_6/ptodata/2/pna/US096C_COMB.seq:*

26: /cgn2_6/ptodata/2/pna/US096D_COMB.seq:*

27: /cgn2_6/ptodata/2/pna/US096E_COMB.seq:*

28: /cgn2_6/ptodata/2/pna/US097A_COMB.seq:*

29: /cgn2_6/ptodata/2/pna/US097B_COMB.seq:*

30: /cgn2_6/ptodata/2/pna/US097C_COMB.seq:*

31: /cgn2_6/ptodata/2/pna/US098A_COMB.seq:*

32: /cgn2_6/ptodata/2/pna/US098B_COMB.seq:*

33: /cgn2_6/ptodata/2/pna/US098C_COMB.seq:*

34: /cgn2_6/ptodata/2/pna/US099A_COMB.seq:*

35: /cgn2_6/ptodata/2/pna/US099B_COMB.seq:*

36: /cgn2_6/ptodata/2/pna/US099C_COMB.seq:*

37: /cgn2_6/ptodata/2/pna/US100_COMB.seq:*

38: /cgn2_6/ptodata/2/pna/US101_COMB.seq:*

39: /cgn2_6/ptodata/2/pna/US6000_COMB.seq:*

40: /cgn2_6/ptodata/2/pna/US6001_COMB.seq:*

41: /cgn2_6/ptodata/2/pna/US6002_COMB.seq:*

42: /cgn2_6/ptodata/2/pna/US6003_COMB.seq:*

43: /cgn2_6/ptodata/2/pna/US6004_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	4111	100.0	4111	1	PCT-US99-06133-1
2	4111	100.0	4111	17	US-09-375-248-1
3	4111	100.0	4795	3	US-07-959-951A-3
4	4111	100.0	4795	6	US-08-257-754-3
5	4111	100.0	4795	15	US-09-169-079-3
6	3912	95.2	4195	3	US-07-959-951A-1
7	3912	95.2	4195	6	US-08-257-754-1
8	3912	95.2	4195	15	US-09-169-079-1
9	3912	95.2	4416	10	US-08-601-132-36
10	3912	95.2	4416	10	US-08-671-573A-36
11	3912	95.2	4416	10	US-08-671-573B-36
12	3912	95.2	4416	17	US-09-355-700-1
13	3912	95.2	4416	18	US-09-440-302A-1035
14	3912	95.2	4416	18	US-09-442-384A-447
15	3912	95.2	4416	20	US-09-534-376A-1
16	3912	95.2	4416	24	US-09-631-092-36
17	3912	95.2	4425	8	US-08-446-648-31
18	3912	95.2	4425	11	US-08-770-449-31
19	3912	95.2	4425	14	US-09-023-655-889
20	3912	95.2	4425	36	US-09-982-610-31
21	3912	95.2	9108	8	US-08-446-648-45
22	3912	95.2	9108	36	US-09-982-610-45
23	3912	82.6	4113	37	US-10-081-126-1
24	3397	77.8	4450	1	PCT-US99-08079-1
25	3198	77.8	4450	37	US-10-012-214-1
26	3198	77.8	4450	37	US-10-012-214-1
27	2721	66.2	4461	55	US-60-167-943-103
28	2573	62.6	4459	71	US-60-324-185-4274
29	2390	58.1	4462	56	US-60-172-373-15763
30	1248	30.4	3277	59	US-60-209-009-455
31	1248	30.4	3277	60	US-60-213-360-951

32 1248 30.4 3277 71 US-60-324-185-4300 Sequence 4300, Ap
c 33 950 23.1 6826 6 US-08-256-769B-19 Sequence 19, Appl
c 34 950 23.1 6827 8 US-08-446-648-17 Sequence 17, Appl
c 35 950 23.1 6827 11 US-08-770-449-17 Sequence 17, Appl
c 36 950 23.1 6827 36 US-09-982-610-17 Sequence 17, Appl
37 440 10.7 575 60 US-60-213-847-55 Sequence 55, Appl
38 401 9.8 415 60 US-60-213-178-1247 Sequence 1247, Ap
39 388 9.4 535 28 US-09-716-953-1245 Sequence 1245, Ap
40 340 8.3 1575 56 US-60-172-373-15761 Sequence 15761, A
41 339 8.2 340 60 US-60-213-847-1271 Sequence 1271, Ap
42 310 7.5 724 57 US-60-184-770-470 Sequence 470, App
43 309 7.5 576 31 US-09-823-241-233 Sequence 233, App
44 253 6.2 256 62 US-60-233-937-796 Sequence 796, App
45 233 5.7 644 18 US-09-474-434-807 Sequence 807, App

ALIGNMENTS

RESULT 1
PCT-US99-06133-1
: Sequence 1, Application PC/TUS9906133
: GENERAL INFORMATION:
: APPLICANT: Ferrelli, Robert E
: APPLICANT: Alitalo, Kari
: APPLICANT: Finegold, David N
: APPLICANT: Karkkainen, Marika
: TITLE OF INVENTION: SCREENING AND THERAPY FOR LYMPHATIC DISORDERS INVOLVING
: TITLE OF INVENTION: THE FLT4 RECEPTOR TYROSINE KINASE (VEGFR-3)
: FILE REFERENCE: 28967/35255
: CURRENT APPLICATION NUMBER: PCT/US99/06133
: CURRENT FILING DATE: 1999-03-26
: NUMBER OF SEQ ID NOS: 18
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 1
: LENGTH: 4111
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (20)..(4111)
: OTHER INFORMATION: Human Flt4 (VEGFR-3) long form cDNA
PCT-US99-06133-1

Query Match 100.0%: Score 4111; DB 1: Length 4111;
Best Local Similarity 100.0%: Pred. No. 0;
Matches 4111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ccacgcgcagcggccggagatgcagcggggcgcgcgcgtgtgctgcgcgactgtggctctg 60
Db 1 ccacgcgcagcggccggagatgcagcggggcgcgcgcgtgtgctgcgcgactgtggctctg 60
QY 61 cctggagactcctgacgcgcctgtgagtgactactcattgaccccccccgaccttgaaat 120
Db 61 cctggagactcctgacgcgcctgtgagtgactactcattgaccccccccgaccttgaaat 120
QY 121 caggaggagtcacagtcacgcgtgcaccccggtgacacccgtgacacccctgtccatctcctgcaggagaca 180
Db 121 caggaggagtcacagtcacgcgtgcaccccggtgacacccctgtccatctcctgcaggagaca 180
QY 181 gcacccctcgagtgaggcttgccaggagctcaggagcgccagccacccggagacaagga 240
Db 181 gcacccctcgagtgaggcttgccaggagctcaggagcgccagccacccggagacaagga 240
QY 241 cagcggagcacgggggtggtgcgagactgcgagggcacagacgcccagccctactgcgaa 300
Db 241 cagcggagcacgggggtggtgcgagactgcgagggcacagacgcccagccctactgcgaa 300
QY 301 ggtgtgtgtgtgcacgaggtatattcccaacacacagcagcgtacgtctgtctactacaa 360
Db 301 ggtgtgtgtgtgcacgaggtatattcccaacacacagcagcgtacgtctgtctactacaa 360

QY 361 gtacatcaaggcacgcacatcaggggcacacagcgcgcagctcctacgtgttcgtgagaga 420
Db 361 gtacatcaaggcacgcacatcaggggcacacagcgcgcagctcctacgtgttcgtgagaga 420
QY 421 ctttgagcagcatttcattcaacaagcctgacacgctcttggtaacaggaagacgcacat 480
Db 421 ctttgagcagcatttcattcaacaagcctgacacgctcttggtaacaggaagacgcacat 480
QY 481 gtgggtgcccctgtgtgtgtccatccccggcctcaatgtcacgctgcgcgcgcaaaagctc 540
Db 481 gtgggtgcccctgtgtgtgtccatccccggcctcaatgtcacgctgcgcgcgcaaaagctc 540
QY 541 ggtgtgtgtgcacagcggcagaggtgtgtgtgggatgacccgcccgggagctgctcgtctc 600
Db 541 ggtgtgtgtgcacagcggcagaggtgtgtgtgggatgacccgcccgggagctgctcgtctc 600
QY 601 cacgcacactgtgcacagatgcccctgtacctgtacgtgcagtcgagaccacccctggggagaccagga 660
Db 601 cacgcacactgtgcacagatgcccctgtacctgtacgtgcagtcgagaccacccctggggagaccagga 660
QY 661 cttcctttccaaaccccttctgtgtgcacatcacaggaacagcagctctatgacatccagct 720
Db 661 cttcctttccaaaccccttctgtgtgcacatcacaggaacagcagctctatgacatccagct 720
QY 721 gttgccaggaagtcgctggagctgctggtaggggagaagctggtcctgaactgcacccgt 780
Db 721 gttgccaggaagtcgctggagctgctggtaggggagaagctggtcctgaactgcacccgt 780
QY 781 gtgggctgagttcaactcaggtgtcactttgactgggactaccacaggaagcagcaga 840
Db 781 gtgggctgagttcaactcaggtgtcactttgactgggactaccacaggaagcagcaga 840
QY 841 gcggggtaagtgggtgccgcagcgcctcccagcagcgcctcccagcagaccacacacacactcccagcat 900
Db 841 gcggggtaagtgggtgccgcagcgcctcccagcagcgcctcccagcagaccacacacacactcccagcat 900
QY 901 cctgacacatccacaacagtcagccagcagcagcagcctgggctcgta tgtgtgcaaggcccaacaa 960
Db 901 cctgacacatccacaacagtcagccagcagcagcagcctgggctcgta tgtgtgcaaggcccaacaa 960
QY 961 cggcatccagcagatttcgggagagaccagcagctcattgtgcatgaaaaatcccttcatcag 1020
Db 961 cggcatccagcagatttcgggagagaccagcagctcattgtgcatgaaaaatcccttcatcag 1020
QY 1021 cgtcgagtggtccaaaggaccatcctctggagccagcgcgcagcagcagcagctggtgaagct 1080
Db 1021 cgtcgagtggtccaaaggaccatcctctggagccagcgcgcagcagcagcagctggtgaagct 1080
QY 1081 gcccgtaagctggcagcagctaccccccccgagttccagtggtacaaaggtcggaaaggc 1140
Db 1081 gcccgtaagctggcagcagctaccccccccgagttccagtggtacaaaggtcggaaaggc 1140
QY 1141 actgtccggggccacagtcacatgcctcctgtgctcgaaggaggtgacagagggccagcac 1200
Db 1141 actgtccggggccacagtcacatgcctcctgtgctcgaaggaggtgacagagggccagcac 1200
QY 1201 agggacctacacccctgcctgtggaaactccgctgctggcctgagggcgcaacatcagcct 1260
Db 1201 agggacctacacccctgcctgtggaaactccgctgctggcctgagggcgcaacatcagcct 1260
QY 1261 ggagctggtggaatgtgccccccacagatacatgagagggaggcctcctccccacagat 1320
Db 1261 ggagctggtggaatgtgccccccacagatacatgagagggaggcctcctccccacagat 1320
QY 1321 ctactcgctgcacagcccgagccctcacctgcagcgcctacggggtgccccctgcctct 1380
Db 1321 ctactcgctgcacagcccgagccctcacctgcagcgcctacggggtgccccctgcctct 1380
QY 1381 cagcatccagtgggcactggcgcctggacacccctgcaagatgtttgtccccagcgtagctct 1440
Db 1381 cagcatccagtgggcactggcgcctggacacccctgcaagatgtttgtccccagcgtagctct 1440
QY 1441 ccggcgggcggcagcagcaagacctcatgcccacagtcgcgtgactggagggcggtgacccac 1500

|||||
Db 1441 ccgycgycgagcagcaagacccatgcccacagtccgtgactgagggcgtgacccac 1500
QY 1501 gcagatgycgctgaaccccatcgagagccctggacacctgaccaggtttgtgagggaaa 1560
Db 1501 gcagga tgcgctgaaccccatcgagagccctggacacctgaccaggtttgtgagggaaa 1560
QY 1561 gaaLaagactgtgagcaagctgggtgataccagaatgccaacgctgtctgcacatgtacaagt 1620
Db 1561 gaaLaagactgtgagcaagctgggtgataccagaatgccaacgctgtctgcacatgtacaagt 1620
QY 1621 tgtgttccaaacaggtggcgaggatgagcgctcatctacttcttatgtgaccacat 1680
Db 1621 tgtgttccaaacaggtggcgaggatgagcgctcatctacttcttatgtgaccacat 1680
QY 1681 cccgcagcgtttaccatcgaa tccaaagcatccgagagctactagagggccacgcggt 1740
Db 1681 cccgcagcgtttaccatcgaa tccaaagcatccgagagctactagagggccacgcggt 1740
QY 1741 gctcctgagctgccaagccgacagctacaagtacgagcatctgcgtggtaaccgctcaa 1800
Db 1741 gctcctgagctgccaagccgacagctacaagtacgagcatctgcgtggtaaccgctcaa 1800
QY 1801 cctgtccacgctcacagatgcgcacgggaacccgcttctgtcgtactgcaagaacgtgca 1860
Db 1801 cctgtccacgctcacagatgcgcacgggaacccgcttctgtcgtactgcaagaacgtgca 1860
QY 1861 tctgttccgcaacccctctggcccgccagcttgagaggtgacacctggggcgcgcaagc 1920
Db 1861 tctgttccgcaacccctctggcccgccagcttgagaggtgacacctggggcgcgcaagc 1920
QY 1921 cagcgtcagctgagtatacccccgctgcgcgccgagcagagggccactatgtgtgcga 1980
Db 1921 cagcgtcagctgagtatacccccgctgcgcgccgagcagagggccactatgtgtgcga 1980
QY 1981 agtgcaagaccgycgagcatgacaagcacgtgccaagaagaatcctgtcgtgcagc 2040
Db 1981 agtgcaagaccgycgagcatgacaagcacgtgccaagaagaatcctgtcgtgcagc 2040
QY 2041 cctggaaagcccttcggctcacgcagaaacttgaccgacctcctggtgaacgtgagcgaactc 2100
Db 2041 cctggaaagcccttcggctcacgcagaaacttgaccgacctcctggtgaacgtgagcgaactc 2100
QY 2101 gctggagatgcagtgcttggtggccgagcgcacgcgcccagcatcgtgtgtacaaaga 2160
Db 2101 gctggagatgcagtgcttggtggccgagcgcacgcgcccagcatcgtgtgtacaaaga 2160
QY 2161 cagagggctgctggaggaaaagtctggagtcgacttggcggaactcctggtgaacgtgagcgaactc 2220
Db 2161 cagagggctgctggaggaaaagtctggagtcgacttggcggaactcctggtgaacgtgagcgaactc 2220
QY 2221 catccagcgtgctgcgagaggaatgcgggacgctatctgtgacgctgtgcaacgcca 2280
Db 2221 catccagcgtgctgcgagaggaatgcgggacgctatctgtgacgctgtgcaacgcca 2280
QY 2281 gggctgctgcactcctccgcagcgtggccgtgaaagctccgaggaataagggcagcat 2340
Db 2281 gggctgctgcactcctccgcagcgtggccgtgaaagctccgaggaataagggcagcat 2340
QY 2341 ggaagatcgtgatactctgtcgttaccggcgctcatcgtcttcttctgtggctcctcct 2400
Db 2341 ggaagatcgtgatactctgtcgttaccggcgctcatcgtcttcttctgtggctcctcct 2400
QY 2401 cctcatctctgtaacatgagagggccggccacgcagacatcaagagggctacctgtc 2460
Db 2401 cctcatctctgtaacatgagagggccggccacgcagacatcaagagggctacctgtc 2460
QY 2461 catcatatggaccggggaggtgcctctgagagcgaatgcaataacctgtcctacga 2520
Db 2461 catcatatggaccggggaggtgcctctgagagcgaatgcaataacctgtcctacga 2520
QY 2521 taccagccagtgggaattccccccgagcgtgcacctggggagagtgtcctcggcctacgg 2580
|||||

Db 2521 tgcaccagctgggaattcccccgagcggctgcacctggggagagtgctcggctacgg 2580
QY 2581 cgcttctgggaaggtggtggaagcctcccgcttctcgcatccacaagggcagcagctgtga 2640
Db 2581 cgcttctgggaaggtggtggaagcctcccgcttctcgcatccacaagggcagcagctgtga 2640
QY 2641 caccgtggccgtgaaaaatgctgaaaagggcgccaagcgagcgagcgagcgctgat 2700
Db 2641 caccgtggccgtgaaaaatgctgaaaagggcgccaagcgagcgagcgagcgctgat 2700
QY 2701 gtcggagctcaagatcctcatccatcgcgaacacacctcaacgtgtcaacctctcgg 2760
Db 2701 gtcggagctcaagatcctcatccatcgcgaacacacctcaacgtgtcaacctctcgg 2760
QY 2761 ggcgtgcaaccaagccgagggccccctcatggtgatactgtggagttctgcaagtacggcaa 2820
Db 2761 ggcgtgcaaccaagccgagggccccctcatggtgatactgtggagttctgcaagtacggcaa 2820
QY 2821 cctctccaaacttctgtgcgcgaagcgggacccctcagccccctgcgaggagaagtctcc 2880
Db 2821 cctctccaaacttctgtgcgcgaagcgggacccctcagccccctgcgaggagaagtctcc 2880
QY 2881 cgagcagcgcgacgcttccgcgccatggtgagctcgcagcgtggatcggagggcgcc 2940
Db 2881 cgagcagcgcgacgcttccgcgccatggtgagctcgcagcgtggatcggagggcgcc 2940
QY 2941 ggggagcagcagacaggttctcttcgcgcggttctcgaagaccgagggcgaggcgagggcg 3000
Db 2941 ggggagcagcagacaggttctcttcgcgcggttctcgaagaccgagggcgaggcgagggcg 3000
QY 3001 ggccttccagaccagaagctgaggaacctgtggtgagcccgctgacctggaagatctc 3060
Db 3001 ggccttccagaccagaagctgaggaacctgtggtgagcccgctgacctggaagatctc 3060
QY 3061 tgtctgtacagcttccaggtggccagagggatggagttcctggcttcccgaagtgcat 3120
Db 3061 tgtctgtacagcttccaggtggccagagggatggagttcctggcttcccgaagtgcat 3120
QY 3121 ccacagagacctggctgtcgtcggaacatctcgtgtcgaaaagcgacgtggtgaaagatctg 3180
Db 3121 ccacagagacctggctgtcgtcggaacatctcgtgtcgaaaagcgacgtggtgaaagatctg 3180
QY 3181 tgactttggccttgcgcgggacatctacaagacctgactacgtcccgaagggcagtgcc 3240
Db 3181 tgactttggccttgcgcgggacatctacaagacctgactacgtcccgaagggcagtgcc 3240
QY 3241 ccggctgccccctgaagtggatggccccctgaaagcatcttcgacaagggtgtacaccacgca 3300
Db 3241 ccggctgccccctgaagtggatggccccctgaaagcatcttcgacaagggtgtacaccacgca 3300
QY 3301 gagtgaactgtggttcttgggtgcttctcgtggagatcttctcgtggggcctcccc 3360
Db 3301 gagtgaactgtggttcttgggtgcttctcgtggagatcttctcgtggggcctcccc 3360
QY 3361 gtacctgggtgtcagatcaatgaggaattcttgcagcggtgagagcggcacaagat 3420
Db 3361 gtacctgggtgtcagatcaatgaggaattcttgcagcggtgagagcggcacaagat 3420
QY 3421 gagggccccgagctggccactcccgccatcgcgcgaatctgtgaaactgctggtccgg 3480
Db 3421 gagggccccgagctggccactcccgccatcgcgcgaatctgtgaaactgctggtccgg 3480
QY 3481 agaccccaagcgagacctgcatctcggagctggtgagatcctgggagacctgtctcca 3540
Db 3481 agaccccaagcgagacctgcatctcggagctggtgagatcctgggagacctgtctcca 3540
QY 3541 gggcaggggctcgaagaggaaggagggtctgtcgtggccccgcgagctctcagagctc 3600
Db 3541 gggcaggggctcgaagaggaaggagggtctgtcgtggccccgcgagctctcagagctc 3600
QY 3601 agaagagggcagcttctcgaaggtgttccaccaatggccctcacatcgtccaggtgcagc 3660
Db 3601 agaagagggcagcttctcgaaggtgttccaccaatggccctcacatcgtccaggtgcagc 3660

Qy	1201	aggcacatcacacctgcgcctctggaactccgctgctgacctgagcgcaacatcacgct	1261
Db	1201	aggcaactacacctgcgcctctggaactccgctgctgacctgagcgcaacatcacgct	1261
Qy	1261	ggagctggtggtgaaatgtgcccccacagatacatgagaaggagcgctctctcccacgcat	1320
Db	1261	ggagctggtggtgaaatgtgcccccacagatacatgagaaggagcgctctctcccacgcat	1320
Qy	1421	ctactcgctgcacagcgccagcgccctcacctgcacgacctacggggtgccccctgcctct	1380
Db	1321	ctactcgctgcacagcgccagcgccctcacctgcacgacctacggggtgccccctgcctct	1380
Qy	1381	cagcatccagtggaactgagcgccctgacacccctgcagaatgtttgccacgctagctct	1440
Db	1381	cagcatccagtggaactgagcgccctgacacccctgcagaatgtttgccacgctagctct	1440
Qy	1441	ccgcgcgcgagcagcaagaactcatctccacagtgcgtgactggaagcggtgaccac	1500
Db	1441	ccgcgcgcgagcagcaagaactcatctccacagtgcgtgactggaagcggtgaccac	1500
Qy	1501	gcaggatgccgtgaaccccatcgagagcctggacacotggaccgagtttggagggaaa	1560
Db	1501	gcaggatgccgtgaaccccatcgagagcctggacacotggaccgagtttggagggaaa	1560
Qy	1561	gaataagactgtgacgaactggttgatccagaatgccaaagtctgtccaatgtacaagt	1620
Db	1561	gaataagactgtgacgaactggttgatccagaatgccaaagtctgtccaatgtacaagt	1620
Qy	1621	tgtgtctccaaagggtggccaggatgagcggtcatctactctctatgtgaccacct	1680
Db	1621	tgtgtctccaaagggtggccaggatgagcggtcatctactctctatgtgaccacct	1680
Qy	1681	ccccgagcgtctcacatcgaaatccaaagcctccgagagcctactagaggcgagccggt	1740
Db	1681	ccccgagcgtctcacatcgaaatccaaagcctccgagagcctactagaggcgagccggt	1740
Qy	1741	gctctgagctgccaaagccgacagctacaagtacagcatactgcgtggtaccgctcaa	1800
Db	1741	gctctgagctgccaaagccgacagctacaagtacagcatactgcgtggtaccgctcaa	1800
Qy	1801	cctgtccacgctgcacgagtgcgcagcggaaccgctctctgcagctgcaagaacgtgca	1860
Db	1801	cctgtccacgctgcacgagtgcgcagcggaaccgctctctgcagctgcaagaacgtgca	1860
Qy	1861	tctgttcgccaccctcttgccgccaagcctggagagggtggcaactggggcgccacgc	1920
Db	1861	tctgttcgccaccctcttgccgccaagcctggagagggtggcaactggggcgccacgc	1920
Qy	1921	caagctcaagctgagatctcccgctgcgcgcccagacgagggccactatgtgtgcga	1980
Db	1921	caagctcaagctgagatctcccgctgcgcgcccagacgagggccactatgtgtgcga	1980
Qy	1981	agtgcgaacggcgcgacgatgacaagcactgcccaagaagtaacctgtcggttcaggc	2040
Db	1981	agtgcgaacggcgcgacgatgacaagcactgcccaagaagtaacctgtcggttcaggc	2040
Qy	2041	cctggaagccctcggtctacgcagaaactgacccgacctctctggtgaacgtgagcactc	2100
Db	2041	cctggaagccctcggtctacgcagaaactgacccgacctctctggtgaacgtgagcactc	2100
Qy	2101	gctggagatgcagtgtctgtgtggccggagcgacgcgcccagactctgtgtgtacaaga	2160
Db	2101	gctggagatgcagtgtctgtgtggccggagcgacgcgcccagactctgtgtgtacaaga	2160
Qy	2161	cgagagctctggagggaaaaagtctggagtcgacttggcgactcccaaccagagctgag	2220
Db	2161	cgagagctctggagggaaaaagtctggagtcgacttggcgactcccaaccagagctgag	2220
Qy	2221	catccagcgcgctgcgcgagagagatgcgggacgctatctgtgcagcgtgtgtcaacycca	2280
Db	2221	catccagcgcgctgcgcgagagagatgcgggacgctatctgtgcagcgtgtgtcaacycca	2280

QY	2281	ggcctgcgtcaactcctccgcagcgtgcccgtggaaggctccagataaaaggcagcat	2340
Db	2281	ggcctgcgtcaactcctccgcagcgtgcccgtggaaggctccagataaaaggcagcat	2340
QY	2341	ggagatcgtatccctgtcgtatccgcgtcaatcgctgtctctcttggggtctctctct	2400
Db	2341	ggagatcgtatccctgtcgtatccgcgtcaatcgctgtctctctcttggggtctctctct	2400
QY	2401	cctcatctttgtaacatgagagcgcgcacacgcagacataaagagcgggtacctatgc	2460
Db	2401	cctcatctttgtaacatgagagcgcgcacacgcagacataaagagcgggtacctatgc	2460
QY	2461	catcatcattggaaccccgaggaggtgcctcttgaggagcaatcgataacctgtctaacga	2520
Db	2461	catcatcattggaaccccgaggaggtgcctcttgaggagcaatcgataacctgtctaacga	2520
QY	2521	tgcagccagtgggaattcccccgagagcgttgcaccttggggagagtgctcgcgtacgg	2580
Db	2521	tgcagccagtgggaattcccccgagagcgttgcaccttggggagagtgctcgcgtacgg	2580
QY	2581	cgccttcggaaaggttggttgaaagcctccgttttcggcataccaaagggcagcagcttga	2640
Db	2581	cgccttcggaaaggttggttgaaagcctccgttttcggcataccaaagggcagcagcttga	2640
QY	2641	caccgtggccgttgaaatctgtgaaagggcgccacgcgcagcagaccgcgcgtcgat	2700
Db	2641	caccgtggccgttgaaatctgtgaaagggcgccacgcgcagcagaccgcgcgtcgat	2700
QY	2701	gtcggagctcaagatcctcattcaatcggcgaacctcaacgttgcgcgtgaggaagtctcc	2760
Db	2701	gtcggagctcaagatcctcattcaatcggcgaacctcaacgttgcgcgtgaggaagtctcc	2760
QY	2761	ggcctgcaccgaacgcgcagggccccctcaatgggtgaggttctcgaagtacgcgcaa	2820
Db	2761	ggcctgcaccgaacgcgcagggccccctcaatgggtgaggttctcgaagtacgcgcaa	2820
QY	2821	cctctccaaactctcgcgcgaacggagacgccttcagccccctgcgcgagaagtctcc	2880
Db	2821	cctctccaaactctcgcgcgaacggagacgccttcagccccctgcgcgagaagtctcc	2880
QY	2881	cgaagcgcgcgcgccttcgcgcctcattggtgaggtctcccaaggtcggatcgcgagggcgc	2940
Db	2881	cgaagcgcgcgcgccttcgcgcctcattggtgaggtctcccaaggtcggatcgcgagggcgc	2940
QY	2941	ggggagcagcgacaaggctcctcttcgcgcgttctcgaagaccggagggcgcgagcgcg	3000
Db	2941	ggggagcagcgacaaggctcctcttcgcgcgttctcgaagaccggagggcgcgagcgcg	3000
QY	3001	ggcttctccagaccagaagctgaggaccttggcgtgagccgtgacccgtgacatggaagtct	3060
Db	3001	ggcttctccagaccagaagctgaggaccttggcgtgagccgtgacccgtgacatggaagtct	3060
QY	3061	tgtctgtacagcttcaggttgccagagggatggagtctctggcttcccgaagtgcat	3120
Db	3061	tgtctgtacagcttcaggttgccagagggatggagtctctggcttcccgaagtgcat	3120
QY	3121	ccacagagactggctgctcggaaacattctgctcggaaagcagcgtggtgaagatctg	3180
Db	3121	ccacagagactggctgctcggaaacattctgctcggaaagcagcgtggtgaagatctg	3180
QY	3181	tgaacttggccttgcgcgggacatctcaaaagacctgactacgtccgcaaggcagtgct	3240
Db	3181	tgaacttggccttgcgcgggacatctcaaaagacctgactacgtccgcaaggcagtgct	3240
QY	3241	ccgcttgccttgaaatggatggcccttgaaagcatctcgacaagtggtacaccagca	3300
Db	3241	ccgcttgccttgaaatggatggcccttgaaagcatctcgacaagtggtacaccagca	3300
QY	3301	gagtgcagctgtgctcttgggggtgcttctctcgagatcttctcttgagggtctcccc	3360
Db	3301	gagtgcagctgtgctcttgggggtgcttctctcgagatcttctcttgagggtctcccc	3360
QY	3361	gtacctgtgggttgcagatacaatgagggttcttgcacagcggctgagagacgcgcacagat	3420

Db 661 CTTCCTTTTCCAACCCCTTCCTGGTGACATCACAGGCAACGAGCTCTATGACATCCAGCT 720
QY 721 gttccccagaaagtgcgtgagctgcgtgtagggagaaagtgcgttcctgaactgcacccgt 780
Db 721 GTTCCCCAGGAAGTCGCTGAGAGTCGCTGTTAGGGAGAAAGCTGGTCTTGAACCTGCACCGT 780
QY 781 gtgggctgagtttaactcagggtgtaacctttgactggagctaccagggaagcaggcaga 840
Db 781 GTGGGCTCAGTTTAACTCAGGTGTCACCTTTGACTGGGACTACCCAGGGAAGCAGCAGA 840
QY 841 gcggggttaagtgggtgcccagagcgaactctcccagcagacccacacagaaactctccagcat 900
Db 841 GCGGGGTAAAGTGGGTGGCCGAGGACGACGCTCCACGACAGCCACACAGAACTCTCCAGCAT 900
QY 901 cctgaaccatccaaacgtcagcagcagcagcctgggctcgtatgtgtgcaagggcccaaca 960
Db 901 CCTGACCATCCACAAAGTCAGCAGCAGCAGCCTGGGCTCGTATGTGTGCAAGGCCAACA 960
QY 961 cggcatccagcatcttcgggagagcaccgaggttcattgtgcatgaaatcccttcatcag 1020
Db 961 CGGCATCCAGCATTTCCGGAGAGCACCAGAGGTCAATTTGTCATGAAAAATCCCTTTCATCAG 1020
QY 1021 cgtcgaatgctcaaaagacccatccttgaggccacgagcagcagcagcagcagcagcagc 1080
Db 1021 CGTCGAGTGGCTCAAAAGGACCCATTCCTTGGAGGCCACGGCAGGAGCAGAGTGGTGAAGCT 1080
QY 1081 gccgtgaagctlggagcgttaccctccgcccgcaggttcagtggtacaaagatgaaagggc 1140
Db 1081 GCCGTGAAGCTGGCAGCGTACCCCCGCCCGAGTTCAGTGGTACAAAGGATGAAAGGC 1140
QY 1141 actgtccggcgccacagtcacatgcccctgggtgctcaaggaggtgacagagccagcac 1200
Db 1141 ACTGTCCGGCGCCACAGTCCACATGCCCTGGTGCTCAAGGAGGTGACAGAGGCCAGCAC 1200
QY 1201 aggcacctacacctggccctgtggaactccgctgctggcctgagcgcgaacatcagcct 1260
Db 1201 AGGCACCTACACCCCTGCCCTGTGGAACTCCGCTTGGCCTGAGCGCAACATCAGCCT 1260
QY 1261 ggaactggtggtgaattgtgccccccagatacatgagaaggagcctctccccccagcat 1320
Db 1261 GGAGCTGGTGGTGAATGTGCCCCCCCAGATACATGAGAGGAGCGCTCTTCCCCCAGCAT 1320
QY 1321 ctactcgttcaagcgcgcagcctcaactgacagcgcctacgggtgcccctgctct 1380
Db 1321 CTACTCGCGTCACAGCGCCAGGCCCTCACTGACAGGGCTACGGGGTGCCCTGCCTCT 1380
QY 1381 cagcatccagtggcactggcgccctggacacccctgcaagatgtttgcccagcgtagct 1440
Db 1381 CAGCATCCAGTGGCAGCTGGCGGCCCTGGACACCCCTGCAAGATGTTTQCCCGAGCGTAGTCT 1440
QY 1441 ccggcgcgagcagcagaagacctcatgcccacagtgccgtgactgagggcggtgaccac 1500
Db 1441 CCGCGCGCGCAGCAGCAACCTCATGCCCACAGTGCCTGAGTGAGGGCGGTGACCAC 1500
QY 1501 gcaggatgcccgtgaaccccatcgagagcctggacactggaactgacaggtttgtggaggaaa 1560
Db 1501 GCAGGATGCCGTGAACCCCATCAGAGCCTTGGACACTGGACCCAGCTTGTGGAGGGAAA 1560
QY 1561 gaataagactgtgagaagcgtgtgatccagaatgccaacgtgtctgccaatgtacaagt 1620
Db 1561 GAATAAGACTGTGAGCAAGCTGGTGTATCCAGAAATGCCAAGTGTCTGCCATGTACAAAGTG 1620
QY 1621 tgtggtctccaaacaaagtggggcagagtgagcgggtcactactctatgtgacaccat 1680
Db 1621 TGTGGTCTCCAAACAGGTGGCCGAGATGAGCGGCTCATCTACTTCTATGTGACCAACCAT 1680
QY 1681 ccccagcggcttcaccatccaaagccatccagccatccgagagctactagagggccagccggt 1740
Db 1681 CCCCAGCGGCTTCACCATCGAATCCAAAGCCATCCGAGGAGCTACTAGAGGGCCAGCGGT 1740
QY 1741 gctcctgagctgccaagcagcagctacaaagtacagatcctgctggtgtaccgctcaa 1800
Db 1741 GCTCCTGAGCTGCCAAGCCGACAGCTACAAGTACGAGCATCTGCGCTGGTACCGCTCAA 1800

QY 1801 cctgtccacgctgacgatgctgcacgggaacccgcttctgctcgtactgcaagaacgtgca 1860
Db 1801 CCTGTCCACGCTGCAGATGCGCACGGGAACCCGCTTCTGCTCAGCTGCAAGAACGTGCA 1860
QY 1861 tctgttccgccaccctctctggcccagcctggaggaggtggcaacctggggcgccacgc 1920
Db 1861 TCTGTTCCGCCACCCCTCTGGCCGCCAGCTTGGAGGAGGTGGCACCTTGGGGCGGCCACGC 1920
QY 1921 cagcctcagcctgagtatccccccgctgcgcgcccgagcagcagcagcagcagcagcagc 1980
Db 1921 CAGCCTCAGCCTGAGTATCCCCCGCTGCGCCCGCAGCAGCAGGAGGCTACTATGTGTGCGA 1980
QY 1981 agtgcaagaccgctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 2040
Db 1981 AGTGCAAGACCGCGCAGCCATGACAAGCACTGCCCAAGAAAGTACTGTGCGGTGCAGGC 2040
QY 2041 cctggaaagcccttcggtctcagcagcaacttgaccgacctcctggtgaaacgtgagcagc 2100
Db 2041 CCTGGAAGCCCTTCGCTCAGGCAGAACTTGACCGACCTCCTGCTGAACGTGAGCGCATC 2100
QY 2101 gctggagatgcaagtgccttgggtggccggagcgcgcgcgcgcgcgcgcgcgcgcgcgc 2160
Db 2101 GCTGGAGATGCAAGTGTGTGGTGGCGGAGCGCACGGCGCCAGCATGCTGTGGTTACAAGA 2160
QY 2161 cgaagagctgctgagagaaagtctgagtcgacttggcgactcgaaccacagaaagctgag 2220
Db 2161 CGAGAGCTGCTGGAGGAAAGTCTGGAGTGCAGTTCGAGGACTCCCAACACAGAAAGCTGAG 2220
QY 2221 catccagcgtgctgcgagagagatgcggagcgtactctgctgagcgtgtgcaacgccaa 2280
Db 2221 CATCCAGCGCTGCGCGAGGAGATGCGGGACGCTATCTGTGCAGCGTGTGCAACGCCAA 2280
QY 2281 gggctgcgtcaactctccgcagcgtggccgtggaagctcccgagataaaggggaagc 2340
Db 2281 GGGCTCGCTCAACTCTCGCCAGCGTGGCCGTGGAGGCTCCGAGGATAAGGCGAGCAT 2340
QY 2341 ggaatgcgtgactctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 2400
Db 2341 GGAGATCGTGATCTTGTCTGCTACCGCGCGCTCATCGCTGTCTTCTGCGGTCTCTCTCT 2400
QY 2401 cctcatcttctgtaacatgagagggcgccacgcagacatcaagacggggtacactgtc 2460
Db 2401 CCTCATCTTCTGTAACTAGGAGGCGGCCCCAGCGCAGACATCAAGACGGGTACCTGTCT 2460
QY 2461 catcatcattggaccccgagggtgctcctgagaggaatagcgaatacctgtcctacga 2520
Db 2461 CATCATCATGGACCCCGGGAGTGCTCTGGAGGAGCAATGCGAATACCTGTCTCTACGA 2520
QY 2521 tgccagcagtgaggaaattcccccgagcgtgacactggggagagtgctcggtacgg 2580
Db 2521 TGCCAGCCAGTGGGAATTCCTCCGAGAGCGGTGTCACCTTGGGGAGAGTGTCTCGGCTACGG 2580
QY 2581 cgcttccgggaaggtggtggaagcctccgcttccggaatcccaagggcagcagctgtga 2640
Db 2581 CGCCTTCGGGAAGGTGTGGAAGCCTCCCTTTCGGCATCCACAGGGCAGCAGCTGTGA 2640
QY 2641 caccgtggccgtgaaaaatgctgaagagggcgccacggccagcagcagcagcagcagcag 2700
Db 2641 CACCGTGGCGGTGAAAATGCTGAAAGAGGGCGCCACGGCCAGCAGCAGCGCGCGCTGAT 2700
QY 2701 gtcgagctcaagatcctcattcacatcgcaacacactcaacgtggtcaacctcctcgg 2760
Db 2701 GTCGGAGCTCAAGATCCTCATTCACATCGGCAACCACTCAACGTGGTCAACCTCTCTCGG 2760
QY 2761 ggcgtgcaacaaagccgagggccccctcatggtgacgtggaggttctgcaagtacggcaa 2820
Db 2761 GCGGTGCACCAAGCCGACGGCCCCCTCATGCTGTGAGAGTCTGCAAGTACGGCAA 2820
QY 2821 cctctccaaacttctgcgcgcaagcgggaacgcttcagccccctgcgaggagaagctctcc 2880
Db 2821 CCTCTCCAACTTCTTGGCGGCCAAGCGGAGCGCTTCAGCCCCCTGCGCGGAGAGTCTCC 2880

Qy 61 cctggactcctggacggcctggtgagtgctactccaagaccccccagacattgaacat 120
Db 61 CCTGGGACTCCTGGACGGCCTGGTGAGTGGCTACTCCATGACCCCCGACCTTGAACAT 120
Qy 121 cacgagagagtcacacgctcatcgacacccggtagacagcctgtcca tctctgtaggggaca 180
Db 121 CACGGAGGAGTCACACGTCATCCACACCGGTGCACAGCCTGTCCATCTCTCGCAGGGACA 180
Qy 181 gacccccctcagatgggcttgccaggagctcagagagccagcaccagggagacaagga 240
Db 181 GACCCCCCTCAGAGTGGGCTTGCCCAAGAGCTCAGGAGCGCCACGACCGGAGACAAGGA 240
Qy 241 cacgagagacacgggggtggtgtagagctgcagagggcacagagccagcctactgcaa 300
Db 241 CACGAGGACACGGGGGTGGTGGAGACTGCGAGGCTGCGAGGGCACAGAGCCAGGCCCTACTGGCAA 300
Qy 301 gtlgtlgtctgctgcacgaggtgtacatgccaaacgacacagcagctacgtctgtactacaa 360
Db 301 GGTGTGTGCTGTGCACGAGGTACATGCCAACACACAGGCAGCTACGTCTGCTACTACAA 360
Qy 361 gfacatcaaggacacgcatacgaaggacacacagccgcccagctcctcgttctcgtgagaga 420
Db 361 GTACATCAAGGACACGCATCGAGGGACCAACGCTTGACAGCTTGTGGTCAACAGGAGCGCCAT 420
Qy 421 ctttgagcagcattcatcaaacgctgacacgctcttgggtcaacagaaagacgcat 480
Db 421 CTTTGGACAGCCATTTCATCAACAGCCTTGACAGCTTGTGGTCAACAGGAGCGCCAT 480
Qy 481 ggggtgcccctgctcgtggtgtccatccccgggctcaatgtlcaagctgcgctgcgaagctc 540
Db 481 CTGGGTGCCCTCTGCTGTGTCTCATCCCCGGCCTCAATGTACGCTGCGCTCGCAAGGCTC 540
Qy 541 ggtgctgtggccagacgggcagagagtggtgtgagatgacagcgccggcgatcgtcgtc 600
Db 541 GGTGTGTGGCCAGACGGGCAGGAGTGTGTGGATGACCGCGGGGCGCATGCTCTGTCTC 600
Qy 601 cagcgaactgctgcagatgcccctgactcagtgagagacacacagcagctctatgacatccagct 720
Db 601 CACGCCACTGCTGCAGATGCCCTGTACTGTGAGTGCAGAGCCACTTGGGGAGACCAAGA 660
Qy 661 ctctcttccaaaccccttctcgtggtgcacatacaggaacagcagctctatgacatccagct 720
Db 661 CTCTCTTCCAAACCCCTTCTGCTGCATCACAGCATCACAGCAAGCAGCTCTATGACATCCAGCT 720
Qy 721 gttgccaggaagtcgctgagactcgtgtagggagagagctggtccctgaaactgcacgct 780
Db 721 GTTGCCCAAGGAAGTCGCTGGAGCTGCTGGTAGGAGAGAGCTGGTCTCTCAACTGCACCGT 780
Qy 781 gtgggctgagtttaactcaggtgtcacctttgactgggactaccagaggaagcagggcaga 840
Db 781 CTGGGCTGAGTTTAAGTGGGTGCCCGAGCGAGCTCCCGAGCAGACCCACACAGAACTCTCCAGCAT 900
Qy 841 gcggggtaagtgggtgcccagagcagctccccagcagaccacacagaaactctccagcat 900
Db 841 CGGGGTAAGTGGGTGCCCGAGCGAGCTCCCGAGCAGACCCACACAGAACTCTCCAGCAT 900
Qy 901 cctgaccatccacaacgctcagcagcagcagcagctgggtcgtgtagtgcgaaggccaaaca 960
Db 901 CCTGACCATCCACAACGCTCAGCCAGCAGCTGGGCTGCTATGTGTGCAAGGGCCAAACA 960
Qy 961 cggcatccagcgaatttcgggagagcagcagagtcattgtgcatgaaatcccttcatcag 1020
Db 961 CGGCATCCAGCGATTTCGGGAGAGGACCGAGGTCATTGTGATGAAATCCCTTCATCAG 1020
Qy 1021 cgtcagtggttcaaaagacccatcctggagccacgcagcagagcagctggtgaaact 1080
Db 1021 CGTCAGTGGCTCAAAAGGACCCATCCTGGAGGCCACGGCAGGAGACGAGCTGGTGAAGCT 1080
Qy 1081 gccctgaaactgagcagcgtacccccccccgagttccagtggtacaaagatgaaagggc 1140
Db 1081 GCCCGTGAAGCTGGCAGCGGTACCCCCCGCCCGAGTTCCAGTGGTACAAAGGATGAAAGGC 1140

Qy 1141 actgtccggcgccacagttccacatgcccctggtgctcaaggaggtgacagagggccagcac 1200
Db 1141 ACTGTCCGGCGCCACACTCCACATGCCCTGGTCTCAAGGAGGTGACAGAGGCCAGCAC 1200
Qy 1201 aggcacctacaccctcgcccctgtgtgaaactccgctgctggtcgtgagggcgaacaatacgacct 1260
Db 1201 AGGCACCTTACACCCCTCGCCCTGTGAACTCCGCTGCTGGCCTGAGGCGCAACATCAGCCT 1260
Qy 1261 ggaactggtggtgaatgtgccccccccagatatataagaaaggagagccctcctccccagcat 1320
Db 1261 GGAGCTGCTGTGTGAATGTGCCCCCCCCAGATACATAGAAGAGAGGCCCTCTCTCCCCAGCAT 1320
Qy 1321 ctactcgcgtcacagcggccagccctcactcgcagccctacggggtgccccctgcccct 1380
Db 1321 CTACTCGGCTCACAGCCGCCAGGCCCTCACCCTGCAGGCCCTACGGGGTGCCTCTGCTCT 1380
Qy 1381 cagcatccagtggcactggcgcccctggacacccctgcaagatggtttgcccagcgtagctct 1440
Db 1381 CAGCATCCAGTGGCAGCTGGCGCCCTGGACACCCCTGCAAGATGTTTGGCCACGCTAGTCT 1440
Qy 1441 ccggcgcgagcagcagaagacccctcatgcccagtgcccagtgccgtgactggagggcggtgaccac 1500
Db 1441 CCGCGCGCGGACGAGCAAGACCTCATGCCACAGTGGCGGTGACTGGAGGGCGGTGACCAC 1500
Qy 1501 gcagatgcccgtgaaccccatcgagagcctgagacacctggaccagttctgtgagggagaaa 1560
Db 1501 GCAGATCCCGTGAACCCCATCGAGAGCCTGGACACCTGGACCCGAGTGTGTGGAGGGAAA 1560
Qy 1561 gaaataagactgtgaaagctgggtgattccagaaatgccaacgtctctgcatgtcaaatgt 1620
Db 1561 GAATAAGACTGTGAGCAAGCTGGTGATCCACAATGCCAACGTGCTGCGCATGTACAAGTG 1620
Qy 1621 tgtggtctccaaaggtggggccaggatgagcggtcctactctctatgtgacacccat 1680
Db 1621 TGTGTCTCTCCAAAGGTGGGCCAGGATGAGCGGCTCATCTACTTCTATGTGACCAACAT 1680
Qy 1681 cccgagcgtctcaccatccgaatccaagccatccgagagactactaagagccagcaggt 1740
Db 1681 CCCGACGGCTTACCATTCGAATCCAAGCCATCCGAGAGCTACTAGAGGGCCAGCCGCT 1740
Qy 1741 gctcctgagctgccaaagccgacagctacaagtacagcatctgcgtggtggtaccgcctcaa 1800
Db 1741 GCTCTGAGCTGCCAAGCCGACAGCTACAAGTACGAGCATCTGCGCTGGTACCGCCCTCAA 1800
Qy 1801 cctgtccacgctgcacgagatgcgcagcggaacccgctctctgctgactgcgaagacgtgca 1860
Db 1801 CCTGTCCACGCTGCACGATGCGCACGGGAACCCGCTTCTGCTCGACTGCAGAACAGCTGCA 1860
Qy 1861 tctgttcgcaacccctctgcgcagccttgagagaggtgacacctgggcgagccacgc 1920
Db 1861 TCTGTTCCGCCACCCCTCTGGCCGCCAGCCTGGAGAGGTGGCACCTGGGGCGCCACGC 1920
Qy 1921 cagcctcagcctgagatcccccccgctgcgcgccgagcagcagggggccactatgtgtcga 1980
Db 1921 CAGCTCAGCCTGAGTATCCCCCGCTGCGCCCGCAGCAGCAGGGGCCACATATGTGTGCGGA 1980
Qy 1981 agtcaagacccggcgagccatgacaaagcactgcacaaagaagtacctgtctggtgcagggc 2040
Db 1981 AGTCAAGACCCGGCGAGCCATGACAAGCACTGCCACAAGAAGTACCTGCGGTGCGAGGC 2040
Qy 2041 cctggaagccctcgctcagcagaaacttgaccgacctcctggtgaactgagcagctc 2100
Db 2041 CCTGGAGCCCTCGGCTCAGCGCAGAACTTGAACCGACCTCTCTGGTGAACTGTGACGACTC 2100
Qy 2101 gctggagatgcagtgctgtgtggccggagcgcgcgcccagcatcgtgtggtacaaaga 2160
Db 2101 GCTGGAGATGCAGTGTCTGTGTGGCCGAGCGCACGCGCCCGAGCATCTGTGTGGTACAAAGA 2160
Qy 2161 cgaagagctcgtggaggaagaaagtctggagtcgacttggcgagctcccaacagagctgag 2220
Db 2161 CGAGAGGCTCTGGAGGAAAAGTCTGGAGTGCAGCTTGGCGGACTTCCAAACAGAGCTGAG 2220
Qy 2221 catccagcgcgtgcgcgagaggatgcggagcgtactctgtgacagcgtgtgcaacgcaaa 2280


```

: EARLIER APPLICATION NUMBER: 07/959,951
:
: EARLIER FILING DATE: 1992-10-09
:
: NUMBER OF SEQ ID NOS: 22
:
: SOFTWARE: PatentIn Ver. 2.0
:
: SEQ ID NO 3
:
: LENGTH: 4795
:
: TYPE: DNA
:
: ORGANISM: Homo sapiens
:
: FEATURE:
:
: NAME/KEY: CDS
:
: LOCATION: (20)..(4108)
:
: US-09-169-079-3

```

Query Match					
Best Local Similarity	100.0%	Score 4111;	DB 15;	Length 4795;	
Matches 4111; Conservative	0;	Mismatches	0;	Indels	0; Gaps
Oy	1	ccacgcgcagcggccgagatgcagcgggcgccgcgcctgtgcttcgcactgctgcctg	60		
Dd	1	ccacgcgcagcggccgagatgcagcgggcgccgcgcctgtgcttcgcactgctgcctg	60		
\ y	61	cctgggaacctcctggacggccttggtgagtgggttactccatgacccccccgcaccttgaacat	120		
Dd	61	cctgggaacctcctggacggccttggtgagtgggttactccatgacccccccgcaccttgaacat	120		
Oy	121	cacgagagatcacacgtcatcgacaccgggtgcagcgcctgtccaatccttcgcaggagaca	180		
Dd	121	cacgagagatcacacgtcatcgacaccgggtgcagcgcctgtccaatccttcgcaggagaca	180		
Oy	181	gcaccccctcagttgggcttggccagagctccagagggcgccacgccacggagacaagga	240		
Dd	181	gcaccccctcagttgggcttggccagagctccagagggcgccacgccacggagacaagga	240		
Oy	241	cagcgagacacgggggttgtgcgagactgcgagggcacagcgcaggccctactgtcaa	300		
Dd	241	cagcgagacacgggggttgtgcgagactgcgagggcacagcgcaggccctactgtcaa	300		
Oy	301	gggtgtgctgtgcacgaggtacatgtccaacgcacacagggcagctacgtctgctactaca	360		
Dd	301	gggtgtgctgtgcacgaggtacatgtccaacgcacacagggcagctacgtctgctactaca	360		
Oy	361	gtacatcaaggcacgcgatcaggggcacacggccgcagctcctaogtgtctgtgagaga	420		
Dd	361	gtacatcaaggcacgcgatcaggggcacacggccgcagctcctaogtgtctgtgagaga	420		
Oy	421	ctttgagcagccattcatcaacagcctgcacgcctcttggtcaacagagagacacccat	480		
Dd	421	ctttgagcagccattcatcaacagcctgcacgcctcttggtcaacagagagacacccat	480		
Oy	481	gtgggtgcctctgtgtgtgtccatccccggccccaatgtcacgctgcgctcgcaaaagctc	540		
Dd	481	gtgggtgcctctgtgtgtgtccatccccggccccaatgtcacgctgcgctcgcaaaagctc	540		
Oy	541	gggtcgtgtggccagacgggcagggaggttggtgtggagtgcacggcggggcatgctcgtgc	600		
Dd	541	gggtcgtgtggccagacgggcagggaggttggtgtggagtgcacggcggggcatgctcgtgc	600		
Oy	601	cacgccactgctgcacgatgcootgttacctgcagtcgagacacaccttggggagaccagga	660		
Dd	601	cacgccactgctgcacgatgcootgttacctgcagtcgagacacaccttggggagaccagga	660		
Oy	661	cttcccttccaaccccttccgtgtgcacatcacaggcaacagagcttatgcacatccagct	720		
Dd	661	cttcccttccaaccccttccgtgtgcacatcacaggcaacagagcttatgcacatccagct	720		
Oy	721	gttgcccaggaaatcgctggagctgctgttaggggagaaagcttggtcctgaactgcacct	780		
Dd	721	gttgcccaggaaatcgctggagctgctgttaggggagaaagcttggtcctgaactgcacct	780		
Oy	781	gtgggctcgaatttaactcaaggtgtcaccttttgactgggactaccagggaagcagggcaga	840		
Dd	781	gtgggctcgaatttaactcaaggtgtcaccttttgactgggactaccagggaagcagggcaga	840		

[illegible]

[illegible][illegible]

QY 1441 ccggcgcgagcagcaagaacctcatgcccacagtgccgtagctggagggcggtgaccac 1500
DB 1441 CCGCGCGCGCAGCAGCAAGACCTCATGCGCACAGTGCCTGACTGGAGGCGGTGACCAC 1500
QY 1501 gaggatgccgtgaacccccatgagagcctggacacctggaccaggttctgtgagggaaa 1560
DB 1501 CGAGGATGCCGTGAACCCCATCGAGAGCCCTGGACACCTGGACCGAGTTTGTGGAGGAAA 1560
QY 1561 gaaLaagactgtgagcaagctggtgatccagaaTgccaacgtgtctgqccatgLaacaagt 1620
DB 1561 GAATAAGCATGTGAGCAAGCTGGTGATCCAGATGCCAACGTGCTGCCATGTACAAAGTG 1620
QY 1621 tgggtctcaacaagtgggccaggatgagcggtctatcttctatgtgaccacct 1680
DB 1621 TGTGGTCTCCAACAAGGTGGCGCAGGATGAGCGGCTCATCTACTTCTATGTGACCACCAT 1680
QY 1681 cccgcagcgcttcacatcgaaTccaaagccatccgaggagctactagagggccagccggt 1740
DB 1681 CCGCGACGGCTTACCATCGAATCCAAGCCATCGAGGAGCTACTAGAGGGCCAGCGGT 1740
QY 1741 gctctgagctgccaagccagactacaagtacgagcatctgctggTaccguctcaa 1800
DB 1741 GCTCTGAGCTGGCAAGCCGACAGCTACAAAGTACGAGCATCTGCGCTGGTACCCTCAA 1800
QY 1801 cctgtccacactgcagatgcgcagggaaacccgcttctgctgactgcaagaacgtgca 1860
DB 1801 CCTGTCCACGCTGCACGATCGGACGGGAACCCGCTTCTGCTCGACTGCAAGAACGTGCA 1860
QY 1861 tctgttcgcaaccccttgccgccagcctggaggaggtggcacctggggcgcgcacgc 1920
DB 1861 TCTGTTCCGCCACCCCTCTGCGGCCACCTGAGGAGGTGGCACCCTGGGGCGGCCACGC 1920
QY 1921 caagctcaagctgagtatccccgcgctgcgcgcgagcaggggcaactatgtgca 1980
DB 1921 CAGGCTCAGGCTTGAGTATCCCGCGCTGCGCGCCGACGACGAGGGCCACTATCTGTGGA 1980
QY 1981 agtgcaagccgagcagccatgacaagcactgccacaagaatacctgtcgtgcagcc 2040
DB 1981 AGTGCAAGACCGCGCAGCCATGACAAGCACTGCCACAAGAATACCTGTGCGGTGCGGC 2040
QY 2041 cctggaaagccctcggtcagcagaaacttgaccgacctcctggtgaaagtgagcgactc 2100
DB 2041 CCTGGAAGCCCTCGGCTCACGAGAACTTGACCGACCTCCTGCTGAACGTGAGCGACTC 2100
QY 2101 gctggagatgactgctgtggtggccggagcgacgcgcgccagcatcgtgtggtacaaga 2160
DB 2101 GCTGGAGATGCACTGTGCTGGTGGCCGAGCGCACGCGCCAGCATCGTGTGTACAAAGA 2160
QY 2161 cgagagctgctggagaaaagtctggagtcgacttggcgagctccaaaccagaagctgaq 2220
DB 2161 CGAGAGGCTGCTGGAGGAAAGTCTGGAGTCGACTTGGCGGACTCCAACGAAAGCTGAG 2220
QY 2221 catccagcgctgcgcgagaggatgcgggaacgtatctgtgcagcggtgtgcaacgccaa 2280
DB 2221 CATCCAGCGGCTGCGCGAGGAGGATCGGGACGCTATCTGTGCAGCGTGTGTCAACGCCAA 2280
QY 2281 ggcctgcgtcaactcctccgcagcagtgccgtggagagctccqaggaataaaggcgact 2340
DB 2281 GGGCTGCGTCAACTCTCTCGCCGACGCTGGCCGTGGAGGCTCCGAGGATGAAGGGCAGCAT 2340
QY 2341 ggagatcgtagtcttgcgtaccggcgctcatcgctgttcttcttcttgcgttctcctct 2400
DB 2341 GGAGATCGTGATCTTGTGCGGTACCGCGCTCATCGCTGTCTTCTTCTTCTTCTTCTTCT 2400
QY 2401 cctcatcttctgtaaatgagggagcgccgccacgcagacataaagacgggctacctgtc 2460
DB 2401 CCTCATCTTCTGTAAATGAGGAGCGCGGCCACGCGAGACATCAAGACGGGCTACCTGTC 2460
QY 2461 catcatatggaacccggggagtgctctgtgagagcaatgcgaatacctgtctctacga 2520
DB 2461 CATCATATGGACCCCGGGAGGTGCTCTTGGAGGAGCAATGCGAATACCTGTCTCTACGA 2520

QY 2521 tgccagccagtgggaaattcccccgagagcggtgcacctggggagagtgctcgggtacgg 2580
DB 2521 TGCCAGCCAGTGGGAATTCCTCCGAGAGCGGTGCACTGGGAGAGTGTCTCGCTACGG 2580
QY 2581 cgccttcgggaaagtgtggaagcctccgcttctcggcataccacaaggagcagcagctgtga 2640
DB 2581 CGCTTTCCGGGAAGGTGGTGAAGCCTCCGCTTTTCGGCATCCCAAGGGCAGCAGCTGTGA 2640
QY 2641 caccgtggcgTgaaaaTgctgaaagaggcgccacgagcgccagcagcaccgcgcgtgat 2700
DB 2641 CACCGTGGCGGTGAAATGCTGAAAGGGCGCCAGCGGACGAGCACCAGCGCGGTGAT 2700
QY 2701 gtcgagctcaagatcctcatctacacTcggaaccacctcaacgtgtgtaacctcctcg 2760
DB 2701 GTCCGAGCTCAAGATCCTCATTTCACTCGCAACCACTCAACGTGTCAACCTCCTCGG 2760
QY 2761 ggcgtacacaagccgacagggcccccctcatgtgtagctgtggagttctgcaagtacggaaa 2820
DB 2761 GCGGTGCACAAGCCGACGGGCCCTCATGTTGATGCTGGAGTTCTGCAAGTACGGCAA 2820
QY 2821 cctctccaaactctctgcgcgccaagcggaacgcttcaagccccctgcgcggagaagtctcc 2880
DB 2821 CCTCTCAACTTCTCTGCGGCCAAAGCGGACGCCCTTTCAGCCCTGCGCGGAGAAGTCTCC 2880
QY 2881 cgagcagcgcgacgcttccgcgcaatggtgagctcgcagctcggaTcggaaggcgcc 2940
DB 2881 CGAGCAGCGGACGCTTCCGGCCCATGTGGAGCTTCGCCAGGCTGGATCGGAGCGGCC 2940
QY 2941 ggggagcagcagaggttctcttcgcgcggttctcgaagaccgagggcgagcagcagcg 3000
DB 2941 GGGGACACGACAGAGGTCTCTTCCGCGGTTCCTCGAAGACCGAGGGCGGAGCGGCG 3000
QY 3001 guctctccagaccaaagaagctgaggacctgTggctgagccccgctgacctggaagatct 3060
DB 3001 GCGTCTCCAGACCAAGAAGCTGAGGACCTGTGGCTGAGCCCCCTGACCATTGGAAGATCT 3060
QY 3061 tgtctgtacagcttccaggttgccagagaggtgagttccttggcttcccgaagaatgcat 3120
DB 3061 TGTGTGCTACAGCTTCCAGGTGGCCAGAGGGATGGAGTTCTCTGGCTTCCCGAAGTGCAT 3120
QY 3121 ccacagagacctggctgcggaacattctgctgcggaagcgagctgtgtgaagatctg 3180
DB 3121 CCACAGAGACCTGGCTGCTCGGAACATTCTGCTGCGGAAAGGACGCTGGTGAAGATCTG 3180
QY 3181 tgactttggccttggccgggacatctacaagaacctgactacTACGTCGCGAAGGCGAGTGC 3240
DB 3181 TGACTTTGGCCTTGGCCGGGACATCTACAAGACCTGACTACGTCGCGAAGGCGAGTGC 3240
QY 3241 ccggctgccccTgaagtggatggccccctgaaagcatcttcgacaagggtgtacacacgca 3300
DB 3241 CCGGCTGCCCTTGAAGTGGATGGCCCCCTGAAAGCATCTTTCGACAAGGTGTACACCACGA 3300
QY 3301 gagtgcagtggtgcttcttgggggtgcttctctgggagatacttctcttgggggctcccc 3360
DB 3301 GAGTGACGTGTGCTTCTTGGGGTGTCTCTCTGCGAGATCTTCTCTCTGCGGGGCTCCCC 3360
QY 3361 gtacctggggTgcagataaaTgaggagttctgtccagcggtgtgagacgggcacaaagat 3420
DB 3361 GTACCTTGGGGTGCAGATCAATCAGAGGTTCTGTCCAGCGGCTGAGACGCGCACAAAGAT 3420
QY 3421 gaggcccccgagctggccactcccgccatccgcgcacatcgtgaaactgctggtccgg 3480
DB 3421 GAGGGCCCCGAGCTGGCCACTCCCGCCATCCCGCCATCATGCTGAACTGCTGTGTCCGG 3480
QY 3481 agacccccaggcgagacctgcatctctcgagctggtgagatactctgggggacctctcca 3540
DB 3481 AGACCCCAAGCGACACCTGCATTCTCGAGCTGTGTGAGATCTCTGCGGGGACCTGCTCCA 3540
QY 3541 gggcgagggccttgcagaaggaagaggtctgtcatgtgccccgcgcagctctcagagctc 3600
DB 3541 GGGCAGGGCCTTGCAAGAGGAAGAGAGGTCTGATGTGCCCGCCGCGCAGCTCTCTAGAGCTC 3600
QY 3601 agaaagggcgagcttctcgaggggtgtccacctagccatcgccccagggctgacgc 3660

Db 3121 CCACAGAGACCTGGCTGCTCGGAACATTTCTGCTCGGAAGCGACGCTGGTCAAGATCTG 3180
QY tgactttggccttgcccgagacatctacaaagacctgactcgtccgcaagggcagtg 3240
|||||
Db 3181 TGACTTTGGCCTTGCCCGGACATCTACAAAGACCTGACTAGCTCCGCAAGCGCAAGTGC 3240
|||||
QY ccggctgccccctgaagtggatggcccccgaagcatcttcgacaaggtgtacacacgcga 3300
|||||
Db 3241 CCGGCTGCCCTCAAGTGGATGGCCCTGAAAGCATCTTCGACAAGGTGTACACACGCA 3300
|||||
QY aagtgcagtgatggtctcttggggtgcttctcttgaggagatcttctctctgggggacctcccc 3360
|||||
Db 3301 GAGTACGCTGTGCTCTTTGGGGTGTCTCTCGGAGATCTTCTCTCTGGGGCCCTCCCC 3360
|||||
QY gtaccctlggggtgcagatacaatgagaggtctctgcagcgctgagagcgagcaaggat 3420
|||||
Db 3361 GTACCTTGGGCTGCAGATCAATCAGAGATTTCTGCCAGCGCTGAGAGACGGCAAGGAT 3420
|||||
QY gagggcccccggagctggccactccccccataacgcccacatctgtaactgtggtccgg 3480
Db 3421 GAGGGCCCGGAGCTGGCCACTCCGCCATACGCCGATCATGCTCAACTGCTGGTCCGG 3480
|||||
QY agaccccaaggcgagacctgcatctctcgagctggtggaagatctctggggagacctgctca 3540
|||||
Db 3481 AGACCCCAAGGCCAGACCTGCATTTCTCGAGCTGGTGGAGATCTCTGGGGACCTGCTCCA 3540
|||||
QY gggcaggggctcgaagagaaagagaggtctgcatggccccgcgagctctcagagctc 3600
Db 3541 GGCAGGGGCTGCAAGAGAAAGAGAGGTCTGCATGGCCCCCGCAGCTCTCAGAGCTC 3600
|||||
QY agaagggggcagcttctcgaggtgtccaccatggccctacacatcgcccagctgacgc 3660
Db 3601 AGAAGGGGAGCTTCTCGAGGTGTCCACCATGGCCCTACACATCGCCAGGCTGACGC 3660
|||||
QY tgaggacagcccccaagcctgcagcgccacacagcctggcccgccaggtattacaactgggt 3720
Db 3661 TGAGGACAGCCCCGCAAGCCTGCGAGCCACAGCCTTGGCGCCGAGGTATTACAACTGGGT 3720
|||||
QY gtcccttcccgggtgctcgccagaggggctgagaccgtggttctctccagagatgaagac 3780
Db 3721 GTCCCTTCCCGGCTGCTGCGCCAGAGGGGCTGAGACCCGTGGTTCCTCCAGGATGAAGAC 3780
|||||
QY atttgaggaattccccatgaccccaacgacctacaaggctctgtggacaaccagacaga 3840
Db 3781 ATTTGAGGAATTCCTCATGCCCAACGACCTACAAAGGCTCTGTGGCAACCCAGACAGA 3840
|||||
QY cagtggagtggtgctgcccgcagagagtttgacagatagagagcagcagcatagacaaga 3900
Db 3841 CAGTGGGATGGTGTGCTGCTCGAGGAGTTTGAGCAGATAGAGGAGGCGCATAGACAAGA 3900
|||||
QY aagcggcttcag 3912
|||||
Db 3901 AAGCGGCTTCAG 3912
|||||

RESULT 8

US-09-169-079-1
: Sequence 1, Application US/09169079
: GENERAL INFORMATION:
: APPLICANT: Alitalo, Kari
: APPLICANT: Kaipainen, Arja
: APPLICANT: Vaitola, Relfa
: APPLICANT: Jussila, Lotta
: TITLE OF INVENTION: File4 (VEGFR-3) as a Target for Tumor Imaging and Anti-Tumor Thera
: FILE REFERENCE: 28113/34891
: CURRENT APPLICATION NUMBER: US/09/169,079
: CURRENT FILING DATE: 1998-10-09
: EARLIER APPLICATION NUMBER: 08/901,710
: EARLIER FILING DATE: 1997-07-28
: EARLIER APPLICATION NUMBER: 08/340,011
: EARLIER FILING DATE: 1994-11-14
: EARLIER APPLICATION NUMBER: 08/257,754
: EARLIER FILING DATE: 1994-07-09

: EARLIER APPLICATION NUMBER: 07/959,951
: EARLIER FILING DATE: 1992-10-09
: NUMBER OF SEQ ID NOS: 22
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 1
: LENGTH: 4195
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (20)..(3913)
US-09-169-079-1

Query Match 95.2%; Score 3912; DB 15; Length 4195;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3912; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ccacgcgcagcggccggagatgcagcggggccgcgctgctgctcgagactgtgctctg 60
Db 1 ccacgcgcagcggccggagatgcagcggggccgcgctgctgctcgagactgtgctctg 60
QY 61 cctgggactcctggacggcctggtgagtggttactccatgacccccccgacacttgaacat 120
Db 61 cctgggactcctggacggcctggtgagtggttactccatgacccccccgacacttgaacat 120
QY 121 caccgaagagtcacacgtcatcgacacccggtgacagcctgtccatctcctcgaggggaca 180
Db 121 caccgaagagtcacacgtcatcgacacccggtgacagcctgtccatctcctcgaggggaca 180
QY 181 gcacccccctcgagtggtggttggccaggagctcagagggccagcgcacccgggagacaagga 240
Db 181 gcacccccctcgagtggtggttggccaggagctcagagggccagcgcacccgggagacaagga 240
QY 241 ccagcagggacacacgggggtggtgcgagactgcaggggacagagcgcagccctactactgcaa 300
Db 241 ccagcagggacacacgggggtggtgcgagactgcaggggacagagcgcagccctactactgcaa 300
QY 301 ggtgtgtcgtcgcacgaggtacatgccaaacacacagcagctacgtctgctactacaa 360
Db 301 ggtgtgtcgtcgcacgaggtacatgccaaacacacagcagctacgtctgctactacaa 360
QY 361 gtacatcaaggcagcgcacgcaggggacccacgcgcgcagctcctacgttctcgtgagaga 420
Db 361 gtacatcaaggcagcgcacgcaggggacccacgcgcgcagctcctacgttctcgtgagaga 420
QY 421 ctttgagagccattcatcaaaagcctgacacgctcttgggtcaaacaggaagagccat 480
Db 421 ctttgagagccattcatcaaaagcctgacacgctcttgggtcaaacaggaagagccat 480
QY 481 gtgggtgcccctgtctgtggtgtccatccccggcctcaatgtcacgctgcgctgcgaagctc 540
Db 481 gtgggtgcccctgtctgtggtgtccatccccggcctcaatgtcacgctgcgctgcgaagctc 540
QY 541 ggtgctgtggccagacggcggcaggggtggtggtggtatgacccggcggggtgctgctgctc 600
Db 541 ggtgctgtggccagacggcggcaggggtggtggtggtatgacccggcggggtgctgctgctc 600
QY 601 cagcgcactgctgcacgatgccctgtacgtgcagtcgcagacacactgggggagaccagga 660
Db 601 cagcgcactgctgcacga tggcctgtacctgcagtcgcagacacactgggggagaccagga 660
QY 661 cttccttttccaaaccccttctggtggtgcacatcacaggcaacagagctctatgacatccagct 720
Db 661 cttccttttccaaaccccttctggtggtgcacatcacaggcaacagagctctatgacatccagct 720
QY 721 gttgcccaaggaagtcgctggagctggtggtggtggtggtggtggtggtggtggtggtggtg 780
Db 721 gttgcccaaggaagtcgctggagctggtggtggtggtggtggtggtggtggtggtggtggtg 780
QY 781 gttgggctgagtttaactcaggtgtcacctttgactgggactacccaggggaaagcagcgaga 840
Db 781 gttgggctgagtttaactcaggtgtcacctttgactgggactacccaggggaaagcagcgaga 840

QY 841 gcygggtaagtgggtgccgagcgagctcccgagcagacccacacagaactctccagcat 900
Db 841 gcygggtaagtgggtgccgagcgagctcccgagcagacccacacagaactctccagcat 900
QY 901 cctgaccatccacaacgctcagccagcagcagctgggctgctatgtgtgcaaggccacaacaa 960
Db 901 cctgaccatccacaacgctcagccagcagcagctgggctgctatgtgtgcaaggccacaacaa 960
QY 961 cggcatccagcgatttcgggagagcagcagagctcaattgtgcaatacccttcacag 1020
Db 961 cggcatccagcgatttcgggagagcagcagagctcaattgtgcaatacccttcacag 1020
QY 1021 cgtcgagtggttcaaaaggaccatcctgtagggccacgagcagagagctggtagaagct 1080
Db 1021 cgtcgagtggttcaaaaggaccatcctgtagggccacgagcagagagctggtagaagct 1080
QY 1081 gcccgtagaagctgggagcgctaccccccccgagcttcagtggttacaaggagtagaaagcc 1140
Db 1081 gcccgtagaagctgggagcgctaccccccccgagcttcagtggttacaaggagtagaaagcc 1140
QY 1141 actgtccgggcccacagctccacatgcccctggtgctcaaggaggtgacagagccagcac 1200
Db 1141 actgtccgggcccacagctccacatgcccctggtgctcaaggaggtgacagagccagcac 1200
QY 1201 aggcacctacacctcgcccctgtggaactccgctgctgctcagggctgagggcgcaacatcagcct 1260
Db 1201 aggcacctacacctcgcccctgtggaactccgctgctgctcagggctgagggcgcaacatcagcct 1260
QY 1261 ggaagctgggtggatgtgcccccccaatatacagaaagagagcctccctccccagcat 1320
Db 1261 ggaagctgggtggatgtgcccccccaatatacagaaagagagcctccctccccagcat 1320
QY 1321 ctactcggttcacagcccgccctccactgctcagcgctcaggggtgcccctgcccct 1380
Db 1321 ctactcggttcacagcccgccctccactgctcagcgctcaggggtgcccctgcccct 1380
QY 1381 cagcatccagtggaactggcgccctggagacccctgcaagatgttgcacagcgtagct 1440
Db 1381 cagcatccagtggaactggcgccctggagacccctgcaagatgttgcacagcgtagct 1440
QY 1441 ccggcgccgagcagcagaacacctcactgcccacagtgccgtgactggaagcggtgaccac 1500
Db 1441 ccggcgccgagcagcagaacacctcactgcccacagtgccgtgactggaagcggtgaccac 1500
QY 1501 gcaggatgcgctgaaccccatcagagaccttgacacacctggaccgagtttgtgagggaaa 1560
Db 1501 gcaggatgcgctgaaccccatcagagaccttgacacacctggaccgagtttgtgagggaaa 1560
QY 1561 gaaataagactgtgagcaagctgggtgataccagaatgccacgctgtctgcaatgtataagtg 1620
Db 1561 gaaataagactgtgagcaagctgggtgataccagaatgccacgctgtctgcaatgtataagtg 1620
QY 1621 tgtggttcccaaaagtgggccagatgagcgctcactctactctctatgtgaccacat 1680
Db 1621 tgtggttcccaaaagtgggccagatgagcgctcactctactctctatgtgaccacat 1680
QY 1681 ccccgagcgcttcacatcgaaatccaaagcactccgagagctactagagggccagccggt 1740
Db 1681 ccccgagcgcttcacatcgaaatccaaagcactccgagagctactagagggccagccggt 1740
QY 1741 gctcctgagctgccaagcagcagctacaaagtagcagcactctgctggttaccgctcaa 1800
Db 1741 gctcctgagctgccaagcagcagctacaaagtagcagcactctgctggttaccgctcaa 1800
QY 1801 cctgtccagctgacagatgcccagggaaacccgcttctgctgactcaagaacgtgca 1860
Db 1801 cctgtccagctgacagatgcccagggaaacccgcttctgctgactcaagaacgtgca 1860
QY 1861 tctgttcgacacccctctggccgagcctggagaggtggacactggggcgccagcgc 1920
Db 1861 tctgttcgacacccctctggccgagcctggagaggtggacactggggcgccagcgc 1920

QY 1921 caogctcagcctgtagtatcccccgctcgccccgagcagcgagggccactatgtgtgcga 1980
Db 1921 caogctcagcctgtagtatcccccgctcgccccgagcagcgagggccactatgtgtgcga 1980
QY 1981 agtgcagaagccgagcgagccatgacaagcactgccaagaagtacctgtcggtgcagcc 2040
Db 1981 agtgcagaagccgagcgagccatgacaagcactgccaagaagtacctgtcggtgcagcc 2040
QY 2041 cctggaagcccttcggtctcacgcagaacttgaccagcctcctgtggaagctgagcagcctc 2100
Db 2041 cctggaagcccttcggtctcacgcagaacttgaccagcctcctgtggaagctgagcagcctc 2100
QY 2101 gctggagatgcagctgcttggctggcgagcgacgcgccccagcatctgtgtgtaacaaaga 2160
Db 2101 gctggagatgcagctgcttggctggcgagcgacgcgccccagcatctgtgtgtaacaaaga 2160
QY 2161 cgagagctgctgtaggagaaagtctggaagctgagctgagcagcctcacaacagagctgag 2220
Db 2161 cgagagctgctgtaggagaaagtctggaagctgagctgagcagcctcacaacagagctgag 2220
QY 2221 catccagcgctgctgtaggagaaagtgcgggagcgtatctgtgcagcgctgtgcaacgcca 2280
Db 2221 catccagcgctgctgtaggagaaagtgcgggagcgtatctgtgcagcgctgtgcaacgcca 2280
QY 2281 gggctgctgctcaactcctccgcccagcgctggcggtggaagctccgaggaataaggcgagcat 2340
Db 2281 gggctgctgctcaactcctccgcccagcgctggcggtggaagctccgaggaataaggcgagcat 2340
QY 2341 ggaagctgctgcttctgctgggtacccgctgctgctgctgctgctgctgctgctgctgct 2400
Db 2341 ggaagctgctgcttctgctgggtacccgctgctgctgctgctgctgctgctgctgctgct 2400
QY 2401 cctcatctctgtaacatgagagggccgccccagcagacatcaagcgggctacctgtc 2460
Db 2401 cctcatctctgtaacatgagagggccgccccagcagacatcaagcgggctacctgtc 2460
QY 2461 catcatcatggaaccccgggaggtgctctgtagaggaacaaagcgaataacctgtcctacga 2520
Db 2461 catcatcatggaaccccgggaggtgctctgtagaggaacaaagcgaataacctgtcctacga 2520
QY 2521 tgcagccagctgggaattcccccgagagcgctgcaactgggagagtgctcggtcagcg 2580
Db 2521 tgcagccagctgggaattcccccgagagcgctgcaactgggagagtgctcggtcagcg 2580
QY 2581 cgctctcgaggaggtgtagaagcctccgcttccgcatccacaaggcgagcgctgag 2640
Db 2581 cgctctcgaggaggtgtagaagcctccgcttccgcatccacaaggcgagcgctgag 2640
QY 2641 caccgtggcggtgaaaatgctgaaaagggcgccagcgccagcgagcgagcgagcgctgat 2700
Db 2641 caccgtggcggtgaaaatgctgaaaagggcgccagcgccagcgagcgagcgagcgctgat 2700
QY 2701 gtcgagctcaagatcctcatccatcgcgcaacacctcaactggtgcaacctctcgg 2760
Db 2701 gtcgagctcaagatcctcatccatcgcgcaacacctcaactggtgcaacctctcgg 2760
QY 2761 ggcgtgcaacagccgagggccctcctcatggtgtagctggtgaggtctgtgcaagtacggaa 2820
Db 2761 ggcgtgcaacagccgagggccctcctcatggtgtagctggtgaggtctgtgcaagtacggaa 2820
QY 2821 cctctcaacttctgctgcgcccaagcgagcgcttccagccctcagccccctgagggagagctccc 2880
Db 2821 cctctcaacttctgctgcgcccaagcgagcgcttccagccctcagccccctgagggagagctccc 2880
QY 2881 cgagcagcgagcgcttccgcccacatggtgagctcgcaggtcgaggtcgagcgcc 2940
Db 2881 cgagcagcgagcgcttccgcccacatggtgagctcgcaggtcgaggtcgagcgcc 2940
QY 2941 ggggagcagcagaggtctctctcgcgcggtctctcgaagacccgagggcgagcgagcg 3000
Db 2941 ggggagcagcagaggtctctctcgcgcggtctctcgaagacccgagggcgagcgagcg 3000
QY 3001 ggccttccagaccagaagctgaggaactgtggtgagccgctgacccatggaagatct 3060

Db 3001 ggccttccagaccaggaagctgaggaacctgtggtgagccgctgaccatggaagatct 3060
Qy 3061 tgtctgtacagcttccagggtggccagaggatggagttctctgcttccccaaaagtgc 3120
Db 3061 tgtctgtacagcttccagggtggccagaggatggagttctctgcttccccaaaagtgc 3120
Qy 3121 ccacagagacctggctgctcggaacattctctgtcggaagcagcgtggtggaagatcg 3180
Db 3121 ccacagagacctggctgctcggaacattctctgtcggaagcagcgtggtggaagatcg 3180
Qy 3181 tgaatttgacctgccccgggacatatcaaaagacctgactacgtcccgcaaggcagtcg 3240
Db 3181 tgaatttgacctgccccgggacatatcaaaagacctgactacgtcccgcaaggcagtcg 3240
Qy 3241 ccggctgccccgagtgagtgagtgccctgaaagcatctcgacaagtggtacacacgca 3300
Db 3241 ccggctgccccgagtgagtgagtgccctgaaagcatctcgacaagtggtacacacgca 3300
Qy 3301 gaggtaacgtgtggttctctggtggtggtctctctggtgagatcttctctggtggtcctccc 3360
Db 3301 gaggtaacgtgtggttctctggtggtggtctctctggtgagatcttctctggtggtcctccc 3360
Qy 3361 gtacctggggtgcagatcaaatgagagtggtctgcccagcggtgagagacgacacaaagat 3420
Db 3361 gtacctggggtgcagatcaaatgagagtggtctgcccagcggtgagagacgacacaaagat 3420
Qy 3421 gagggtcccgagctggcactcccgccatcagccgcatcatgctgaactgctggtccgg 3480
Db 3421 gagggtcccgagctggcactcccgccatcagccgcatcatgctgaactgctggtccgg 3480
Qy 3481 agaccccaaggcgagacctgcatctctcgagctggtgagatcctctggtggtcctgctcca 3540
Db 3481 agaccccaaggcgagacctgcatctctcgagctggtgagatcctctggtggtcctgctcca 3540
Qy 3541 gggcaggggcctgcaagaggaagagggtctgcatggcccgccagctctcagagctc 3600
Db 3541 gggcaggggcctgcaagaggaagagggtctgcatggcccgccagctctcagagctc 3600
Qy 3601 agaagaggagctctctcgagggtgtccacatggccctacacatcgcccgagctgacgc 3660
Db 3601 agaagaggagctctctcgagggtgtccacatggccctacacatcgcccgagctgacgc 3660
Qy 3661 tgaggacagcccgccagctgagcggccacagcctgagcccgaggtatcacactgggt 3720
Db 3661 tgaggacagcccgccagcctgagcggccacagcctgagcccgaggtatcacactgggt 3720
Qy 3721 gtcttttcccggtgtgctggccagagggtgtgagaccgtggttcttcccgagtgagagac 3780
Db 3721 gtcttttcccggtgtgctggccagagggtgtgagaccgtggttcttcccgagtgagagac 3780
Qy 3781 attgaggaattcccatgaccctcaacacagcactacaaaggctctgtggaacacacagaga 3840
Db 3781 attgaggaattcccatgaccctcaacacagcactacaaaggctctgtggaacacacagaga 3840
Qy 3841 cagtggaatggtgtggtcctcgaggagggtttgagcagatagagagcaggtacagacaaga 3900
Db 3841 cagtggaatggtgtggtcctcgaggagggtttgagcagatagagagcaggtacagacaaga 3900
Qy 3901 aagcggttcag 3912
Db 3901 aagcggttcag 3912

RESULT 9
US-08-601-132-36
: Sequence 36, Application US/08601132
: GENERAL INFORMATION:
: APPLICANT: Allitalo, Karl
: APPLICANT: Joukov, Vladimir
: TITLE OF INVENTION: Receptor Ligand
: NUMBER OF SEQUENCES: 41
: CORRESPONDENCE ADDRESS:

: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
: STREET: 6300 Sears Tower, 233 South Wacker Drive
: CITY: Chicago
: STATE: Illinois
: COUNTRY: United States of America
: ZIP: 60606-6402
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/601,132
: FILING DATE:
: CLASSIFICATION: 530
: ATTORNEY/AGENT INFORMATION:
: NAME: Gass, David A.
: REGISTRATION NUMBER: 38,153
: REFERENCE/DOCKET NUMBER: 28113/33118
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312/474-6300
: TELEFAX: 312/474-0448
: TELEX: 25-3856
: INFORMATION FOR SEQ ID NO: 36:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 4416 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: US-08-601-132-36

Query Match 95.2%; Score 3912; DB 10; Length 4416;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3912; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ccacgcgcagcggccggagatgcagcggcgccgcgctgtgctgcgactgtggctctg 60
Db 1 CCACGGCAGCGCGGAGATGACGGGGCGCGCGCTGTGCTGGACTGTGGCTCTG 60
Qy 61 cctgggactcctggagcggcctggtgagtggtactccatgacccccccgacctgaacat 120
Db 61 CTGGGACTCTTGAGCGGCTTGGTGTGCTACTTCATGACCCCGCCGACCTTGAACAT 120
Qy 121 cagcggaggagtcacacgtcatcagaccggtgacacgctgacacgctcctgctcctgagggaca 180
Db 121 CACGGAGGAGTCAACGTATCATGACACCGGTGACACGCTGTCCATCTCTTCAGGGGACA 180
Qy 181 gcacccctcctgagtggtggttggccaggagctcaggcggcggcggagacaaggga 240
Db 181 GCACCCCTCGAGTGGGCTTGGCCAGGAGCTCAGGAGGCGCCAGCCAGCCGAGACAAGGA 240
Qy 241 cagcggagacacggggtggtgagactgcgagggcacagacgagcggcctactgcaa 300
Db 241 CACGGAGGACACGGGGGTGTTGGGAGACTTCCGAGGCGACAGCGCCGCGCTTACTGCAA 300
Qy 301 ggtgttgctgtcagcagaggtacatgtcccaacacacagcagcagctcgtctgctactacaa 360
Db 301 GGTGTTGCTGCTGCACAGGTACATGCCAACACACACAGGAGCTAGCTGTGCTACTACAA 360
Qy 361 gtacatcaagggaacgcagtcaggggaccacgcccgcagctcctactcgttctgtagaga 420
Db 361 GTACATCAAGGACGATCATGAGGGGACACGCGCGCGAGCTCTTCTGTCTGTAGAGA 420
Qy 421 ctttgagcagcattcatcaaacgctgacagcgtcttgggtcaaacaggaagacgcat 480
Db 421 CTTTGAGCAGCCATTTCATCAACAGCCTTACACGCTTTGGTCAACAGAGAGAGCGCCAT 480
Qy 481 gtgggtgcccctgtctggtgtccatccccggcctcaatgtcacgctgctgcgaagctc 540
Db 481 GTGGGTGCCCTGTCTGTGGTGTCCATCCCCGGCCTCAATGTACAGCTGTCCGCTCGAAGCTC 540

QY 541 gggtgtgtgcccagcagcggcagaggtgggtgtgtgtgtgacccgagggcgatgctcgtgtc 600
Db 541 GGTGCTGTGCCAGACAGCGGACGAGAGTGGTGTGGATGATACCGCGGGGCATGCTCGTGTc 600
QY 601 cagccactgtgtcacgatagccctgttacctgcagtgtagacacacctggggagaccagga 660
Db 601 CAGCCCACTCTGTCAGGATGCCCTGTACCTGCACTGCGAGACCACTGGGGAGACCAGGA 660
QY 661 ctctcttccaaccccttctgggtgacatcacaggcaacagagctctatgacatccagct 720
Db 661 CTTCCTTTTCCAAACCCCTTCTGTTGCACATCACAGCAACGAGCTCTATGCATCCAGCT 720
QY 721 gttgccagagaagtcgtgagctgctgtgttaggggagaagctggtcctgaactgacacct 780
Db 721 GTTGGCCAGGAAGTCTGCTGGAGCTGCTGTGTAGGGGAGAAGCTGCTCTGAATGCAACCGT 780
QY 781 gtgggtgaagttaaactcagggtgtcacctttagctggactacccagggaagcagcagga 840
Db 781 GTGGGCTGACTTTAACTCAGTGTCACTTTTACTGGGACTACCCAGGGAAGCAGGCAGA 840
QY 841 qcggggtlaagtcgggtgcccagcagcgtctcccagcagaccacacagaaacttccaacct 900
Db 841 GCGGGGTAACTGGGTGCCAGGACGCGCTCCACAGCAGACCCACACAGAATCTTCCAGCAT 900
QY 901 cctgaccatccacaacgctcagccagcacgacctggcctcgtatgtgtgcaaggccaaacaa 960
Db 901 CCTGACCATCCAAAGCTCAGCCAGCAGCACTGGGCTCGTATGTGTGCAAGGCCAACAA 960
QY 961 cggcatccagcgtattcgggagagcaccgaggtcattgtcatgaaaaatcccttcatcag 1020
Db 961 CGCATCCACCGATTTCCGGGAGAGCACCGAGGTCAATTTGCATGAATAATCCCTTTCATCAG 1020
QY 1021 cgtcgaatggctcaaggagaccatctctggaggccacggaaggcagcagagcagctgctaagct 1080
Db 1021 CGTGCAGTGGCTCAAGAGGACCCATCTCTGGAGGCCACGCGCAGGAGCAGCTGGTGAAGCT 1080
QY 1081 gccgtgaagctggcagcttaccctcccgcccgagttlccagtggtcaaggatggaagcc 1140
Db 1081 GCCCGTGAACCTGGCAGCTTACCCCGCCCGCCGAGTTCCAGTGGTGTACAGGATGGAAGGC 1140
QY 1141 actgtccggggcgcacagtcacatagccctgggtgctcaaggaggtgacagagaccagcac 1200
Db 1141 ACTGTCCGGCGCCACAGTCCACATGCCCTGGTGCTCAAGGAGGTGCACAGAGGCCAGCAC 1200
QY 1201 aggcacctacacctgacctgtggaactccgctgctggcctgagcgcgaacataagcct 1260
Db 1201 AGGCACCTACACCTCGCCCTGTGGAACTCCGCTGTGGCTGTAGCGCGCAACATCAGCCT 1260
QY 1261 ggaagctggtgtgaattgtgccccccagatacatgagaagaggcctcctccccagcat 1320
Db 1261 GGAGCTGGTGTCAATGTGCCCCCCCCAGATACATGAGAAGGAGGCCCTCTCCCCAGCAT 1320
QY 1321 ctactcgcgtcaacagcgcagggcctcaactgcacggtcactcaggggtgacctgacct 1380
Db 1321 CTACTCGCGTACAGCGCGCCAGCGCCCTCACTGCAAGGGCTACCGGGTGCCTGCTCT 1380
QY 1381 cagcatccagtgacactggcggccctggacacctcgaagatgtttggccagcgtagtct 1440
Db 1381 CAGCATCCAGTGGCACTGGCGGCCCTTGGACACCCCTGCAAGATGTTTGGCCAGCGTAGTCT 1440
QY 1441 ccggcgcgagcagcagaagacctcatgccaagtgccgtgactggaggggcggtgaccac 1500
Db 1441 CCGCGCGGCGCACAGCAAGCCTCATGCCACAGTCCCGCTGACTGGAGGGCGGTGACCAC 1500
QY 1501 qcaggatgcggtgaaccccatcagagagcctggacacctggaacagatttgtggaggga 1560
Db 1501 GCAGGATGCGGTGAACCCCATCGAGAGCCTTGGACACTGGACCGAGTTTGTGGAGGGA 1560
QY 1561 gaataagactgtgacaagctggtgatccagaatgccaagctgtctgacctatcaagtg 1620
Db 1561 GAATAAGACTGTGAGCAACCTGGTGATCCAGAAATGCCAACGCTGTGCCATGTACAAGTG 1620
QY 1621 tgtggtctccaacaaggtgggcaggatgagcgggtcactacttctatgtgaccacct 1680

Db 1621 TGTGCTCTCCAAACAGGTGGGCGAGGATCAGCGGCTCATCTACTTCTATGTGACCACCAT 1680
QY 1681 cccccagcggcttcaaccatcgaaatccaagccatccagagagctactagagggccagccggt 1740
Db 1681 CCCCAGCGCTTTCAGCATCGAAATCCAAGCCATCCGAGGAGCTACTTAGAGGGCCAGCGGT 1740
QY 1741 gctcctgagctcgaagcgcagacagctacaagtacagacatctcgctagtaccgctcaa 1800
Db 1741 GCTCTGAGCTGCCAAGCGGACAGCTACAAGTACGAGCATCTGCCGTGGTACCGGCTCAA 1800
QY 1801 cctgtccacgctgcacgatgagcagggaaacccgctctctgctcgactgcaagaacgtgca 1860
Db 1801 CTTGTCCAGCTGTCAGGATGCGCAGCGGAACCCGCTTCTGCTCGACTCCAAGAAGCTGCA 1860
QY 1861 tctgttcgcaacccctctggccgccagcctggagaggtggcaccctggggcgccacgc 1920
Db 1861 TCTGTTGGCCACCCCTCTGGCGCCGACGCTGGAGGAGTGGCACCTGGGGCGCGCACGC 1920
QY 1921 caagctcaagctgagtaatccccccgctcgcgcccgagcagcagggccactatgtgtgga 1980
Db 1921 CACGCTCAAGCTGAGTATCCCCCGCTCGCGCCGAGCAGCAGGGCCACTATGTGTGCGA 1980
QY 1981 agtgaagaccgcgcagccatgacaagcactgccaagaagtaacctgctggtgcaggc 2040
Db 1981 AGTGAAGACCCGCGCAGCCATGACAGCACTGCCACAGAAGTACCTGTGCGTGCAGGC 2040
QY 2041 cctgaagccctcggtctcacgcagaaacttgaccacacctcctggtgaacgtgagcagctc 2100
Db 2041 CTTGGAAGCCCTCGGCTCACGCAGAACTTGACCGACCTCTCTGGTGAACGTGAGCGACTC 2100
QY 2101 gctggagatgagtgcttggtagcgaggagcagcagcgcacacatcgtgtggtacaaaga 2160
Db 2101 GCTGAGATGCAAGTCTTGTGGCGCGAGCGCACCGCGCCACGATCGTGTGTGTAAGA 2160
QY 2161 cgagagctgctggaggaagagctctggagtcgacttggcgagctcaaccagaaagctgag 2220
Db 2161 CGAGAGCTGCTGGAGGAAAAGTCTGGAGTCACTTTGGCGGACTCCAACCAAGACTCAG 2220
QY 2221 catccagcgcgtgctgcgagggaggaatgcgggagcgtatctgtgcagcgtgtgcacgc 2280
Db 2221 CATCCAGCGCTGCGCAGGAGGATCGCGGAGCGCTATCTGTGCAAGCTGTGCAACGCCAA 2280
QY 2281 gggctgcgtcaactcctccgcccagcagcgtgcgtgaaaggctccagagataaggcagcat 2340
Db 2281 GGGCTGCGTCAACTCTCTCGCCAGCGTGGCCGTGGAAGGCTCCGAGGATAAGGGCAGCAT 2340
QY 2341 ggagatcgtgtatccttgcgttaccggggtcactcgtctcttctgggtcctcctcct 2400
Db 2341 GGAGATCGGTGATCTTGTGCGGTACCGCGCTCATCGCTGTCTTCTTCTGGGTCTCTCT 2400
QY 2401 cctcatcttctgtaacatgagagggccgcccacgcagacatacaagagcgggtacactgtc 2460
Db 2401 CCTCATCTTCTGTAACATGAGGAGGCGCGCCACGCAGACATCAAGAGCGGGTACTGTCT 2460
QY 2461 catcatcatgacccccggggaggtgcctctgagagacaatcgcaataacctgtctcag 2520
Db 2461 CATCATATGGAACCCCGGGAGGTGCCCTGTGAGGAGCAATCCGAATACCTGTCTCTACA 2520
QY 2521 tggcagcagtgagggaattccccccgagagcggcgtgcacctggggagagtgctcggtacgg 2580
Db 2521 TGCCAGCCAGTGGGAATTTCCCCCGAGAGGGGTGCACCTGGGGAGAGTGCCTCGGTACGG 2580
QY 2581 qcctctcggggaaggtgggtggaaagcctcgcgttctcgcatccaagaggcagcagctgtga 2640
Db 2581 CGCCTTCGGGAAGGTGGTGGAAAGCCTCCGCTTTCGGCATCCACAAGGGCAGCAGCTGTGA 2640
QY 2641 caccgtgcccgtgaaaaatgctgaagaagggcgccacgcccagcagcagccgcgctgat 2700
Db 2641 CACCGTGGCCGTGAAAAATGCTGAAAAGAGGGGCCACGCGCCAGCAGCAGCCGCCCTGAT 2700
QY 2701 gtcgagctcaagatctcatctcagtcggcaacacacctcaacgtggtcaacctcctcgg 2760

us-09-373-21-
-atagacaaga 3900

1 16 09:39:20 2002

[illegible][illegible]

[illegible]


```

: REGISTRATION NUMBER: 38,153
: REFERENCE/DOCKET NUMBER: 289667/33348
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312/474-6300
: TELEFAX: 312/474-0448
: TELEX: 25-3856
: INFORMATION FOR SEQ ID NO: 36:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 4416 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: CDNA
US-08-671-5738-36

```

[illegible]

Db	781	GTGGCTGAGTTTAACTCAGGTGTACCTTTGACTGGACTACCCAGGAAGCAGCCAGA	840
Qy	841	gcggggtaagtgggtgcccagagcagcgtcccagcagagccacacagaactctccagcat	900
Db	841	GCGGGTAAGTGGGTGCCGAGCAGCCTCCAGCAGACCACACAGAACTCTCCAGCAT	900
Qy	901	cctgaacatccaaacagtcagcagcagcagacctgggctcgtatgtctgcaaggccaaaca	960
Db	901	CTTGACCATCCACAACAGTTCAGCCAGCAGCACTGGGCTCGTATGTCTGCAAGGCCAACA	960
Qy	961	cggcatccagcgatttcgggagagcaccgaggtcattgtgcatagaataccctcatcag	1020
Db	961	CGGCATCCAGCGATTTCGGGAGAGCACCGAGGTCATTGTGCATGAATACTCCTTCATCAG	1020
Qy	1021	cgtcagtggtctcaaaagaccatcctggaggccacgaggagcagcagctggtgaagct	1080
Db	1021	CGTCAGGTGGCTCAAAAGGACCCATCTCTGGAGGCCAGCGGAGGAGCAGCTGGTGAAGCT	1080
Qy	1081	gcgcgtgaagctggcagcgtaccctccgcgcggaggtccaggtccagtggtacaagatggaaagc	1140
Db	1081	GCCCTGAAGCTGGCAGCGTACCCCGCCCGAGTTCCAGTGGTACAAAGATGGAAGGC	1140
Qy	1141	actgtccgggcgcacagtcacatgcccctggtgtctcaaggaggtgcacagagccagcac	1200
Db	1141	ACTGTCCGGGGCCACAGTCACATGCCCTGTGTCTCAAGAGAGTGCACAGAGCCAGCAC	1200
Qy	1201	aggcactcacacctgccctgtggaaatccgcctgtgccttgagcgcacaatcagcct	1260
Db	1201	AGGCACCTACACCTCGCCCTGTGGAATCCCGTGTGCCCTGAGCGCGAATCAGGCT	1260
Qy	1261	ggagctgggtggaatgtgccccccacagatcacatgagaaggaggtcctctccccagcat	1320
Db	1261	GGAGCTGTTGTGAATGTGCCCCCCACAGATACATGAGAAGAGGCTCTCTCCCCAGCAT	1320
Qy	1321	ctactcgttcacagccgcagccctcactgtcacggcctcaggggtgcccttcctct	1380
Db	1321	CTACTCGGCTCACAGCCGCCAGGCCCTCACCTGCAGGGCTACGGGGTGCCCTGCCCT	1380
Qy	1381	cagcatccagtggcactggcgccctggacacctgtcaagatgtttgccagcgtagtcct	1440
Db	1381	CAGCATCCAGTGGCACTGGCGGCCCTGGACACCCCTGCAAGATGTTTGGCCAGCTAGTCT	1440
Qy	1441	ccggcggcgcagcagcaagaacctatgccagtgccgtgactggaggcgggtgaccac	1500
Db	1441	CCGGCGGCGCAGCAGCAAGCTCATGCGCACAGTGCCTGTACTGGAGGGCGGTGACCAC	1500
Qy	1501	gcaggatgcgcgtgaaaccccatcgagagcctggaacctggaccggagtgttgaggaggaaa	1560
Db	1501	GCAGSATGCCGTGAACCCCATCGAGAGCCTGGACACCTGGACCGAGTTTGTGGAGGGAAA	1560
Qy	1561	gaataagacttgagcaagctggatccagaaatgccaaacgtgtctgccatgtacaagt	1620
Db	1561	GAATAAGACTGTGAGCAAGCTGGTGTATCCAGAAATGCCAAACGTGTCTGCATGTACAAGTG	1620
Qy	1621	tgtggtctcaacaagttgggcagatgagcgcctcactctctatgtgaccacat	1680
Db	1621	TCGTGCTCCAAACAGTGGCGCAGATGAGCGGCTCATCTACTTCTATGTGACCCACAT	1680
Qy	1681	ccccgcgcgtctcacatcgaatccaaagcattccgaggagctactagaggccagccggt	1740
Db	1681	CCCCGACGGCTTCAACATCGAATCCAAGCCATCCCGAGGAGTACTAGAGGGCCAGCCGT	1740
Qy	1741	gctcctgagctgccaaagccagctacaagtacagcatctgcgctgggtaccgcctcaa	1800
Db	1741	GCTCCTGAGCTGCCAAAGCCGACAGCTACAAGTACAGCATCTGGGCTGTGTACCGCTCAA	1800
Qy	1801	ctgtccaagctgcagatgcccgcaggaacccgctctctgcacactgcagaacgtgca	1860
Db	1801	CCTGTCCAGCTGCAGATGCCGACGGNACCCGGTCTCTGCTGCATGCAAGAACGTGCA	1860
Qy	1861	tctgttcgcaacctctggcggccagcctggagggtggcaactggcgccgagccagc	1920

Db 1861 TCCTTTCCACCCTCTGCCCGCCAGCCTTGAGGAGGTGGCACCTTGGGGCGGCCACGC 1920
Qy 1921 caecctcagcctgagatccccccgclgagcccgagacagagggccaciatatgltcga 1980
Db 1921 CACGCTCAGCCTGAGTATCCCCCGCTGGCCCGACGAGGGCCACTATGTGTGCGA 1980
Qy 1981 aqtcagagacggcgagccatgacaagacactgacacaagaagtacctgltcgtgagggc 2040
Db 1981 AGTCAAGACGGCGCAGCCATGACAAGCACTGCCACAAGAAGTACCTGTGCGTGCAGGC 2040
Qy 2041 ctgagaagccctcggctacgagagaacttgaccgaacctctcgtgagacgtgagcgactc 2100
Db 2041 CCTGAAGCCCTCGGCTCACGAGAACTTGTACCGACTCTCTGTGTAACCTGAGCGCACTC 2100
Qy 2101 qctgagatgcagtgcttggtggccgagcgacgagcccgagcatcgltgltacaaaga 2160
Db 2101 GCTGCAATGCAGTGTCTTGGTGGCCGAGCGACCGCCCGCCAGCATCTGTGTGTACAAGA 2160
Qy 2161 caqaggrtgctlgaggaagttctgagtcgacttgaggactccaacacagaagctlgag 2220
Db 2161 CGAGAGGCTGCTGAGGAAAGTCTGGAGTCGACTTGGCGGACTCCAAACCAGAAGCTGAG 2220
Qy 2221 calccagcgctcgcgagagagatgcgggacgctatctgtgcagcgtgtgcaacgccaa 2280
Db 2221 CATCCAGCGCTGCGGAGAGATGCGGACGCTATCTGTGAGCGCTGTGTCAACGCCAA 2280
Qy 2281 gggctgcgtcaactctccgcccagclgagcgltgagagctccaacacagaagctlgag 2340
Db 2281 GGGCTGCGTCAACTCTCCGCCAGCGTGGCCGTGGAAAGGCTCCGAGGATAAAGGGCAGCAT 2340
Qy 2341 gggagtcgtgactctgtcgtggtaccggcgctcagctgctgtctctctgggtctctcct 2400
Db 2341 GGAGATCGTCACTCTTCTCGGTACCGGCGTCACTCGTGTCTTCTTCTGGGTCTCTCTCT 2400
Qy 2401 cctcatctctgttaaatgagagggccgcccacgacacatacaagcggcgtacctgtc 2460
Db 2401 CCTCATCTTCTGTAAATGATGAGGAGGGCGGCCACGACAGATCAAGACGGGCTTACCTGTCT 2460
Qy 2461 caLcatatggaacccgggaggtgctctlgagaggaatgcgaalacctgtcctacga 2520
Db 2461 CATCATCATGACCCCGGAGGTGCTCTGGAGAGCAATGCGAATACCTGTCTTACGA 2520
Qy 2521 tgcagcagtggaattccccgagagaggtgacacctggggagagtgctcggctacgg 2580
Db 2521 TGGCAGCAGTGGGAATTCGCCCGGAGAGGGCTGCACCTGGGGAGAGTGTCTCGCTACGG 2580
Qy 2581 cgcctlcgggaaggtggtggaagcctccgcttctcgcatccacaagggcagcagctgtga 2640
Db 2581 CGCCTTCGGGAAGGTGTTGGAAGCCTCCCGCTTTCGGCATCCACAAGGGGAGCAGCTGTGA 2640
Qy 2641 caccgtggccgtgaaatgctgaaagaggcgccacgycagcgagcagcgccgctgat 2700
Db 2641 CACCGTGGCGGTCAAAATGCTGAAAGAGGGCGCCACGGCAGCGACACCGCGCGCTGAT 2700
Qy 2701 gtcggagctcaagatcctcatcatcgccgaacacctcaacgtggtcaacctctcgg 2760
Db 2701 GTCGGAGCTCAAGATCCTATTACATCGCAACCACTTCAACGTGGTCAACCTCTCTCGG 2760
Qy 2761 ggcgtcaccaagccgagggccctcatggtgactgagagttctgcaagtaaggcaaa 2820
Db 2761 GGGCTGCACCAAGCCCGAGGGCCCCCTCATGTGTGATCTGTGGAGTTCTGCAAGTACGGCAA 2820
Qy 2821 cctctccaactctcgtcgccgaagcggaagcgcttccagccctcgcgaggaagctctcc 2880
Db 2821 CCTCTCAACTTCTTCGGCGCCAAAGCGGACGCCCTTTCAGCCCTTGGCGGAGAACTCTCC 2880
Qy 2881 cyagagcgcgagcgtctccgcacatggtgagctgcgaggtggaatcgagagcgcc 2940
Db 2881 CGAGCAGCGGACGCTTCCGGCCCATGTTGGAGCTTCGCGAGCTGATCGGAGCGGCC 2940
Qy 2941 gggagcagcagcaggtctctcgcggtctctcgaagacggagggcgagcagggcg 3000
Db 2941 GGGAGCAGCGACAGGGTCTCTTCTCGCGGTTCTCGAAAGACCGAGGGCGGCGGCGC 3000

RESULT 12

US-09-355-700-1

; Sequence 1, Application US/09355700

; GENERAL INFORMATION:

; APPLICANT: Ludwig Institute for Cancer Research

; Helsinki University Licensing

; Alitalo, Kari(U.S. only)

Qy 3001 ggccttccagacccaagaagctgagacctgtgctgagcccgctgacatggaagatct 3060
Db 3001 GGCTTCTCCAGACAAGAGCTGAGGACCTGTGGCTTGAGCCCGCTGACCATGGAAGATCT 3060
Qy 3061 tgcctctacagctccaggtggccagaggaatggaggtlccctggtctccgaaaagtgcat 3120
Db 3061 TGCTCTGTACAGCTTCCAGGTGGCCAGAGGGATGGAGTTCTCTGGCTTCCGAAAGTGCAT 3120
Qy 3121 ccacagagacctggctgctcggaacattctgctgctcggaagcgagctggtaagatctg 3180
Db 3121 CCACAGAGACCTGGCTGCTCGGAACATTTCTGCTGTCGGAAGCGACGTGCTGTAAGATCTG 3180
Qy 3181 tgactttggccttggccgggacatctacaaaagacctgactacgtccgcaagggcgagtc 3240
Db 3181 TGACTTTGGCTTGGCCGGGACATCTACAAAGACCTGACTAGCTCCGAAGGGCAGTGC 3240
Qy 3241 ccggctgccccctaaatggatggccctgaaagcatcttcgacaaggtgtlacaccacga 3300
Db 3241 CCGGCTGCCCTCGTAGTGGATGGCCCTTGAAGCATCTTCGACAAAGGTGTACACACAGCA 3300
Qy 3301 gagtgcgtgtggtcctttgggggtgcttctctggggagatcttctctctggggcctcccc 3360
Db 3301 GAGTGCAGTGTGGTCTTTGGGGTGTCTTCTGAGAGATCTTCTCTCTGGGGCCTCCCC 3360
Qy 3361 gtacctgggggtgcagatcaatgagagttctgcagcggtgcgagagacggcaagagat 3420
Db 3361 GTACCTGGGGTGCAGATCAATGAGGAGTTCTGCCAGCGGCTGAGAGCGCACAAAGAT 3420
Qy 3421 gaggggcccgagctggccactcccgccatagcgccgcatcagctgaaactgctggtccgg 3480
Db 3421 GAGGGCCCGGAGCTGGCCACTCCCCCATACGCCGCATCATGCTGAACTGCTGTGTCGG 3480
Qy 3481 agaccccaaggcgagacctgcattctcggagctgggtggagatcctggggagacctgtcca 3540
Db 3481 AGACCCAAAGGCGAGACCTGCATTTCTCGAGCTGGTGGAGATCTCTGGGGACCTGTCTCA 3540
Qy 3541 gggcagggccctgcagagagaagagaggtctgcattggccccgcgcagctctcagagctc 3600
Db 3541 GGCAGGGGCCCTGCAAGAGAAAGAGAGGTCTGCATGGCCCGCGCAGCTCTCAGAGCTC 3600
Qy 3601 agaagaggcgactctctgcaggtgtccaccattggccctacacatcgcccaggtcgagcg 3660
Db 3601 AGAAGAGGCGAGCTTCTCGCAGGTCTCCACCATGGCCCTTACACATCGCCAGGCTGACGC 3660
Qy 3661 tgagagaccccgcaagcctgcagcgccacagcctggcgccaggtattacaactgggt 3720
Db 3661 TGAGGACAGCCCGCAAGCCTGCAGCGCCACAGCCTGGCCGCGCAGGTATTACAACCTGGGT 3720
Qy 3721 gtcctttccgggtgcctggccagaggggtgagaccgtggttctctcaggatgaagac 3780
Db 3721 GTCTTTTCCGGGTGCCTGGCCAGAGGGGCTGAGACCCGTGGTTCTCTCAGGATGAAGAC 3780
Qy 3781 attgagggaattccccatgaaccccaacacctacaaagctctgtggacaaccagacaga 3840
Db 3781 ATTTGAGGAATTTCCCATGATGACCCCAACGACCTTACAAAGGCTCTGTGGACAACACACAGA 3840
Qy 3841 cagtgggatggtgctggtcgtcgagaggtttgagcagatagagagcagggcatagacaaga 3900
Db 3841 CAGTGGGATGTTGCTGGCTCGGCTCGGAGAGTTTTCAGCAGATAGAGAGCAGCATAGACAAGA 3900
Qy 3901 aagcggtctcag 3912
Db 3901 AAGCGGCTTCAG 3912

RESULT 12

US-09-355-700-1

; Sequence 1, Application US/09355700

; GENERAL INFORMATION:

; APPLICANT: Ludwig Institute for Cancer Research

; Helsinki University Licensing

; Alitalo, Kari(U.S. only)

OY 1321 ctactcgcgtcaagccgacagccctcacctgcacggttacggggtgccccctcctct 1380
DB 1321 CTACTCGCGTCAACGCCGCCAGCCCTCACCTGCACGGCTACGGGGTGCCCCCTCCT 1380
OY 1381 caagctcaagtggcactggcgccctgacacccctgcaagatggttggccagcgtagtcct 1440
1381 CAGCATCCAGTGGCACTGGCGCCCTGGACACCCCTGCAAGATGTTGGCCACGCGTAGTCT 1440
OY 1441 ccggcgcgccagcagcaagacctcatgccacagtgccgctgactgagggcggtgaccac 1500
DB 1441 CCGGGCGGCGAGCAGCAAGACCTCATGCCACAGTGCCTGACTGGAGGGCGGTGACCAC 1500
OY 1501 gcagatgctgtaaccccatcgagagctgacacccctggaccgagtttggagggaaa 1560
DB 1501 GCAGGATGCCGTGAACCCCATCGACAGCTGGACACCTGGACCGAGTTTGGAGGGAAA 1560
OY 1561 gaataagactgtagcaagctggtgatccagaaatccaaagctgtctgcatgtacaaagt 1620
DB 1561 GAATAGACTGTGAGCAAGCTGGTGATCCAGAAATGCCAAGCTGTGGCCATGTACAAGTG 1620
OY 1621 tgggtctccaacaaggtgggcccaggatgagcggctcatctacttctatgtgaaccacat 1680
DB 1621 TGTGCTCTCCAAAGCTGGCGCAGGATGACGGGCTCATCTACTTCTATGTGACCAACCAT 1680
OY 1681 ccccgacggcttcacatgcaatccaaagccatccgagagctactagaggccagccggt 1740
DB 1681 CCCCACAGCGCTTACCATCGAATCCAAAGCCATCCGAGGAGCTACTAGAGGGCCAGCCGT 1740
OY 1741 gctctgagctgccaagcgacagctacaagtacagacatctgcgctgtgtaccgctcaa 1800
DB 1741 GCTCTGAGCTGCCAAGCGCAGAGCTACAAAGTACGAGGATCTGCGCTGTACCGCTCAA 1800
OY 1801 cctgtccacgctgacgatgcccagggaaacccgcttctgtctgactgcaaaagctgca 1860
DB 1801 CCTGTCCAGCTGCACGATGCGCACGGAAACCCGCTTCTGTCTGACTGCAAGAAGCTGCA 1860
OY 1861 tctgttcgcaacccctctggcgccagcctggagagctggcaactcctggcgccgcacgc 1920
DB 1861 TCTGTTCGCCACCCCTCTGGCGCGCAGCCTGGAGGAGTGGCACCTGGGGCGCGCACGC 1920
OY 1921 caagctcaagctgagatatacccccgctgcgcccagcagcagagggccactatgtgcga 1980
DB 1921 CAGGCTCAGCCTGAGTATCCCCCGCTCGCGCCCGCAGCAGGAGGCCACTATGTGTGCGA 1980
OY 1981 agtgcgaacccggcagccatgacaagcactgccacaagaagtacctgtcggtgcagcc 2040
DB 1981 AGTGCAAAGCCGGCGAGCCATGACAAGCACTGCCACAAGAAGTACCTGTCTCGTGACGC 2040
OY 2041 cctggaagccctcggtcagcagaaactgaaccagcctcctgtgcaagctgagcgactc 2100
DB 2041 CCTGGAAGCCCTCGGCTCACGCAACTTGACCAGCCTCTCTGGTGAACGTGAGCGACTC 2100
OY 2101 gctggagatgcagtgcttggtagggagcgacgcgcccagcatcgtgtgtacaaaga 2160
DB 2101 GCTGGAGATGCAGTGTGGTGGCGGAGCGCACGCGCCAGCATCGTGTGTACAAAGA 2160
OY 2161 cgagagctgctggagaaaagtctggagtcgactggcggaactccaaccagaagctgag 2220
DB 2161 CGAGAGGCTGTCTGGAGAAAAGTCTGGAGTGGACTTGGCGGACTCCAAACCAAGCTGAG 2220
OY 2221 catcagcgcgtagcgagaggatgtagggagcgtatctgtgacgctgtgcaacgcaa 2280
DB 2221 CATCAGCGCGTGGCGAGGAGATGGCGGAGCCTATCTGTGCACGCTGTGCAAGCCCAA 2280
OY 2281 gggctgcgtcaactcctcccgcaagcgtggccgtggaaggtccgaggataaaggcgagcat 2340
DB 2281 GGGCTGCGTCAACTCTCCCGCAGCGTGGCGGTGGAGGCTCCGAGGATAAGGGCAGCAT 2340
OY 2341 ggaagatgatcctgtcggtacggcgctcatcgctgtcttcttctgggtccctcctct 2400
DB 2341 GGAGATCGTGATCTCTGTGGTACCGGGGTATCGCTGTCTTCTGGGTCTCTCTCT 2400
OY 2401 cctcatctctgttaacatgaggagggcgggccacgcagacatcaagacgggctacctgtc 2460

DB 2401 CCTCATCTTCTGTAAATGAGAGCGCGGCCACGACACATCAAGACGGGCTACCTGTCT 2460
OY 2461 catcatcatgaaacccccggggaggtgcctcttgagaggaacaatgcgaataacctgtcctcaga 2520
DB 2461 CATCATCATGACCCCGGGAGGTGCCCTCTGGAGGAGCAATGCGAATACCTGTCTCTACGA 2520
OY 2521 tgcagcgagtgaggaaattccccccgagagcggtctgcacctggggagagtgctcggctcagc 2580
DB 2521 TGCCACGACGTGGGAATTCCTCCCGCAGAGCGGCTGCACCTGGGGAGAGTGTCTCGCTACGG 2580
OY 2581 cgccttcggggaagtggtgggaagcctccgcttcgggcatccacaaggcgacgactgtga 2640
DB 2581 CGCCTTCGGGAAGGTGGTGGAAAGCTCCGCTTTCGGCATCCACAAGGCGACGACTGTGA 2640
OY 2641 caccgtggccgtgaaatgctgaaaagagggcgccacggccaagcgacgacgcgcgcat 2700
DB 2641 CACCGTGGCCGTGAAATGCTGAAAGAGGGCGCCACGGCCACGAGCACCCGCGCGCTGAT 2700
OY 2701 gtcggagctcaagatcctcatctcaatcgcgcaacacacctcaacgtgggtcaacctcctcgg 2760
DB 2701 GTCGGAGCTCAAGATCCTCATTTACATCGGCAACCACTCAACGTGGTCAACCTCCTCGG 2760
OY 2761 ggcgtgcaccaagccggaaggcccccctcatgtgatcgtggagttctgcgaagtacggcaa 2820
DB 2761 GCGCTGCAACCAAGCGCAGGCGCCCTCATGTGTGATCTGTGAGTCTTGCAAAAGTACGGCAA 2820
OY 2821 cctctcaactctctgcgcgccaagcagcgacgttcagccccctgcgcgagagaagtcctcc 2880
DB 2821 CCTCTCAACTTCTCTGCGCGCCAAAGCGGACGCTTACGCCCTTCGCGGGAAGTCTTCC 2880
OY 2881 cgagcagcgcggaagcgttccgcgcctatggtggagctgcgcagggctggatcgaggcgcc 2940
DB 2881 CGAGCAGCGCGGACGCTTCCGCGCATGGTGGAGCTCGCCAGGCTGGATCGATCGAGCGCGCC 2940
OY 2941 ggggagcagcagcaggggtcctcttcggcggtctctgaaagaccgagggcgagcgagggcg 3000
DB 2941 GGGGAGCAGCAGCAGGGTCTCTTCGCGCGGTTCTCGAAGACCCGAGGGCGGAGGCGG 3000
OY 3001 ggccttcacagacccaagaagctgaggacctgggtgagctgcgcagccgctgaccatggaaga 3060
DB 3001 GGCTTCTCCAGACCAAGAGCTGAGGACCTGTGCTGAGCCCGCTGACCATGGGAAGATCT 3060
OY 3061 tgcctgtacagcttccaggtaggcagaggatggagttcctctgccttcctccgaaagtgcac 3120
DB 3061 TGTCTGTCTACAGTTCAGAGTGGCGCAGAGGATGGAGTTCCTTGGCTTCTCCGAAAGTGCAT 3120
OY 3121 ccacagagacctgctcgtcgaaacattctgctatcgaaagcagcgtggtgaaagactg 3180
DB 3121 CCACAGAGCCTGGCTGCTCGGAACATTTCTGCTGTGGAAAGCAGCTGGTGAAGATCTG 3180
OY 3181 tgactttggccttgcccgggacatctacaagacccctgactacgtccgcaaggcgagtcg 3240
DB 3181 TGACTTTGGCCTTGCCCGGGACATCTCAAAAGACCCCTGACTACGTCCGCAAGGCGAGTGC 3240
OY 3241 ccggctgccccgaagtggatggccccctgaaagcatcttcgacaagggtgtcacacaagca 3300
DB 3241 CCGGCTGCCCCCTGAAGTGGATGGCCCCCTGAAAGCATCTTCGACAAGGTGTACACACGCA 3300
OY 3301 gagtgaagctgtggtccttctggggtgcttctctggagatcttctctctgggggctctccc 3360
DB 3301 GASTGACGTGTGTCTTTGGGGTGTCTCTCTGGGAGATCTTCTCTCTGGGGGCTTCCCC 3360
OY 3361 gtacccctggggtgcagatcaatgaggagttctgccagcgctgagagacggcacaagat 3420
DB 3361 GTACCCCTGGGTGCAGATCAATGAGGAGTTCTGCCAGCGCTGAGAGACGCGCACAGGAT 3420
OY 3421 gagggccccgagctggccactccgcacatacgccgcatcatgtgtaactgtctgctcgg 3480
DB 3421 GAGGGCCCCGAGGTGCCACTCCCGCCATACGCGCGCATCTGCTGAACCTGCTGTCTCGG 3480
OY 3481 agaccccaagcgagacctgcattctcgagctggtgagatcctcggggacctgcctcca 3540

```
Db 3481 AGACCCCAAGCGAGACCTGCATTCTCGAGCTGGTGGAGATCCTGGGGAGCCTGCTCCA 3540
QY 3541 qggcaggccctgcaagaaagagaggtctgtgcatggcccgcgagctctcagagctc 3600
Db 3541 GGCAGCGGCTTGCAGAGAGAGAGAGGTCTGCATGGCCCGCCGAGCTCTCAGAGCTC 3600
QY 3601 aqaagaggcagcttctcagagtgltcaacatggccctaacacatcgccrccgctgaagc 3660
Db 3601 AGAAGAGGCGAGCTTCTCGAGGTGTCCACCATGTGCCCTTACACATCGCCACGCTGACGC 3660
QY 3661 tgaggacagccgcuaagcctgacgcgcacagcctggcccgaggtatcaaacctgggt 3720
Db 3661 TGAGGACAGCCGCCAAGCTGTCAGCGCCACAGCCTGGCCGCGCAGGTATTACAACTGGGT 3720
QY 3721 gtcccttccggggtgcccaggggaggggctgagaccctgttccctccaggtgaagac 3780
Db 3721 GTCCCTTCCGGGTGCCCTGGCCAGAGGGGCTGAGACCCGCTGGTCTCCAGGATCAAGAC 3780
QY 3781 atttaggaattccccatgaaccccaacagcctacaaagcctctgtggacaaccagacaga 3840
Db 3781 ATTTGAGGAATTCCTCATGACCCCAACGACCTTACAAAGGCTCTGTGGACAACACAGACA 3840
QY 3841 cagtgaggatggctggcctcgagaggttttgagcagatagagagcagggcatagacaaga 3900
Db 3841 CACTGGGATGTGCTGGCTCGGCTCGAGGAGTTTGAGCAGATAGAGACGCGATAGACAAGA 3900
QY 3901 aagcgagctcag 3912
Db 3901 AAGCGGCTTTCAG 3912
```

RESULT 13

```
US-09-440-302A-1035
; Sequence 1035, Application US/09440302A
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; TITLE OF INVENTION: Human Neurobiology Array
; FILE REFERENCE: CLON-006CIP11
; CURRENT APPLICATION NUMBER: US/09/440.302A
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 09/053,375
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 1193
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1035
; LENGTH: 4416
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 4243
; OTHER INFORMATION: n = A,T,C or G
US-09-440-302A-1035
```

```
Query Match 95.2%; Score 3912; DB 18; Length 4416;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3912; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 ccacgcagcagcgcggagatgacggcgccggcgctgtgctgcgactgtggctctg 60
Db 1 ccacgcagcagcgcggagatgacggcgccggcgctgtgctgcgactgtggctctg 60
QY 61 cctgggactcctggacggcctgtgagtgagtgactctcatgaccccccgacctgaacat 120
Db 61 cctgggactcctggacggcctgtgagtgagtgactctcatgaccccccgacctgaacat 120
QY 121 cacggagagtcacagctcatcagaccggtgacagcctgtccatctcctgcaggggaca 180
Db 121 cacggagagtcacagctcatcagaccggtgacagcctgtccatctcctgcaggggaca 180
QY 181 gcacccctcagtggtggcttggcagagctcagaggcgccagggcgccagccaggaaga 240
```

```
Db 181 gcaacccctcagtggtgcttggccagagctcagagggcgccagccacgcggagacaaaga 240
QY 241 cagcagagacacaggggggtgggtgcgagactgcgagggcacagacgcagccctactgcaa 300
Db 241 cagcagagacacaggggggtgggtgcgagactgcgagggcacagacgcagccctactgcaa 300
QY 301 ggtgtgtcgtgcacagaggtacatggcaacgacacagcagcagctactactactacaa 360
Db 301 ggtgtgtcgtgcacagaggtacatggcaacgacacagcagcagcagctactactactacaa 360
QY 361 gtacatcaaggaacagcatcgaggggacacacgcgcgcagctcctacgtgttctlgagaga 420
Db 361 gtacatcaaggaacagcatcgaggggacacacgcgcgcagctcctacgtgttctlgagaga 420
QY 421 ctttgagcagcactcatcaacaagcctgacacgctgtgacacgaggaagacgcacat 480
Db 421 cttlgagcagcactcatcaacaagcctgacacgctgtgacacgaggaagacgcacat 480
QY 481 gtgggtgcctgtgtgttccatcccccgccctcaatgtcacgctgcgctgcgaagcctc 540
Db 481 gtgggtgcctgtgtgttccatcccccgccctcaatgtcacgctgcgctgcgaagcctc 540
QY 541 ggtgtgtggcagacggcgaggggtgtgtgtgggatgacggcggggagctgtcgtgtc 600
Db 541 ggtgtgtggcagacggcgaggggtgtgtgtgggatgacggcggggagctgtcgtgtc 600
QY 601 cagccactgtgcagcatgccctgtacctgtcagtcgagacacacacctggggagacccaga 660
Db 601 cagccactgtgcagcatgccctgtacctgtcagtcgagacacacacctggggagacccaga 660
QY 661 cttcctttccaaaccccttctctgggtgcacatcacaggcaacgagctctatgacatccagct 720
Db 661 cttcctttccaaaccccttctctgggtgcacatcacaggcaacgagctctatgacatccagct 720
QY 721 gtctgcaggaaagtgcgtggagctgtgtgttaggggaaagctggtcctgaactgcaccgt 780
Db 721 gtctgcaggaaagtgcgtggagctgtgtgttaggggaaagctggtcctgaactgcaccgt 780
QY 781 gtgggctgagtttaactcaggtgtcacctttgactgggactaccagggagagcaggcaga 840
Db 781 gtgggctgagtttaactcaggtgtcacctttgactgggactaccagggagagcaggcaga 840
QY 841 gcggggtaagtgggtgcccagcagcagctccccagcagacccacacagaactctccagcat 900
Db 841 gcggggtaagtgggtgcccagcagcagctccccagcagacccacacagaactctccagcat 900
QY 901 cctgacacatccacaacgtcagccagcagcagcagcagctgggctcgtatgtgtgaagggccaa 960
Db 901 cctgacacatccacaacgtcagccagcagcagcagcagcagctgggctcgtatgtgtgaagggccaa 960
QY 961 cggcatccagcgatttcgggagagcaccaggttcattgtgcatgaaaaatcccttccatcag 1020
Db 961 cggcatccagcgatttcgggagagcaccaggttcattgtgcatgaaaaatcccttccatcag 1020
QY 1021 cgtcagtggtcctcaaggaccctcctgtgagccacgcgcagggagagcagctggtgaagct 1080
Db 1021 cgtcagtggtcctcaaggaccctcctgtgagccacgcgcagggagagcagctggtgaagct 1080
QY 1081 gccctgaaagctggcagcagctacccccgcgcaggttccagtggttacaagagtggaagggc 1140
Db 1081 gccctgaaagctggcagcagctacccccgcgcaggttccagtggttacaagagtggaagggc 1140
QY 1141 actgtccggggccacagtcaccatgtccctgtgtctcaaggagggtgacagagggccagcac 1200
Db 1141 actgtccggggccacagtcaccatgtccctgtgtctcaaggagggtgacagagggccagcac 1200
QY 1201 aggcacctacacccctgcgcctgtggaactccgctgctggtgcagggcgcaacatcagct 1260
Db 1201 aggcacctacacccctgcgcctgtggaactccgctgctggtgcagggcgcaacatcagct 1260
QY 1261 ggagctgggtggatgtgccccccacgatatcatgagaagagggcctcctccccagcat 1320
```

Db 1261 ggagctggtggaatgtgccccccacagatacatgagaaaggaggcctcctccccccagcat 1320
Qy 1321 ctactcgctgtaacagcgcagccctcaactgacagcctacagggtgccccctgctct 1380
Db 1321 ctactcgctgtaacagcgcagccctcaactgacagcctacagggtgccccctgctct 1380
Qy 1381 caqcatccagtggcactggcgccctggacacccctgcaagatgtttgcccaaqgtagtct 1440
Db 1381 caqcatccagtggcactggcgccctggacacccctgcaagatgtttgcccaaqgtagtct 1440
Qy 1441 ccgctggcgagcagcaagaacctcatgcccacagtgccgctgactggaggcgcgtgacac 1500
Db 1441 ccgctggcgagcagcaagaacctcatgcccacagtgccgctgactggaggcgcgtgacac 1500
Qy 1501 qcagatgcccgtgaaccccatcgagacccctggacacactgacccagtttgtgagggaaa 1560
Db 1501 qcagatgcccgtgaaccccatcgagacccctggacacactgacccagtttgtgagggaaa 1560
Qy 1561 gaaataaactgtgagcaagctgtgtatccagaaatgcccagaaatgctgccatgtacaagt 1620
Db 1561 gaaataaactgtgagcaagctgtgtatccagaaatgcccagaaatgctgccatgtacaagt 1620
Qy 1621 tgtggttccaaagtgggccagagatgacgactcatctacttctatgtgacacacat 1680
Db 1621 tgtggttccaaagtgggccagagatgacgactcatctacttctatgtgacacacat 1680
Qy 1681 cccgcagcgttaccatcgaaatccagccatccgagagactactagaggccagccggt 1740
Db 1681 cccgcagcgttaccatcgaaatccagccatccgagagactactagaggccagccggt 1740
Qy 1741 gclctgaactgccaagcagactacaagtacagacatctgctgctggatccctcaa 1800
Db 1741 gclctgaactgccaagcagactacaagtacagacatctgctgctggatccctcaa 1800
Qy 1801 cctgtccacgtgcacatgcgcaggaacccgcttctgctgactgcaagaacgtgca 1860
Db 1801 cclgtccacgtgcacatgcgcaggaacccgcttctgctgactgcaagaacgtgca 1860
Qy 1861 trtlttcgcacccctctggcccgacgctggaggagtgacactggggcgccacgc 1920
Db 1861 trtlttcgcacccctctggcccgacgctggaggagtgacactggggcgccacgc 1920
Qy 1921 cagctgaactgaatctcccccgctgcgcgcagcctggaggagtgacactggggcgccacgc 1980
Db 1921 cagctgaactgaatctcccccgctgcgcgcagcctggaggagtgacactgtgtgcga 1980
Qy 1981 agtgaagccgcgcagcctgacaagcactgccaagaagtacactgtcggtgcaggc 2040
Db 1981 agtgaagccgcgcagcctgacaagcactgccaagaagtacactgtcggtgcaggc 2040
Qy 2041 cctggaagccctcggtcacgcgaacttgaccgaactcctgtgacgtgagcgactc 2100
Db 2041 cctggaagccctcggtcacgcgaacttgaccgaactcctgtgacgtgagcgactc 2100
Qy 2101 gctggagatgagtgctgtgtgcccgcagcagcagcgcacagcctggtggtacaaga 2160
Db 2101 gctggagatgagtgctgtgtgcccgcagcagcagcgcacagcctggtggtacaaga 2160
Qy 2161 cgagaggtcgtggagaaaagtctggaagtgcacttgccgactccaacgaagctgag 2220
Db 2161 cgagaggtcgtggagaaaagtctggaagtgcacttgccgactccaacgaagctgag 2220
Qy 2221 catccagcgtgcgcagggagatgggggacgtatatgtgacgctgtgtcaacgcaa 2280
Db 2221 catccagcgtgcgcagggagatggcggcgtatatgtgacgctgtgtcaacgcaa 2280
Qy 2281 gggctgctcaactcctccgcagcgtggccgtggaaggtccgaggaataaggcagcat 2340
Db 2281 gggctgctcaactcctccgcagcgtggccgtggaaggtccgaggaataaggcagcat 2340
Qy 2341 ggagatcgtgatcctgtcggtaccgcgctcatcgctgtcttcttctgggtccctcct 2400
Db 2341 ggagatcgtgatcctgtcggtaccgcgctcatcgctgtcttcttcttctgggtccctcct 2400

Qy 2401 cctcatcttctgtaacatgagggagccgcccacgcagacatcaagacgggctacctgtc 2460
Db 2401 cctcatcttctgtaacatgagggagccgcccacgcagacatcaagacgggctacctgtc 2460
Qy 2461 catcatatggaccccgggaggtgctctgaggagcaatgcgaataacctgtccctacga 2520
Db 2461 catcatatggaccccgggaggtgctctgaggagcaatgcgaataacctgtccctacga 2520
Qy 2521 tgcagccatggaaattccccgagagagcctgcacctggggagagtgctcggtacgcg 2580
Db 2521 tgcagccatggaaattccccgagagagcctgcacctggggagagtgctcggtacgcg 2580
Qy 2581 cgcttcgggaaggtggtgaaagcctccgcttccgcatcccaaaaggcagcgtglga 2640
Db 2581 cgcttcgggaaggtggtgaaagcctccgcttccgcatcccaaaaggcagcgtglga 2640
Qy 2641 caccgtggccgtgaaatgctgaaagagggcgccacggccagcgagcaccgcgcgtgat 2700
Db 2641 caccgtggccgtgaaatgctgaaagagggcgccacggcgagcaccgcgcgtgat 2700
Qy 2701 gtcggagctcaagatcctcatcggaacccactcaacgctggtaacctcctcgg 2760
Db 2701 gtcggagctcaagatcctcatcggaacccactcaacgctggtaacctcctcgg 2760
Qy 2761 ggcgtgcacaaagccgcagggccccctcatgtgtgagtcttcgaaglacggcaa 2820
Db 2761 ggcgtgcacaaagccgcagggccccctcatgtgtgagtcttcgaaglacggcaa 2820
Qy 2821 cctctcaaatctctgcgcgccaagcgagccttcagccccctgcgcgagagctcctc 2880
Db 2821 cctctcaaatctctgcgcgccaagcgagccttcagccccctgcgcgagagctcctc 2880
Qy 2881 cgagcagcgcgagcgttccgcgcctatgggtgagctgcgcagcctggatcggaggcgcc 2940
Db 2881 cgagcagcgcgagcgttccgcgcctatgggtgagctgcgcagcctggatcggaggcgcc 2940
Qy 2941 ggggagcagcgacagggctcctcttcgcgcggttctcgaagaccgagggcgagcgagcg 3000
Db 2941 ggggagcagcgacagggctcctcttcgcgcggttctcgaagaccgagggcgagcgagcg 3000
Qy 3001 ggccttccagacaaagaactgagacctgtggtgcagccctgacctgacctggaagatct 3060
Db 3001 ggccttccagacaaagaactgagacctgtggtgcagccctgacctgacctggaagatct 3060
Qy 3061 tgcgtctacagcttcagatggccagaggtatggagtctcctggctcccgaaagtgc 3120
Db 3061 tgcgtctacagcttcagatggccagaggtatggagtctcctggctcccgaaagtgc 3120
Qy 3121 ccacagagacctggctcgcgaacatctctgctgcggaagcgagcgtggtgaagatctg 3180
Db 3121 ccacagagacctggctcgcgaacatctctgctgcggaagcgagcgtggtgaagatctg 3180
Qy 3181 tgccttggccttgcgcgggacatctacaagacccctgacacgctccgcaaggcgagctgc 3240
Db 3181 tgccttggccttgcgcgggacatctacaagacccctgacacgctccgcaaggcgagctgc 3240
Qy 3241 ccggtcctccctgaagtggatggcctgaaagcatcttcgaaaggtgtacacacgca 3300
Db 3241 ccggtcctccctgaagtggatggcctgaaagcatcttcgaaaggtgtacacacgca 3300
Qy 3301 gagtgcagctgtgttcttgggtgcttctctgggagatcttctctgggggctcctccc 3360
Db 3301 gagtgcagctgtgttcttgggtgcttctctgggagatcttctctgggggctcctccc 3360
Qy 3361 gtaccttggggtgcagatcaatgaggagtctgcacagcgtgaagacggcacaagat 3420
Db 3361 gtaccttggggtgcagatcaatgaggagtctgcacagcgtgaagacggcacaagat 3420
Qy 3421 gaggggccccgagctggcactccgcatacgcgcgtcatctgctgaactgctgggtccgg 3480
Db 3421 gaggggccccgagctggcactccgcatacgcgcgtcatctgctgaactgctgggtccgg 3480

|||||
Db 1201 aggcactcacacctcgccctgtggaactccgctgctgacctgagcgcgaacatcaagct 1260
Qy 1261 ggaagctgggtgaaatgtgtccccccagatacatagagaaggagccctctcccccaagcat 1320
|||||
Db 1261 ggaagctgggtgaaatgtgtccccccagatacatagagaaggagccctctcccccaagcat 1320
Qy 1321 ctactcgctcacagccgcagccctcctaccctgacagccctacgaggtgcccctgacct 1380
|||||
Db 1321 ctactcgctcacagccgcagccctcctaccctgacagccctacgaggtgcccctgacct 1380
Qy 1381 cagcatccagtgacctggcgccctggacacccctgcaagatgtttggccagcgtagtct 1440
|||||
Db 1381 cagcatccagtgacctggcgccctggacacccctgcaagatgtttggccagcgtagtct 1440
Qy 1441 ccggcgccgcagcagcaagaactctatgccaaagtccgtgacctgagagggcggtgaccac 1500
Db 1441 ccggcgccgcagcagcaagaactctatgccaaagtccgtgacctgagagggcggtgaccac 1500
Qy 1501 gcaagatggccgtgaaaccccatcgagagcctggacacccctggaccgagtttgtgagaggaaa 1560
|||||
Db 1501 gcaagatggccgtgaaaccccatcgagagcctggacacccctggaccgagtttgtgagaggaaa 1560
Qy 1561 gaataagacttgtgacaagctgggtgatccagaatgccaaagtgtctgacctgtaragtg 1620
|||||
Db 1561 gaataagacttgtgacaagctgggtgatccagaatgccaaagtgtctgacctgtlacaagt 1620
Qy 1621 tgttggtctcaacaagggtgggcagagatgagcggctlcatctacttctatgtgaccacct 1680
|||||
Db 1621 tgttggtctcaacaagggtgggcagagatgagcggctlcatctacttctatgtgaccacct 1680
Qy 1681 cccgcagcgcttcaccatcgaaatccaaagccatccgaggaactactagaggccagccggt 1740
|||||
Db 1681 cccgcagcgcttcaccatcgaaatccaaagccatccgaggaactactagaggccagccggt 1740
Qy 1741 qctctgagctgccaagccgcagcagctacaaagtacagagatctgctgctgggtaccgctcaa 1800
Db 1741 qctctgagctgccaagccgcagcagctacaaagtacagagatctgctgctgggtaccgctcaa 1800
Qy 1801 cctgtccagctcacagatcgacaggggaacccgcttctgtcgtactgcaagaacutgca 1860
|||||
Db 1801 cctgtccagctcacagatcgacaggggaacccgcttctgtcgtactgcaagaacutgca 1860
Qy 1861 tctgttccgacccctctggcccgagctggagggaggtggcaccctggggcgccacgc 1920
Db 1861 tctgttccgacccctctggcccgagctggagggaggtggcaccctggggcgccacgc 1920
Qy 1921 caegctcagctgagtatcccccgctcgccgcagcagcagcagagggccacttatgtgcga 1980
Db 1921 caegctcagctgagtatcccccgctcgccgcagcagcagcagagggccacttatgtgcga 1980
Qy 1981 agtgcagagccgcagcccatgacaagcactgccaagaagtagtacctgtcgtgagcgc 2040
Db 1981 agtgcagagccgcagcccatgacaagcactgccaagaagtagtacctgtcgtgagcgc 2040
Qy 2041 cctggaagccctcggtcacgagaacttgaccgacctctggtgaacgtgagcgactc 2100
Db 2041 cctggaagccctcggtcacgagaacttgaccgacctctggtgaacgtgagcgactc 2100
Qy 2101 gctgagagatgcagtgtctgtgtgcccagagcagcagcccgagcatcgtgtggtacaaaga 2160
Db 2101 gctgagagatgcagtgtctgtgtgcccagagcagcagcccgagcatcgtgtggtacaaaga 2160
Qy 2161 cgagagcgtcgtgaggaagaagtctgtgagtcgacttgcggactccaacacagagctgag 2220
Db 2161 cgagagcgtcgtgaggaagaagtctgtgagtcgacttgcggactccaacacagagctgag 2220
Qy 2221 catccagcgtgcgcgagagagatgcgggacgctaactgtgcagcgtgtgcacgcca 2280
Db 2221 catccagcgtgcgcgagagagatgcgggacgctaactgtgcagcgtgtgcacgcca 2280
Qy 2281 gggctgcgtcaactcctcccgagcgtggccgtggaagcgtccgaggaataaggcgagcat 2340
|||||

Db 2281 gggctgcgtcaactcctcccgccagcgtggccgtggaaggctccgaggaataaggcgagcat 2340
Qy 2341 ggagatcgtgatccctgtcggtaccggcgtcatcgtctatcttctctgggtccctctct 2400
|||||
Db 2341 ggagatcgtgataccctgtcggtaccggcgtcatcgtcttcttctctgggtccctctct 2400
Qy 2401 cctcatcttctgtaacatgagagggccggccacgcagacatcaagagcgggtactcgtc 2460
Db 2401 cctcatcttctgtaacatgagagggccggccacgcagacatcaagagcgggtactcgtc 2460
Qy 2461 catcatcatggacccccggggagggtccctctggagaggaatacgaaatcctctctactaga 2520
Db 2461 catcatcatggacccccggggagggtccctctggagaggaatacgaaatcctctctactaga 2520
Qy 2521 tgccagcagtgaggaaatcccccgagagcgtgcacctggggagagtgctctcggtactcgg 2580
Db 2521 tgccagcagtgaggaaatcccccgagagcgtgcacctggggagagtgctctcggtactcgg 2580
Qy 2581 cgccctcgggaaagggtggtggaagcctccgcttccggcatccacaagggcagcagctgtga 2640
Db 2581 cgccctcgggaaagggtggtggaagcctccgcttccggcatccacaagggcagcagctgtga 2640
Qy 2641 caccgtggccgtgaaaaatgctgaaagagggccacggccagcgagcagccgcgctgat 2700
Db 2641 caccgtggccgtgaaaaatgctgaaagagggccacggccagcgagcagccgcgctgat 2700
Qy 2701 gtcgagctccaagatcctcatctcaatcggcaacacacctcaacgttgtcaacctctctcgg 2760
Db 2701 gtcgagctccaagatcctcatctcaatcggcaacacacctcaacgttgtcaacctctcgg 2760
Qy 2761 ggcgtgcacaaagccgagggccccctcatgtgtgatcgtggagttctgcaaglacggcaa 2820
Db 2761 ggcgtgcacaaagccgagggccccctcatgtgtgatcgtggagttctgcaaglacggcaa 2820
Qy 2821 cctctccaacttctgtcgcccaagcgggaaccccttcagccctcgcgagaaagtctcc 2880
Db 2821 cctctccaacttctgtcgcccaagcgggaaccccttcagccctcgcgagaaagtctcc 2880
Qy 2881 cgaagcagcggagcgttcccgcccatgtgtgagctcgccaggtgtgactcgagggcgcc 2940
Db 2881 cgaagcagcggagcgttcccgcccatgtgtgagctcgccaggtgtgactcgagggcgcc 2940
Qy 2941 ggggagcagcagaggttctcttcgcggttctcgagacagagggcgagggcgagggcg 3000
Db 2941 ggggagcagcagaggttctcttcgcggttctcgagacagagggcgagggcgagggcg 3000
Qy 3001 ggccttccagacccaagaagctgagagcctgtggctgagcccgctgacctggaagatct 3060
Db 3001 ggccttccagacccaagaagctgagagcctgtggctgagcccgctgacctggaagatct 3060
Qy 3061 tgtctgtacagcttccagtgggccagagggatggaggttcttggttcccgaagtgcat 3120
Db 3061 tgtctgtacagcttccagtgggccagagggatggaggttcttggttcccgaagtgcat 3120
Qy 3121 ccacagagacctggctgtctgggaacattctgtctcggaagcagcgtggtgaagatctcg 3180
Db 3121 ccacagagacctggctgtctgggaacattctgtctcggaagcagcgtggtgaagatctcg 3180
Qy 3181 tgactttgccttgcggggacatctacaaagacctgactacgttcgcaaggcgagtg 3240
Db 3181 tgactttgccttgcggggacatctacaaagacctgactacgttcgcaaggcgagtg 3240
Qy 3241 ccggctgcccctgaagtggatggccctgaaagcatcttcgacaaggtgtacaccccgca 3300
Db 3241 ccggctgcccctgaagtggatggccctgaaagcatcttcgacaaggtgtacaccccgca 3300
Qy 3301 gagtgcagctggtgccttgggggtcttctctgggagatcttctctggggcgctcccc 3360
Db 3301 gagtgcagctggtgccttgggggtcttctctgggagatcttctctggggcgctcccc 3360
Qy 3361 gtaccttgggtgcagatcaatgagagttctgcccagcgtgagagcgggcacaaaggat 3420
Db 3361 gtaccttgggtgcagatcaatgagagttctgcccagcgtgagagcgggcacaaaggat 3420

|||||
Db 1081 gcccgtgaagctggcagcgtaccctcccgaggtccagtgglacaaaggaaggaaagc 1140
Qy 1141 actgtccggggccacagatccacatgcccctggctcraaggaggtgacagaggccagcac 1200
Db 1141 actgtccggggccacagatccacatgcccctggctcraaggaggtgacagaggccagcac 1200
Qy 1201 aggcacctacacctcgcgcctgtggaactcgcgtcgtggcctgagggccaacatcacgct 1260
Db 1201 aggcacctacacctcgcgcctgtggaactcgcgtcgtggcctgagggccaacatcacgct 1260
Qy 1261 ygaagctggglggatgtgcccccccagatatacatgagaagaggcctcctccccagcat 1320
Db 1261 qgaagctggglggatgtgcccccccagatatacatgagaagaggcctcctccccagcat 1320
Qy 1321 ctactcgcgtctacaagccgcagccctcacctgcaacggcctacggggtgccccctgctct 1380
Db 1321 ctactcgcgtctacaaccccgagccctcacctgcaacggcctacggggtgccccctgctct 1380
Qy 1381 caqcatccagtgagctggcgccttgacacccctgcaagatggttggccccagctagttct 1440
Db 1381 caqcatccagtgagcactggcgccttgacacccctgcaagatggttggccccagctagttct 1440
Qy 1441 ccggcggggagcagcaagacctcatgcccagtgccctgactggaaggcggtgacac 1500
Db 1441 ccgycggcgagcagcaagacctcatgcccagtgccctgactggaaggcggtgacac 1500
Qy 1501 gcaagatgccgtgaaaccccatcgaagagcctggacacccctggacacaggttctgtgaaggaaa 1560
Db 1501 gcaagatgccgtgaaaccccatcgaagagcctggacacccctggacacaggttctgtgaaggaaa 1560
Qy 1561 gaaataagacttgagcaagctggtgatccagaatgccacgtgctgcccattgacaaatg 1620
Db 1561 gaaataagacttgagcaagctggtgatccagaatgccacgtgctgcccattgacaaatg 1620
Qy 1621 tglggtctccaaaggtggggccagatgagcggctcatctacttctatgtgaaccacat 1680
Db 1621 tgtggtctccaaaggtggggccagatgagcggctcatctacttctatgtgaaccacat 1680
Qy 1681 ccccgagcgtctcacatccgaatccaaacctccgagagctactagaggjccagccggt 1740
Db 1681 ccccgagcgtctcacatccgaatccaaacctccgagagctactagaggjccagccggt 1740
Qy 1741 gctcctgagctgccaaagccagactacaagtacagagatctgcgtgglacgcctcaa 1800
Db 1741 gctcctgagctgccaaagccagactacaagtacagagatctgcgtgglacgcctcaa 1800
Qy 1801 cctgtccacgctgacagatgacgacgggaacccgcttctgctcgcactgcaagaacgtgca 1860
Db 1801 cctgttccacgctgacagatgacgacgggaacccgcttctgctcgcactgcaagaacgtgca 1860
Qy 1861 tctgttccgacccctctggcccgccagcctggagagatgacactggggcgccacgc 1920
Db 1861 tctgttccgacccctctggcccgccagcctggagagatgacactggggcgccacgc 1920
Qy 1921 caegctcagcctgagta tcccccgctgcgcgccgagcacgaggccactatgtgtgcga 1980
Db 1921 caegctcagcctgagta tcccccgctgcgcgccgagcacgaggccactatgtgtgcga 1980
Qy 1981 aqtcgaagacggcgacagccatgacaacactgcaacagaatcctctgctcagtgacggc 2040
Db 1981 aqtcgaadacggcgacagccatgacaacactgcaacagaatcctctgctcagtgacggc 2040
Qy 2041 cctggaaagccctcggtctacgcagaacttgaccgacctcctlggtggaacgtgagcgactc 2100
Db 2041 cctggaaagccctcggtctacgcagaacttgaccgacctcctlggtggaacgtgagcgactc 2100
Qy 2101 gctggagatgcaagtcttgggtggcgagcgacgcgcccgactcgtgtgtgtaaaaaga 2160
Db 2101 gctggagatgcaagtcttgggtggcgagcgacgcgcccgactcgtgtgtgtaaaaaga 2160
Qy 2161 cgaagagctactgagagaaaagctctgaggtcgacttgcgtgcgagactccaccagaaagctag 2220
|||||

Db 2161 cgagaggctgctggaggaaaaagctctggagtcgacttggcgactccaccagaaagctgag 2220
Qy 2221 catcaacgctgcgcagagagagatgcggacgcctactctgcagcgtgtgcacgcgcaa 2280
Db 2221 catcaacgctgcgcagagagagatgcggacgcctactctgcagcgtgtgcacgcgcaa 2280
Qy 2281 gggctgctcaactcctcccgccagcgtggccgtggaaggctccgagataaaggcagcat 2340
Db 2281 gggctgctcaactcctcccgccagcgtggccgtggaaggctccgagataaaggcagcat 2340
Qy 2341 ggaagtcgtgataccttctcgttlaccggcgtcatcgtctgtcttcttcttcttcttcttct 2400
Db 2341 ggaagtcgtgataccttctcgttlaccggcgtcatcgtctgtcttcttcttcttcttcttct 2400
Qy 2401 cctcatcttctgtaacatgagagagcggcccacgcagacatcaagacgggctaccctgtc 2460
Db 2401 cctcatcttctgtaacatgagagagcggcccacgcagacatcaagacgggctaccctgtc 2460
Qy 2461 catcatgagaccccggggaggtgctctctggagagcaatgcgaatacctgtcclacga 2520
Db 2461 catcatgagaccccggggaggtgctctctggagagcaatgcgaatacctgtcclacga 2520
Qy 2521 tgcagccagtgggaaattcccccgagagcggtgcacctgggggaggtgctcggctacgg 2580
Db 2521 tgcagccagtgggaaattcccccgagagcggtgcacctgggggaggtgctcggctacgg 2580
Qy 2581 cgccttcgggaaggtggtggaagcctccgcttctcggcatccacaaggcgagcagctgtga 2640
Db 2581 cgccttcgggaaggtggtggaagcctccgcttctcggcatccacaaggcgagcagctgtga 2640
Qy 2641 caccgtggccctgaaaaatgctgaaagaggcgccacagcgagcagcagcgcgctgcat 2700
Db 2641 caccgtggccctgaaaaatgctgaaagaggcgccacagcgagcagcagcgcgctgcat 2700
Qy 2701 gtcggagctcaagatcctcatctcacatcgggcaacacactcaacgtggtlcaacacctctcgg 2760
Db 2701 gtcggagctcaagatcctcatctcacatcgggcaacacactcaacgtggtlcaacacctctcgg 2760
Qy 2761 ggcctgacacaagccgagagggccccctcatggtgatcgtgaggtctctgcaagtagcgcaa 2820
Db 2761 ggcctgacacaagccgagagggccccctcatggtgatcgtgaggtctctgcaagtagcgcaa 2820
Qy 2821 cctctcaacacttctgcgcgcaagcgagcgttgcacctgcgccccctgcgcgagagagctctcc 2880
Db 2821 cctctcaacacttctgcgcgcaagcgagcgttgcacctgcgccccctgcgcgagagagctctcc 2880
Qy 2881 cgacgagcgagcagcgttccgcgcctatggtgagctcgcagggctggtatcgagagcgagcc 2940
Db 2881 cgacgagcgagcagcgttccgcgcctatggtgagctcgcagggctggtatcgagagcgagcc 2940
Qy 2941 gggagcagcagcagaggtcctcttccgcgcgttctgaaagaccgagggcgagcgagcg 3000
Db 2941 gggagcagcagcagaggggtcctcttccgcgcgttctgaaagaccgagggcgagcgagcg 3000
Qy 3001 ggccttctccagacaaagaagctgagggacctgtggtcgtgagccccctgcacctggaagatct 3060
Db 3001 ggccttctccagacaaagaagctgagggacctgtggtcgtgagccccctgcacctggaagatct 3060
Qy 3061 tgtctgtacagcttccaggtgagcagagggatggaggttctctggtcttcccgaagagtgcat 3120
Db 3061 tgtctgtacagcttccaggtgagcagagggatggaggttctctggtcttcccgaagagtgcat 3120
Qy 3121 ccacagagacctggtcgtcggaaacattctgctgctggaagcgagctggttgaagatctg 3180
Db 3121 ccacagagacctggtcgtcggaaacattctgctgctggaagcgagctggttgaagatctg 3180
Qy 3181 tgactttggccttgcgggggacatctcaaaagaccttgactacgtccgcaaggcgagtg 3240
Db 3181 tgactttggccttgcgggggacatctcaaaagaccttgactacgtccgcaaggcgagtg 3240
Qy 3241 ccggtcgtccctcgagtgagtgagtgccctgaaagcatcttctgcaagagtggtacacacgca 3300
Db 3241 ccggtcgtccctcgagtgagtgagtgccctgaaagcatcttctgcaagagtggtacacacgca 3300

QY 841 gcgggtaagtgggtgcccagagcagcgtcccagcagagacccacacagaaactctccagcat 900
DB 841 gcgggtaagtgggtgcccagagcagcgtcccagcagagacccacacagaaactctccagcat 900
QY 901 cctgaccatcccaacagtcagccagacagacactggcctcgatgtgtacaaggccaacaa 960
DB 901 cctgacca tcccaacagtcagccagacagacactggcctcgatgtgtacaaggccaacaa 960
QY 961 cggcatccagcatttccggagagacacagagtcatttgcgatgaaaatcccttccatcag 1020
DB 961 cggcatccagcatttccggagagacacagagtcatttgcgatgaaaatcccttccatcag 1020
QY 1021 cgttctgagtcgctcaaaaggaccatctctggagccacgagccagagagcgtgtgaaagct 1080
DB 1021 cgttctgagtcgctcaaaaggaccatctctggagccacgagccagagagcgtgtgaaagct 1080
QY 1081 gccctgtgaagcttggcagcgtaccccccccgagttccagttgttacaaggatgaaaggc 1140
DB 1081 gccctgtgaagcttggcagcgtaccccccccgagttccagttgttacaaggatgaaaggc 1140
QY 1141 actgtccggagccacagtcacatgcctgtgtctcaaggaggttgacagagccagcac 1200
DB 1141 actgtccggagccacagtcacatgcctgtgtctcaaggaggttgacagagccagcac 1200
QY 1201 aggcacctacacctgcgacctgtgaaactccgctgctggcctgagggcgcaacatcagctc 1260
DB 1201 aggcacctacacctgcgacctgtgaaactccgctgctggcctgagggcgcaacatcagctc 1260
QY 1261 ggaagctgggtggaaatgtgtcccccacagatacatgagaaggagggcctctccccagcat 1320
DB 1261 ggaagctgggtggaaatgtgtcccccacagatacatgagaaggagggcctctccccagcat 1320
QY 1321 ctactgcgtctacagccgacaggccctcaactgcacggcctacgggtgcacctgcctct 1380
DB 1321 ctactgcgtctacagccgacaggccctcaactgcacggcctacgggtgcacctgcctct 1380
QY 1381 cagcatccagctggcactggcgccctggacacccctgcaagatgtttgccagcgtagctc 1440
DB 1381 cagcatccagctggcactggcgccctggacacccctgcaagatgtttgccagcgtagctc 1440
QY 1441 ccggcgccgagcagcaagaacctcatgcccagctgcctgactggagggcggtgaccac 1500
DB 1441 ccggcgccgagcagcaagaacctcatgcccagctgcctgactggagggcggtgaccac 1500
QY 1501 gcaggatccgtgaaaccccatcgaaagcctgcacacctggacaggtttgtgaaggaaa 1560
DB 1501 gcaggatccgtgaaaccccatcgaaagcctgcacacctggacaggtttgtgaaggaaa 1560
QY 1561 gaataagactgtgagcaagctggatccagaaatgccaaagtgtctgccatgtacaagtgt 1620
DB 1561 gaataagactgtgagcaagctggatccagaaatgccaaagtgtctgccatgtacaagtgt 1620
QY 1621 tgtgttcccaacaagctgggccaagatgagcggtctacttctctatgtgaccacat 1680
DB 1621 tgtgttcccaacaagctgggccaagatgagcggtctacttctctatgtgaccacat 1680
QY 1681 ccccgagcgttcaccatcgaaatccaaagccatccagagagctactagaaggccagccgt 1740
DB 1681 ccccgagcgttcaccatcgaaatccaaagccatccagagagctactagaaggccagccgt 1740
QY 1741 gctcctgagctgccaaagccagactacaaagtacgaagctatcgctgtgtacgcgtctcaa 1800
DB 1741 gctcctgagctgccaaagccagactacaaagtacgaagctatcgctgtgtacgcgtctcaa 1800
QY 1801 cctgtccacgctgacagatgagcagcgggaaacccgctctctgctcagctgcaagaacgtgca 1860
DB 1801 cctgtccacgctgacagatgagcagcgggaaacccgctctctgctcagctgcaagaacgtgca 1860
QY 1861 tctgttccgacccctctgtggccgagcctggaggaaggtggcacctggggcgccagcgc 1920
DB 1861 tctgttccgacccctctgtggccgagcctggaggaaggtggcacctggggcgccagcgc 1920

QY 1921 cagctcagcctgagtatccccccgctcgcccccagcagcagggccactatgtgtgcga 1980
DB 1921 cagctcagcctgagtatccccccgctcgcccccagcagcagggccactatgtgtgcga 1980
QY 1981 agtgcagaccggcgcagcctgacaaagcactgccacaagaagtacctgttcggtgcaggc 2040
DB 1981 agtgcagaccggcgcagcctgacaaagcactgccacaagaagtacctgttcggtgcaggc 2040
QY 2041 cctgaaagccctcggctcagcgagaacttgacgagacctcctgtgtgaaagctgcagcactc 2100
DB 2041 cctgaaagccctcggctcagcgagaacttgacgagacctcctgtgtgaaagctgcagcactc 2100
QY 2101 gctggagatgcagtgcttgggtggcggaagcagcagcccaagcatcgtgtgtacaaga 2160
DB 2101 gctggagatgcagtgcttgggtggcggaagcagcagcccaagcatcgtgtgtacaaga 2160
QY 2161 cgagaggtgctggaggaagaaagctcggagtcgagcttggcggaactcccaacagagctgag 2220
DB 2161 cgagaggtgctggaggaagaaagctcggagtcgagcttggcggaactcccaacagagctgag 2220
QY 2221 catccagcgctgcgcgagggaggtgcgggagcgtatcgtgcagcgtgtgcacgcgcaaa 2280
DB 2221 catccagcgctgcgcgagggaggtgcgggagcgtatcgtgcagcgtgtgcacgcgcaaa 2280
QY 2281 gggctgcgtcaactcctcccgagcgtggcgtggaaggtcccagagataagggcagcat 2340
DB 2281 gggctgcgtcaactcctcccgagcgtggcgtggaaggtcccagagataagggcagcat 2340
QY 2341 ggagatcgtgatccttgcgtaccggcgctcagctgtcttcttctgggtccctcctct 2400
DB 2341 ggagatcgtgatccttgcgtaccggcgctcagctgtcttcttctgggtccctcctct 2400
QY 2401 cctcatcttctgtaacatgagaggccggccacagcagacatcaagagcgggctacctctc 2460
DB 2401 cctcatcttctgtaacatgagaggccggccacagcagacatcaagagcgggctacctctc 2460
QY 2461 catcatcatgaccccgggagggtgcctctctgagagacaaatgcgaataacctgtcctacga 2520
DB 2461 catcatcatgaccccgggagggtgcctctctgagagacaaatgcgaataacctgtcctacga 2520
QY 2521 tqccagccagtgggaaatccccccagagcgcctgcacctggggagagtgctcggctacgg 2580
DB 2521 tqccagccagtgggaaatccccccagagcgcctgcacctggggagagtgctcggctacgg 2580
QY 2581 qcqcttcgggaagtggtggaagcctccgcttccgacatccacaaggcagcagctgtga 2640
DB 2581 qcqcttcgggaagtggtggaagcctccgcttccgacatccacaaggcagcagctgtga 2640
QY 2641 caccgtgcccgtgaaatgctgaaagagggcgccacgcccagcgagcaccgcgcgtgat 2700
DB 2641 caccgtgcccgtgaaatgctgaaagagggcgccacgcccagcgagcaccgcgcgtgat 2700
QY 2701 gtcgagctcaagatctcctcatttccatcctgcggcaacacacatcaacgttggtcaacctcctcgg 2760
DB 2701 gtcgagctcaagatctcctcatttccatcctgcggcaacacacatcaacgttggtcaacctcctcgg 2760
QY 2761 ggcgtgcaccagcgcagggccctcctcatgtgtgagctgtgaggtctctgcaagtacggcaa 2820
DB 2761 ggcgtgcaccagcgcagggccctcctcatgtgtgagctgtgaggtctctgcaagtacggcaa 2820
QY 2821 cctctcccaacttcttcgcgcgaagggcgcccttcagccccctgcgcgggagaagtctccc 2880
DB 2821 cctctcccaacttcttcgcgcgaagggcgcccttcagccccctgcgcgggagaagtctccc 2880
QY 2881 cgagcagcgcggaagccttccgcgcctatgttgagagctcggaggtcggagggcgcc 2940
DB 2881 cgagcagcgcggaagccttccgcgcctatgttgagagctcggaggtcggagggcgcc 2940
QY 2941 ggggagcagcagaggtcctcttcgcgcgttcttcgaagaccagggcgagcgagcg 3000
DB 2941 ggggagcagcagaggtcctcttcgcgcgttcttcgaagaccagggcgagcgagcg 3000
QY 3001 ggccttccagaccagaagagctgaggaacctgtggctgagcccgctgaccatgggaagatct 3060

Oy 421 ctttgagcagccattcatcaacaagcctgacacgctcttggtcaacaggaagagccat 480
|||||
Db 421 CTTTGAGCAGCCATTCAACAAGCCTGACACGCTCTTGGTCAACAGGAAGAGCCCAT 480
Oy 481 gagggtgacctgctggtgagcctcccgccctcaatgtcaagctgagcctgcaagctc 540
|||||
Db 481 GTGGGTGCCCTCTCTGTCTCATCCCGGCCCTCAATGTACAGCTGCCCTGCCAANGCTC 540
Oy 541 qylgctgtgagccagagcggaagaggtggtggtgagatgacccggcgagagctgctgctc 600
|||||
Db 541 GGTGTCTGTGGCCAGACGGCAGAGAGTGGGTGGATGACCCGGCGGCCATCTCTGTCTC 600
Oy 601 cagcgaactgctgacagatgacctgtacgtgaglgcagagaccactggaagagacaga 660
|||||
Db 601 CAGCGCACTGCTGCAGATGCCCTGTACCTGTGAGTGCAGACACCACTGGGGAGACAGAGA 660
Oy 661 cttcttccaaacctctctggtgacatcacaggaacagagctctatgacatccagct 720
|||||
Db 661 CTTCTCTTCCAAACCCCTTCTCTGGTGCACATCACAGGAACAGAGCTCTATGACATCCAGCT 720
Oy 721 qttgccaggaagtcgctgagcctgctggtgagggagagctggttccctgaaactgacgct 780
|||||
Db 721 GTTGCCACAGAAAGTCCGTGGAGCTCTGGTAGGGAGAGAGCTGGTCTCAACTGCACCCGT 780
Oy 781 ggggctgagtttaactcagggtgtcacctttgactgggactaccacaggaagcagcaga 840
|||||
Db 781 CTGGCTGAGTTTAACACAGGTGTCACTTTCACCTTTCACCTGGGACTACCCAGGAGCAGCAGA 840
Oy 841 gggggtaagtggtggtgagcagcagctccagcagacccacacagaaactctccagct 900
|||||
Db 841 GCGGGGTAAAGTGGGTGCCGAGCAGCTCCAGCAGTCCAGCAGACCCACACAGAACTCTCCAGCAT 900
Oy 901 cctgaccatcccaacaglcagccagcagcagcagcagcagcagcagcagcagcagcagc 960
|||||
Db 901 CTTGACCATCCACACAGTTCAGCCACACAGCTGGGCTGGCTGTGTGTGCAAGGCCAAGCAA 960
Oy 961 gggcctcagcagatttcgggagagcagcagcagcagcagcagcagcagcagcagcagc 1020
|||||
Db 961 CGGCATCCAGCATTTTCGGGAGAGCACCGAGTCACTTGTGATGAAATCCCTTTCATCAG 1020
Oy 1021 cgtcagagtgctcaagagaccatctctgagggcagcagcagcagcagcagcagcagcagc 1080
|||||
Db 1021 CTTGAGGTGGCTCAAGAGACCCATCTTGAGGCCACCGCAGGAGACGAGCTGTTGAAGCT 1080
Oy 1081 gcccctgagctggcagcgttcccccctcccgagltccagltgglacaagagagagagagc 1140
|||||
Db 1081 GCCCTGGAAGCTGGCAGCGTACCCCTCCCGCCGAGTTCCAGTGTACAGAGATGGAAGGC 1140
Oy 1141 actgtccgggagcagcagctccacatgcccctggtgtcagagaggtgacagagggccagcac 1200
|||||
Db 1141 ACTGTCCGGGGGCCACAGTCCACATGCCCTGTGTCTCAAGGAGGTGACAGAGGCCAGCAC 1200
Oy 1201 aggcacctacacctcgcctctggaacctcgcctgctgagcagcagcagcagcagcagcagc 1260
|||||
Db 1201 AGGCACCTTACACCTTCGCCCTCTGGAAGTCCGCTGTGCTGAGAGGCCAGCATCAGCCT 1260
Oy 1261 ggaagctggtgtgagatgtgccccccacagatatacagagagagagcctcctccccagcat 1320
|||||
Db 1261 GGAGCTGGTGTGATGTGCCCTCCCGCCAGATACATGAGAGAGAGGCTCTCTCCCGCAGCAT 1320
Oy 1321 ctactcgtgtcacagcgcagcagcctcacctgacgagcagcagcagcagcagcagcagcagc 1380
|||||
Db 1321 CTACTCGCGGTACAGCCCGCCAGGCCCTCACCTGCAGGCCCTACGGGTGCCCCCTGCCCTCT 1380
Oy 1381 cagcatccagtgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1440
|||||
Db 1381 CAGCATCCAGTGGCACTTGGCGGCCCTGGACACCCCTGCAAGATGTTTGCCAGCGTAGTCT 1440
Oy 1441 ccggcgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1500
|||||
Db 1441 CCGGGCGCGCAGCAGCAAGACCTTCATGCCACAGTGGCGGTGACTGGAGGGCGGTGACCCAC 1500
Oy 1501 gcaggatgcccgtgaacccccatcgagagccttggaacacctggaccaggtttgtggagggaaa 1560
|||||

Db 1501 GCAGGATGCCGTGAACCCCATCGAGAGCTTGACACCTGGACCCGAGTTTGTGGAGGGAAA 1560
Oy 1561 gaaataagactgtgagcaagctggtgagtcgaataagcgaagcagcagcagcagcagcagcagc 1620
|||||
Db 1561 GAAATAAGACTGTGAGCAAGCTGGTGTATCCAGATGCCAAGCTGTCTGCCATGTACAAAGTG 1620
Oy 1621 tgtgcttcccaacaaggtgaggccaggatgagcggctcatctacttctatgtgacacacat 1680
|||||
Db 1621 TGTGTCTTCCAAACAGGTGGGCCAGGATGAGCGGCTCATCTACTTCTATGTGTGACACCAT 1680
Oy 1681 cccgagagccttccacatcgaatccaagcagcagcagcagcagcagcagcagcagcagcagc 1740
|||||
Db 1681 CCCGACCGCTTACCATCGAATCCAGCCATCCGAGGAGCTACTAGAGGGCCAGCCGGT 1740
Oy 1741 gctcgtgagctgccaagccgacagctacaagtacgagcatctgagcagcagcagcagcagcagc 1800
|||||
Db 1741 GCTCTGAGCTGCCAAGCCGACAGCTACAAGTACGAGCATCTGCGCTGCTACCGCCCTCAA 1800
Oy 1801 cctgtccagctgcaagatgcaagcgggaacccgctctgctgactgcaagaaacgctga 1860
|||||
Db 1801 CTTGTCCACGCTGCAGATGCGCAGCGGAACCCGCTTCTGCTCGACTGCAAGAAGCTGCA 1860
Oy 1861 tctgttccacccctctgcccagcagcctgagagagltgacactgagcagcagcagcagcagc 1920
|||||
Db 1861 TCTGTTCGCCACCCCTCTGGCGCCAGCCTGGAGAGGTGGCAGCTGGGGCGCCGCCACGC 1920
Oy 1921 cagctcagcctgagttatccccccgctgctgcccagcagcagcagcagcagcagcagcagc 1980
|||||
Db 1921 CAGCTCAGCTGAGTATCCCGCGCTGCGCCCGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1980
Oy 1981 agtcaagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 2040
|||||
Db 1981 AGTCAAGACCGCGCAGCCATGACAAGCTGCAAGAAAGTACCTGCTCGGTGCGAGGC 2040
Oy 2041 cctgaaagcctcctgctcagcagaaactgacagcagcagcagcagcagcagcagcagcagc 2100
|||||
Db 2041 CCTGGAAGCCCTCGGCTCACGCAAGCTTGCACGACCTCTCTGCTGAACGTGACGGACTC 2100
Oy 2101 gctggagatgagtgcttgggtggcggagcagcagcagcagcagcagcagcagcagcagcagc 2160
|||||
Db 2101 GCTGCAGATGAGTGTCTGTGGTGGCGGAGCGCAGCGCCAGCATCGTGTGTGTACAAGA 2160
Oy 2161 cgaagagcgtgagagaaagtctgaagtcgaacttggcagcagcagcagcagcagcagcagcagc 2220
|||||
Db 2161 CGAGAGGCTGTGGAGAAAGTCTGGAGTGCAGTTTGGCGGACTTCCAACACAGAGCTGAG 2220
Oy 2221 catccagcgtgagcagagagatgagggagcagcagcagcagcagcagcagcagcagcagcagc 2280
|||||
Db 2221 CATCCAGCGGTGCGCAGGAGGATGCGGGAGCGTATCTGTGCAAGCTGTGCAACGCCAA 2280
Oy 2281 gggctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 2340
|||||
Db 2281 GGGTGTGCTCAACTCTCTCCCGCAGCGTGGCGTGGAAAGCTCCGAGGATAAGGGCAGCAT 2340
Oy 2341 ggaagc 2400
|||||
Db 2341 GGAGATCGTATCTTGTGGGTACCGCGCTCATCGCTGTCTTCTTCTTCTTCTTCTTCTTCT 2400
Oy 2401 cctcatctctgtaacatgagggagcagcagcagcagcagcagcagcagcagcagcagcagcagc 2460
|||||
Db 2401 CCTCATCTTCTGTAACATGAGGAGCGCGCCACAGCAGACATCAAGACGGGCTACCTTGTCT 2460
Oy 2461 catcatcatggaaccccgagggtgctctctggaggagcaatgcgaatcacctgtctctacga 2520
|||||
Db 2461 CATCATGAGCCCGGGGAGGTGCTCTTGAGGAGCAATGCGAATACCTGTCTTCTTCTTCTTCT 2520
Oy 2521 tggcagc 2580
|||||
Db 2521 TGGCAGCCAGTGGGAAATTCCTCCCGCAGAGCGGCTGCACCTGGGAGAGTGTCTCGGCTACGG 2580
Oy 2581 cgccttcggagaggtggtggaagcctccgcttccgcatcccaaggggagagcagcagcagcagc 2640
|||||

QY 2221 catccagcgcgtgcgcagagagatgcggagcgtctctgtcagcgtgtgcaacgcaa 2280
|||||
Db 2232 CATCCAGCGCGTGGCGAGGAGATCGGACGCTATCTGTGAGCGTGTGCAACGCCAA 2291
|||||
QY 2281 gggctgcgtcaactctccgccagcgtggccgtggagggctccgagataaaggcagcat 2340
|||||
Db 2292 GGGCTGCGTCAACTCTCCGCCAGCGTGGCCGTGGAAGGCTCCGAGGATAAGGGCAGCAT 2351
|||||
QY 2341 qgagatcgatcctctgtcgtaccggcgtcatcgtgtcttcttcttcttcttcttct 2400
|||||
Db 2352 GGAGATCGTGATCTTGTGCGTACC GGCGTCACTCGTGCTTCTTCTTGGGTCTCTCTCT 2411
|||||
QY 2401 cctcatcttctgtlaacatgaggagcgcccaacgcagacatcaaacagggctacctgtc 2460
|||||
Db 2412 CTTCACTTCTGTAAATGANGAGCGGCCCCACGCAGACATCAAGACGGGTACCTGTG 2471
|||||
QY 2461 catcaatgagccccggggaggtgctctggaggagcaatgcgaatacctgtcctacga 2520
|||||
Db 2472 CATCATATGGACCCGGGAGGTGCTCTGGAGAGCAATGCGAATACCTGTCTTACCA 2531
|||||
QY 2521 tgcayccagtggaatctcccccagagcgctgcaacctggggagagtgctcggctacgg 2580
|||||
Db 2532 TGCACGCCAGTGGGAATTTCCCGAGAGCGGCTGCAACCTGGGAGAGTGTCTCGGCTACGG 2591
|||||
QY 2581 cgccttcgggaagtggtggaagcctccgctttcggcatcccaagggcgagcagctgtga 2640
|||||
Db 2592 CGCCTTCGGGAAGTGTGTGAAGCCTCCGCTTTCGGCATCCACAAAGGGCAGCAGTGTGA 2651
|||||
QY 2641 caccgtggcgtgaaatgctgaaagaggggccacagcgacgcgcgcgtgat 2700
|||||
Db 2652 CACCGTGGCGGTGAAANTGCTGAAGAGGGCGCCACGGCCAGCGAGCAGCCGCGCTGAT 2711
|||||
QY 2701 gtcggagctcaagatcctcatlcaatcgcgaacacacctcaacgtggtcaacctctcgg 2760
|||||
Db 2712 CTCGGAGCTCAAGATCCTCATTCATCGCAACCACTCAACGTGCTCAACCTCTCTCGG 2771
|||||
QY 2761 ggcgtgcaccaagccagggccccctcatggtgatcgtggagtcttgcgaatcagggaa 2820
|||||
Db 2772 GCGGTGCACAAAGCCGACGGGCCCCCTCATGCTGATCGTGGAGTTCTGCAAGTACGGCAA 2831
|||||
QY 2821 cctctccaactlcttcgcgcgaagcggaaccccttcagccccctgcggagaaagtctcc 2880
|||||
Db 2832 CTTCTCCAATCTCTCGCGGCCAAGCGGACGCCCTTCAGCCCCCTCGCGGAGAACTCTCC 2891
|||||
QY 2881 cgagcgcgcgcagctcccgccatggtggagctcgccagctggatcgagcgccgc 2940
|||||
Db 2892 CGAGCAGCGGACGCTTCCGGCCATGCTGGAGCTCGCAGCTGGATCGGAGCGGCC 2951
|||||
QY 2941 ggggagcgcgcaggggtcctcttcgcgcggttctcgaagacccgagggcgagcgagcg 3000
|||||
Db 2952 GGGGAGCAGCGACAGGGTCTCTTCGCGCGGTCTCTCGAAGACCGAGGCGGAGCGGCG 3011
|||||
QY 3001 ggcctctccagaccgaagctgaggaacctgtggtgagcccgctgaccatggaagatct 3060
|||||
Db 3012 GCGTTCTCAGACCAAGAAGCTGAGAGCTGTGGGTGAGCCGGCTGACCATGGAAAGATCT 3071
|||||
QY 3061 tglctgtacagcttccaggtggccagagagtgagttcctlggcttcccgaagtgcac 3120
|||||
Db 3072 TGTCTGCTACAGCTTCCAGGTGGCCAGAGGATGAGTTCTTGCTTCCCAAGATGCTAT 3131
|||||
QY 3121 ccacagagacctgggtgctcggaacattctgtgtcggaaagcgacgtggtggaagatctg 3180
|||||
Db 3132 CCACAGAGACCTTGGCTGCTCGGAACATTTCTGTGTGCGAAAGCGACGCTGCTGAAGATCTG 3191
|||||
QY 3181 tgaacttggcttggccgggacatctacaagacctgactactcgcgaagggcagltgc 3240
|||||
Db 3192 TGACTTTGGCTTGGCCGGGACATCTACAAAGACCTTACTACTCTCCGCAAGGGCAGTGC 3251
|||||
QY 3241 cggcgtccccctggaagtggatggccccctgaaagcatcttcacaagatgtacacacga 3300
|||||
Db 3252 CCGGCTGCCCTGAAGTGGATGGCCCTGAAAGCATCTTCGACAAGGTGTACACACGCA 3311
|||||
QY 3301 gagtgaocgtgtgttcttgggtgtctctctctgaggagatcttctctctctctctctct 3360

Db 3312 GAGTGACGCTGTGTGCTCTTTTGGGGTGTCTTCTCTGGAGATCTTCTCTCTGGGGCTCCCC 3371
|||||
QY 3361 gtaccctgggtgcagatcaatgagagttctgccagcgctgagagcgcgcacaagat 3420
|||||
Db 3372 GTACCTTGGGTGCAATCAATGAGAGTTCGTGCCAGCGGCTGAGAGACGGCACAAAGAT 3431
|||||
QY 3421 gggggccccggagctggccactcccgccatacgcgcgcgcacatcgtgaaactgctgltccgg 3480
|||||
Db 3432 GAGGGCCCCGAGCTGGCCACTCCCGCCATACGCCGCATCATGCTGAACGTGCTGTCTCGG 3491
|||||
QY 3481 aqaccccaaggcgagacctgcattctcggagctgggtgagatccttggggagacctctctcca 3540
|||||
Db 3492 AGACCCCAAGCGAGACCTTCTCGAGCTGTGAGATCCTTGGGGACCTCTCTCCA 3551
|||||
QY 3541 gggcaggggctgcgaagaggaagaggtctgcctggcccgcgagctctccagagctc 3600
|||||
Db 3552 GGGCAGGGGCTTGAAGAGGAGAGAGGTCTGCATGGCCCGCCGACGCTCTCAGAGCTC 3611
|||||
QY 3601 aqaaagggagctctctcgcaggtgtccaccatggccctacacatcgccccaggtgcgc 3660
|||||
Db 3612 AGAAGAGGGCAGCTTCTCGCAGGTGTCCACCATGCGCCCTACACATCGCCACGCTGACGC 3671
|||||
QY 3661 tgaagacagccgcgaagcctgcagcgcacagcctggcccgaggtattacaactgggt 3720
|||||
Db 3672 TGAGACAGCCCGCCCAAGCTTGCAGCGCCACAGCCTTGCCCGCCAGGTATTACAACTGGGT 3731
|||||
QY 3721 gtcttctcccggtgcctggccagaggggtgagaccggtgttctctccagagatgaaac 3780
|||||
Db 3732 GTCTTCTCCGGTGCCTGGCCAGAGGGCTGAGACCCGTGGTCTCTCCAGGATCAAGAC 3791
|||||
QY 3781 attgagaattccccatgacccccaacgacctacaaaaggtctctgtggaacaccagacaga 3840
|||||
Db 3792 ATTTGAGGAATTTCCCATGACCCCAACACCTTACAAAGGCTCTGTGGACAACACACAGA 3851
|||||
QY 3841 cagtggagtgctgcctgcggaggttgaacagatagagcagcagcagcagcagcagcagc 3900
|||||
Db 3852 CAGTGGGATGTTGCTGGCTCGGAGGAGTTTGAGCGATAGAGCAGGATAGACAAGA 3911
|||||
QY 3901 aagcggtctcag 3912
|||||
Db 3912 AAGCGCTTCAG 3923
|||||

RESULT 19

US-08-770-449-31

; Sequence 31, Application US/08770449

; GENERAL INFORMATION:

; APPLICANT: Bennett, Brian D.

; APPLICANT: Goeddel, David

; APPLICANT: Lee, James M.

; APPLICANT: Matthews, William

; APPLICANT: Tsai, Siao Ping

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES

; NUMBER OF SEQUENCES: 42

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 460 Point San Bruno Blvd

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WinPatIn (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/770,449

; FILING DATE: 20-Dec-1996

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

```

: APPLICATION NUMBER: PCT/US93/00586
: FILING DATE: 22-JAN-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/826935
: FILING DATE: 22-JAN-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/222616
: FILING DATE: 04-APR-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Lee, Wendy M.
: REGISTRATION NUMBER: 40,378
: REFERENCE/DOCKET NUMBER: P0821P2D1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415/325-1994
: TELEFAX: 415/952-9881
: TELEX: 910/371-7168
: INFORMATION FOR SEQ ID NO: 31:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 4425 base pairs
: TYPE: Nucleic Acid
: STRANDEDNESS: Single
: TOPOLOGY: Linear
: US-08-770-449-31

```

Query Match	95.2%	Score 3912	DB 11	Length 4425	
Best Local Similarity	100.0%	Prod. No. 0			
Matches 3912	Conservative	0	Mismatches	0	Indels
		0			Gaps
					0
Qy	1	ccacqcgagcgccgagagatgcagcgggcgccgcgcgtgtgcctgcgactgtgactctg	60		
Db					
Db	12	CCACGCGCAGCGCGGAGATGCAGCGGGCGCGCGCTGTGCTTGCACACTGGCTCTG	71		
Qy	61	ctctggagactctggaacggccctggtgagtggctactccatgaccccccccgacctgaacat	120		
Db					
Db	72	CCTGGGACTCTTGACGGCCCTGCTGAGTGGCTACTTCCATGATACCCCGCCAGCCTTGACAT	131		
Qy	121	cacggagagtcacacgtcatcgacacggctgacagcctgtccatctctcgcaggggaca	180		
Db					
Db	132	CACGGAGAGTCAACAGTCATCGACACGGTGCACAGCCTGTCCATCTCTCGACGGGACA	191		
Qy	181	qacccctcgtggtggcttggccaggagctcaggaggcgccagccacccgagacaagga	240		
Db					
Db	192	QCACCCCTCGAGTGGGCTTGCCGACGAGAGTCAAGGAGCGCAGCACCGGAGACAAGGA	251		
Qy	241	cagcagagacacggggttggtgcagactcgagggacacacacacagccctactcgaa	300		
Db					
Db	252	CAGCGAGACACGGGGTGGTGCAGACTGCGAGGCACTGCGGGCACACGCGCCGCTACTGCAA	311		
Qy	301	ggtctgctgctgcacgaggtacatgccaacgacacagcgagctacgtctcgtactacaa	360		
Db					
Db	312	GCTGTGCTGCTGCACGAGGTACATGTCACACGACACGCGAGTACGTCTGCTACTACAA	371		
Qy	361	gtacatcaagcagcagcatcgaggggcacacagggcgccagctcctcagtgctcgtgagaga	420		
Db					
Db	372	GTATATCAAGGCACGCATCGAGGGGCACACGGCCGCCAGCTCCTACGTTGCTGAGAGA	431		
Qy	421	cttggagcagccattcatcaacagcctgcacgcctcttggccaacaggaagagcccat	480		
Db					
Db	432	CTTTGACAGCCATTTCATCAACAGCCTGACAGCCTCTTGGTCAACAGGAAGACGCCAT	491		
Qy	481	gtgggtgccctgtctgtgtgtccatcccccgccctcaatgtcaacgtgcgctcgcaagctc	540		
Db					
Db	492	GTGGGTGCCCTGTCTGTGTGTCATCTCCCGGCTCAATGTCAAGCTGCGCTCGCAAGCTC	551		
Qy	541	ggctcgttggccagcagggcagagtggtgtgggatgacgcggcgggcatcgtcgtctc	600		
Db					
Db	552	GGTCTGTGGCCACAGCGGACGAGGAGTGGTGTGGGATGACCGCGCGGGCATGCTCGTCTC	611		
Qy	601	cacgccactgctgcacgatgccttgtacctgcagtcgagacacacctggggagacagga	660		
Db					
Db	612	CACGCCACTGCTGACAGTGCCTGTACTTGCAGTGCAGACACCACTGGGAGACGAGA	671		

|||||
Db 1752 GCTCCTGAGCTGCAAGCCGACAGCTTACAAGTACGAGATCTCGCGTGTACCGCTCAA 1811
|||||
QY 1801 cctgtccacgctgcacgatagcgcacgggaacccgcttctgctgcagctgcaagaacgtgca 1860
|||||
Db 1812 CTTGTCTCAGCTGTCAGATCGGCACGGAACCGCTTCTGCTCGACTGCAAGAACGTGCA 1871
|||||
QY 1861 tctgttgcacacccctctgcgcgcacgactgagagaagtgagcaactggagcgcgcacgac 1920
|||||
Db 1872 TCTGTTCCGCACCCCTCTGGCCGCCAGCCTGGAGAGGTGGACCTTGGGGCGGCCACGC 1931
|||||
QY 1921 cagcctcagcctgagtatcccccgctgcgcgcgcagcagcagggccactatgtgtgca 1980
|||||
Db 1932 CACGCTCAUGCTGAGTATCCCCCGCTCGCCCGAGCAGAGGGCCACTATCTGTGCGA 1991
|||||
QY 1981 aqtcgaagaccgcgagcactagcaagcactgcacaaagagLaacctgtcgtgcaggc 2040
|||||
Db 1992 AGTGAAGACCGCGCAGGCATGACAAAGCACTGCCAAGAAAGTACCTTCTCGTGTGACGC 2051
|||||
QY 2041 cctggagccctcggtctcacgcagaacttgaccgacctcctggLgaacgtgaagcactc 2100
|||||
Db 2052 CTTGGAAGCCCTCGGCTCACCCAGAACTTGACCGAACTTCTGGTGAAAGTGAAGCACTC 2111
|||||
QY 2101 gctggagatgcagtgctgtggtggcggagcgacgcgcgcagcactgtgtgtlacaaga 2160
|||||
Db 2112 GCTGGAGATGCAAGTGTGCTGGCCGAGCGCACUCGCCACGATCGTGTGTACAAAGA 2171
|||||
QY 2161 caagagctgcctggagaaagtctggagtcgacttgcgagactccaaacgaagctgag 2220
|||||
Db 2172 CCAGAGGCTGCTGGAGGAAAGTCTGGAGTGCACCTTGGCGGACTCCAAACGAAAGCTGAG 2231
|||||
QY 2221 caLcagcgcgtgcgcgagaggaLgcgcgagcgtatctgtLgcagcgtLgtcaacgcgcaa 2280
|||||
Db 2232 CATCCAGCCGCTGCGGAGGAGATCGCGGAGCCCTATCTGTGCACCGTGTGCAACGCCAA 2291
|||||
QY 2281 gggctgcgtcaactcctccgcagcgtgcccgtggaaagctcccgaggaLaaggcgagcat 2340
|||||
Db 2292 GGGCTGCGTCAACTCTCCGCCAGCGTGGCCGTGGAAGGCTCCGAGGATAGGCGCAGCAT 2351
|||||
QY 2341 ggagatcgtgtaLcctgtLcgtLaccgcgcgtcatcgtgttcttctgtggctcctcct 2400
|||||
Db 2352 GGAGATGTGTATCTTGTGCGTACC CGCGGTATCGCTGTCTTCTGCGGTCTCTCTCT 2411
|||||
QY 2401 cctcatcttctgtaacatgagagcgccgcacgcagacacatcaagagcggtactctgc 2460
|||||
Db 2412 CTTATCTTCTTAACATGAGGAGCGCGCCACCCAGACATCAAGCGGCTACTCTGTC 2471
|||||
QY 2461 catcatatggaccgccggagggtcctctgtggagagcaatgcgaataacctgtcctacga 2520
|||||
Db 2472 CATCATCATGGACCCGGGGAGTGCCTCTGGAGGAGCAATGCGAATACCTGTCTACGA 2531
|||||
QY 2521 tqccagccagLgggaaattccccgcagagcgctacacctggagagtgctcgcgtacgg 2580
|||||
Db 2532 TGCCAGCCAGTGGGAATTTCCCCCGAGACGGCTGCACCTGGGGAGAGTGTCTCGGCTACGG 2591
|||||
QY 2581 cgccttcgggaaggtgggtggagcctccgctttcggcatccacaaaggcgagcagctgtga 2640
|||||
Db 2592 CGCCTTCGGGAAGTGTGTGAAGCTTCGCGCTTTCGGCATCCACAAAGGCGCAGCTGTGA 2651
|||||
QY 2641 cacgctggcgtgaaaaLgctgaaagagggccacgcccagcagcaccgcgctgat 2700
|||||
Db 2652 CACCGTGGCCGTGAAAATTCCTGAAGAGGGCGCCACGCGCCAGCGAGCACCCCGCTGTAT 2711
|||||
QY 2701 gtcgagctcaagatcctcatcattcatcgcgaaccactcaacgtggtcaacctcctcgg 2760
|||||
Db 2712 GTCCGAGCTCAAGATCTCTATTACATCGGCAACCACTCAACGTGGTCAACCTTCTCGG 2771
|||||
QY 2761 ggcgtgcaccaagcgcagggcccccctcatggtgatcgtgagttctgcgaagtacggcaa 2820
|||||
Db 2772 GCGGTGCACCAAGCGCAGGCGCCCTCATGTGTGATCGTGTGAGTCTTGCAGATACGGCAA 2831
|||||
QY 2821 cctctcaacttctgcgcgcgaagcgaggacgttcagccccctgcgcgagaagctccc 2880
|||||

Db 2832 CTTCTCCAACTTCTCTCCCGCCCAAGCGGACGCCCTTCAGCCCCCTCGCGGAGAACTCTCC 2891
|||||
QY 2881 cgaagcagcgcgagcacttctccgcgcactggtggagctcgcacagctggatcgagagcgccc 2940
|||||
Db 2892 CGAGCAGCGCGACGCTTCCCGGCCCATGGTGGAGCTCGCCAGGCTGGATCGGAGCGCGCC 2951
|||||
QY 2941 ggggagcgcgcacaggggtcctcttcgcgcgggttctcgaaagcccgaggcgagcgagcg 3000
|||||
Db 2952 GGGGAGCAGCGACAGGGTCTCTTCCCGCGGTCTTCGAAGACCGAGCGGCGAGCGCGC 3011
|||||
QY 3001 ggccttctcaagaccgaagctgagacactgagctggcctgagcccgctgacacatLgaagaLct 3060
|||||
Db 3012 GGCCTTCTCAAGACCAGAAGCTGAGACCTGTGGCTGAGCCCGCTGACCATGGAAGATCT 3071
|||||
QY 3061 tglctgtctacagcttccaggtggccagaggtgaggttctctggcttccccgaaaatgcat 3120
|||||
Db 3072 TGTCTGCTTACAGTTCACAGGTGGCCAGAGGATGAGTTCCTGGCTTCCCCAAAGTGCAT 3131
|||||
QY 3121 ccacagagaacctggtgctcggaaacatctcgtgcgaaagcgacgtLggLgaagatctg 3180
|||||
Db 3132 CCACAGAGACCTTGGCTGCTCGGAACATTTCTGCTCGGAAAGCGACGTGCTGAAGATCTG 3191
|||||
QY 3181 Lgaecttggccttgcgcgggacatctacaagacctgactactcgcgaagggcagtgcc 3240
|||||
Db 3192 TGACTTTGGCCTTGCCCGGGACATCTACAAACCTGACTACGTCCCGCAAGGGCAGTGC 3251
|||||
QY 3241 ccgctgcctcctgaagtggatggccctgaaagcatcttcgacaaggLgtacaccacgca 3300
|||||
Db 3252 CCGGCTGCCCTGAAGTGCATGGCCCTTGAAGCATCTTCGACAAAGGTGTACACCACGCA 3311
|||||
QY 3301 gagtgaagctgtggctccttgggggtgcttctctctggagagatctctctctgggggctcccc 3360
|||||
Db 3312 GAGTGACGTGTGGTCTTTGGGGTGTCTTCTGAGAGATCTTCTCTGTTGGGGGCTTCCCC 3371
|||||
QY 3361 gtacccctgggtgcagatcaatgagaggtctctgcagcgctgagagcgccacaagat 3420
|||||
Db 3372 GTACCTTGGGTGCAGATCAATGAGAGTCTTGCACGGCTGAGAGACGCGCACAGAT 3431
|||||
QY 3421 gagggcccgagctggccactccgcacatacgcgcgcatcatgctgaactgtggtccgg 3480
|||||
Db 3432 CAGGCCCCCGAGCTGGCCACTCCCGCATACGCCGATCATGTGAACCTGCTGCTCGG 3491
|||||
QY 3481 agaccccaaggcgagacctgcatctcggagctggtggagatcctgggggacctgtccca 3540
|||||
Db 3492 AGACCCCAAGCGAGACTGCAATTTCTCGAGCTGGTGAGATCTCTGGGGGACCTTGCTCCA 3551
|||||
QY 3541 gggcagggcgctgcaagaggaagggaggtctctgcatggccccgcgcagctctcagagctc 3600
|||||
Db 3552 GGGCAGGGCCTGCAAGAGGAAGAGGAGGTCTGCATGGCCCCCGCGCAGCTCTCAGAGCTC 3611
|||||
QY 3601 agaagagggcagcttctcgcagggtgtccacatggccctacacatcgccccagctgcagc 3660
|||||
Db 3612 AGAAGAGGGAGCTTCTCGCAGGTGTCCACCATGGCCCTACACATGCCCCAGGCTGACGC 3671
|||||
QY 3661 tgagcagagcccgcaagcctgagcccaagcctggcccgcaaggtattacaactgggt 3720
|||||
Db 3672 TGAGCAGACCCCGCAAGCCTGACGCCACAGCTTGGCCCTGGCCCGCAGGTATTACAACTGGGT 3731
|||||
QY 3721 gtcctttccccgggtgctcgtggccagaggggtgagaccctggttctctccaggtatgaagac 3780
|||||
Db 3732 GTCCTTTCCCGGGTGCCTGGCCAGAGGGCTGAGACCCCGTGGTTCTCTCCAGGATGAAGAC 3791
|||||
QY 3781 atttgaggaattccccatgaccccaacgacctacaaggctctgtggaacccagacaga 3840
|||||
Db 3792 ATTTGAGAAATTCCTCATGTACCCCAAGCTTACAAAGGCTCTGTGGACAACACAGACAGA 3851
|||||
QY 3841 cagLggagatggtcgtgcctcgagaggtttgacagatatagagcagcgcatagacaaga 3900
|||||
Db 3852 CAGTGGGATGCTGCTGCTCGGAGGAGTTTGAGCAGATAGAGCAGGCGCATAGACAGA 3911
|||||
QY 3901 aagcggcttcag 3912
|||||
Db 3912 AAGCGGCTTCAG 3923

QY 1381 cagcatccagtgacatggcgccctggacacccctgcaagatgtttgcccagcgtagtct 1440
DB 1392 CAGCATCCAGTGGCACTGGCGGCCCTGGACACCCCTCAAGATGTTTGGCCACGGTAGTCT 1451
QY 1441 ccggcgcgagcagcagaagaactcatgccacagtgccctgactggagggcggtgacac 1500
DB 1452 CCGCGCGCGCGACACAGACCTCATGCCACAGTGCCTGTGATGCCGTGGAGGGCGTGAACCA 1511
QY 1501 qcaggatgcggtgaaaccccatgagagcctgacacctgacccgagtttgtaggggaaa 1560
DB 1512 GCAGGATGCCGTCAACCCCATCGAGAGCCTGGACACCTGGACCGAGTTTGTGAGAGGAAA 1571
QY 1561 gaataagactgtgagcaagactggatccagaatgccaaagtgcttgccatglacaagtg 1620
DB 1572 GAATAAGACTGTGAGCAAGCTGTGATCCAGATGCCAAAGTGTCTGCCATGTACAAGTG 1631
QY 1621 tgggttctccaagaagtgaggccaagatgagcggctcaactctctctatgtgacaccat 1680
DB 1632 TGTGTCTCCAAACAGGTGGGCCAGATGAGCGGCTCATCTACTTCTATGTGACCACCAT 1691
QY 1681 cccgacggcttcaccatgaaaccagccatccgagagactacagagggccagccggt 1740
DB 1692 CCCCAGCGCTTCACCATCGAATCCAAAGCCATCCGAGGAGCTACTAGAGGGCCACCGCGT 1751
QY 1741 gctcctgaactgccaaagccgacagctacaagtacgagacatctgctggglaccgctcaa 1800
DB 1752 GCTCTCTGAGCTGCCAAGCGCACAGGTACAAAGTACGAGCATCTGCGCTGTGATCCGCTCAA 1811
QY 1801 cctgtccagctgacgaatgcacagggaaacccgctctgtcgcagactcaagaagacgtgca 1860
DB 1812 CTTGTCCAGCTGTCAGATGCCGACGGGAACCCGCTTGTGCTGAGTGCAGAAAGCTGCA 1871
QY 1861 tctgttgcgcaacccctctggcgccagcctggagaggttggaacctggggcgccacgc 1920
DB 1872 TCTGTTCCGCCACCCCTCTGGCGCCAGCTGGAGGAGTGGCACCTGGGGCGGCCACGC 1931
QY 1921 caegctcaegctgaatctcccccgctcgcgcccgagcaacacctggtgaaactgtgtgca 1980
DB 1932 CACGCTCAGCTTGATATCCCCCGCGTGGCGCCGAGACGAGGCCACTATGTGTGCGA 1991
QY 1981 agtgaagaccggcgagccaagcaagcaactgcccacagaagtacctgtcgtgtgagggc 2040
DB 1992 ACTGCAAGACCGCGCAGCCATGACAAGCACTGCCACCAAGAACTACCTGTGGTGCAAGC 2051
QY 2041 cctggaagccctcggctcaagcagaacttgaccgacctcctggtgaacgtgagcagtc 2100
DB 2052 CCTGGAAGCCCCTCGGCTCAGCGAAGCTTGACCGACCTCTGCTGTAACGTGAACGACTC 2111
QY 2101 gctggagatgcagtgcttggtagccgagcagcagcgcccaagcatcgtgtgtacaaaaga 2160
DB 2112 GCTGGAGATGCAGTCTTGTGTGGCCGGAGCGCACGCCGCCAGCATCGTGTGTACAAAGA 2171
QY 2161 cgagaggtgctggagggaaaagtctggagtgcacttgggactcccaaccagagctgag 2220
DB 2172 CGAGAGCTGTGTGAGGAAAAGTCTGGAGTGCAGCTTGGCGGACTCCAAACGAGACCTGAG 2231
QY 2221 catccagcgctgagcagaggagatgcgggacgtatctgtgcagcgtgtgcaacgcaaa 2280
DB 2232 CATCCAGCGCGTGGCGAGGAGGATGCGGGAGCGTATCTGTGCAAGCGTGTGCAACGCCAA 2291
QY 2281 gggctgctcaactcctccgcagcgtggcggtggaagctccagagataaaggcaycat 2340
DB 2292 GGGCTGGCTCAACTCTCCGCCACGCTGGCCGTGGAAGGGCTCCCGAGGATAAGGGCAGCAT 2351
QY 2341 ggagatcgtatccttctgtgtagccggcgctatcgtgtcttcttctgtgttctcctcct 2400
DB 2352 GCAGATCGTGTATCTTGTGCGTACCGCGCTCATCGCTCTCTTCTGCGTCTCTCTCT 2411
QY 2401 cctcatcttctgaactgaagagcgccgcccacgagacatacgaagcggtacctgctc 2460
DB 2412 CCTCATCTTCTGTAACTGTAGGAGCGCGGCCACGCACGACATCAAGACGGGCTACCTGTC 2471

QY 2461 catcatcattggacccccgggaggtgcctctgagagagcaatgcgaaatcacctgtcctacga 2520
DB 2472 CATCATCATGGACCCCGGGAGGTGCCCTGGAGGAGCAATGCGAATACCTCTCTACGA 2531
QY 2521 tgcagccagtgaggaaattccccccgagagcgctgcacctggggagagtgctcggctacgg 2580
DB 2532 TGCCACGACGATGGGAAATTCGCCGAGAGCGGTGCACCTGGGGAGAGTGTCTCGGTACGG 2591
QY 2581 ggccttccgggaaggtggtgggaagcctccgcttctggcattccacaaggagcagaactglga 2640
DB 2592 GCGCTTCGGGAAGGTGTGGGAAGCCTCCGCTTTCCGGCATCCACAAGGGCAGACGCTGTGA 2651
QY 2641 caccgtggccgtgaaaaatgctgaagaaggcgccacgcccagcgagcaccgcgcgctgat 2700
DB 2652 CACCGTGGCGGTGAAAAATGCTGAAAGAGGGCGCCACGCCAGCGAGCACCGCGCTCAT 2711
QY 2701 gtcggagctcaagatcctcatctcacatcggcaacacacctcaacgtggtlcaacctcctcgg 2760
DB 2712 CTCGGAGCTCAAGATCTCTTCAATCGCAACCACTCAACGTGGTCAACCTCTCTCGG 2771
QY 2761 ggcgtgacccaagcgcagggcccccctcatggtgaatcgtggagttctcgaagtacggcaa 2820
DB 2772 GCGTGTCAACAAAGCGCAGGGCCCCCTCATGTGATCGTGAGTTCTGCAAGTACGGCA 2831
QY 2821 cctctccaaactccttgcgcgccaaaggcgaccttccagccccctgcgaggaagtctcc 2880
DB 2832 CCTCTCCAACCTCTTGC CGCCCAAGCGGAGCGCCTTCAGCCCCCTGCCGCGAGAACTCTCC 2891
QY 2881 cgagcagcgcgagcgtctcccgccatggtgagctgcgcaggtctggaatcggagcgcc 2940
DB 2892 CGAGCAGCGCGAGCGTTCGCCGCGCATGTGTGGAGCTGCCAGGTGGATCGGAGCGCGCC 2951
QY 2941 gggagcagcagcagggctccttctcgcgcttctcgaagaccagggcgagggcgagggcg 3000
DB 2952 GGGAGCAGCCACAGGGTCTCTTCGCGCGGTCTCTGAAGACCAGGGCGGAGCGAGCGC 3011
QY 3001 ggccttccagaccacaagaagctgaggacctgtgctgagcccgctgaccttgggaagatct 3060
DB 3012 GGCTTCTCAGACCAAGAAGCTGAGGACCTGTGGCTGAGCCGCTGACCATGGAAGATCT 3071
QY 3061 tgcctgtcacagctccaggtggccagagggatgagttcctggcttcccgaaagtcat 3120
DB 3072 TGTCTGTCTACAGCTTTCAGGTGGCCAGAGGGATGGAGTTCTTGGCTTCCCGAAAAGTGCAT 3131
QY 3121 ccacagagacctggctcctcggaacattctgctgcgaaagcagctgggtgaagatctg 3180
DB 3132 CCACAGACCTGCTGCTCGGAACATTCCTGCTCGGAAAGCAGCCTGGTGAAGATCTG 3191
QY 3181 tgaatttggcccttgcggggacatctacaagaccctgactaogtccgcgaagggcagtcg 3240
DB 3192 TGACTTTGGCCTTGGCGGGACATCTACAAGACCCCTGACTACGTCGCGCAAGGCGAGTGC 3251
QY 3241 ccggctccccctgaagtggatggccctgaagcatcttcgaaggtgtacaccagca 3300
DB 3252 CCGCTGCCCTGAAAGTGGATGGCCCCCTGAAAGCATCTTCGACAAGGTGTACACCACGCA 3311
QY 3301 gagtgaagtggtgttcttgggtgcttctctgggagatcttctctgggggacctcccc 3360
DB 3312 GAGTGCAGTGTGTGCTTGGGTGCTTCTTCTGGAGATCTTCTCTCTGGGGGCTTCCCC 3371
QY 3361 gtaccttgggggtgcagatcaatgaggagtcttcccaagcgctgagagacggcacaagga 3420
DB 3372 GTACCTTGGGTTGCAGATCAATGAGGAGTTCTGCCAGCGCTGAGAGACGGCACAAAGAT 3431
QY 3421 gaggccccggagctggccactccgcctaccccatcagcccatcatctgaactgctggctcgg 3480
DB 3432 GAGGGCCCCGGAGCTGGCCACTCCCGCCATACCGCGCATCTGCTGAATGCTTGGTCCGG 3491
QY 3481 agacccaagggcgagacctgcatctcggagctggtggagatcctcgggggacctgctcca 3540
DB 3492 AGACCCCAAGCGCAGACCTGCATTCTCGGAGCTGGTGAGATCTCTGGGGGACCTGCTCCA 3551
QY 3541 gggcaggggctgcagaagagaagaggtctgtcatggcccccgcgagctctcagagctc 3600

Db 912 CCTGACCATCCACAACTCAGCCAGCACGACCTGGGCTCGTATGTGTGCAAGGCCAACAA 971
Qy 961 cggcatccagcgtatttcgggagagcaaccgaggtcattgtgcatgaaaaatcccttcatcag 1020
Db 972 CGGCATCCAGCGATTTTCGGGAGAGCACCGAGGTCATTGTGCATCAAAATCCCTTTCATCAG 1031
Qy 1021 cgtcgagtgactcaaggagcccaatccctggaagcccaaggcaggaagacgagctnqtgaagct 1080
Db 1032 CGTGAGTGGCTCAAGAGGACCCATTCCTGGAGGCCACGGCAGGAGACGAGCTGGTGAAGCT 1091
Qy 1081 gccctgaaagctggcagcgtaccctcccccgcgcgcaggttcccaagtgtacaagagatgaaagcc 1140
Db 1092 GCCCGTGAAGCTGGCAGCGTACCCCGCCCGCCGAGTTCACAGTGGTACAAGGATGCAAGGCC 1151
Qy 1141 acgtgcccggcgccacagtcacatatgccctgggtgtctcaaggaggtgacagagccagcac 1200
Db 1152 ACTGTCCGGCGGCACAGTCCATGCCCCCTGGTGCCTCAAGGAGGTGACAGAGGCCAGCAC 1211
Qy 1201 aggcacctacacccctgcgcctgtggaactccgctgctggcctgaaggcgaacataagcct 1260
Db 1212 AGCACCTACACCTTGCCCTGTGGAACTCCGCTGTGCTGAGGCTGAGGCGCAACATCAGCCT 1271
Qy 1261 ggaagctgggtggaatgtgcccccccagatacacatgaaagagagcctcctccccagcat 1320
Db 1272 GGAGCTGGTGGTCAATGTGCCCCCCCAGATACATGAAAGGAGGCCCTCTCCCCAGCAT 1331
Qy 1321 ctactcggcgtcacagcgcgcagcgcctcaactcgtcaaggctacgaggtgcccctgcctct 1380
Db 1332 CTACTGCGGTACAGCGCGGCAGGCCCTCACTGACAGGGCTACGGGGTGCCCCGTGCTCT 1391
Qy 1381 cagcatccagtggaactggcgccctggacacccctgcaagatgtttgcccagcgtagctt 1440
Db 1392 CAGCATCCAGTGGCAGTGGCGGCCCTGGACACCCTGCAAGATGTTTGGCCAGCGTAGCT 1451
Qy 1441 ccggcgggcagcagcaagacctcatgccacagtgccgtgactgagggcggtgaccac 1500
Db 1452 CCGCGCGCGGCAGCAGCAAGACCTCATGGCCACAGTGCCTGTACTGGAGGGCGGTGACCAC 1511
Qy 1501 qcaggatgcgcgtgaaccccatcgagcctggacacctggacacctgagccgaatttgtgagggaaa 1560
Db 1512 GCAGGATGCGGTGAACCCCATCAGAGCCTTGGACACTGACCGAGTTCCTGACCGAGTTTGTGGAGGAAA 1571
Qy 1561 gaataagactgtgagcaagctggatgcagaaatgccaaagtgctctgccatgtlacaagtgt 1620
Db 1572 GAATAAGACTGTGAGCAAGCTGGTGATCCAGAAATGCCAAAGTCTCTGCCATGTACAAAGTG 1631
Qy 1621 tglgggtctcaacaaggtgggcccagatgagcggctcaletactctctatgtgacacacat 1680
Db 1632 TGTGGGTCTCCAAACAAGGTGGGCCAGGATGAGCGGCTCATCTACTTATGTGACCACCAT 1691
Qy 1681 ccccggcggcttcaccatcgaaatcccaagccatccgagggagctactagaggccagccggt 1740
Db 1692 CCCCAGCGGCTTCACCATCGAATCCAAAGCCATCCGAGGAGCTACTAGAGGGCCAGCCGGT 1751
Qy 1741 gctcctgagctgccaagccgacagctacaaagtacgagcatctgctggtgataccgcctcaa 1800
Db 1752 GCTCTTGAGCTGCGCAAGCGCACAGCTTACAAGTACGAGCATCTGCGCTGTTACCGGCTCAA 1811
Qy 1801 cctgtccacgctgcacgatgcgcacggggaacccgcttctgctcagactgcaagaacgtgca 1860
Db 1812 CTTGTCCACGCTGCACGATGCGGCACGGGAACCCGCTTCCTGCTCGACTGCAAGAACGTGCA 1871
Qy 1861 tctgtttgcacacccctcttgccgcgcagcctggagagggtggcacctggggcgccacgc 1920
Db 1872 TCTGTTCCGCAACCCCTCTGGCCCGCAGCTGGAGGAGGTGGCACCTTGGGGCGGCCACGC 1931
Qy 1921 cacgctcagcctgagtatcccccgctcgcgcccgagcagcaggggccaactatgttgcga 1980
Db 1932 CAGGCTCAGCCTGAGTATCCCCCGCTCGCGCCCGAGCACGAGGGCCACTATGTGTGCGCA 1991
Qy 1981 aqtcgaagaccggcgagccatgacaagcactgcacaaagaagtacctctcgtgtcaggc 2040
Db 1992 AGTGAAGAACCCGCGCAGCCATGACAAGCACTGCCACAAAGAAGTACCTGTCTGGTGCAGGC 2051

Qy 2041 cctgggaagccccctcggctcacgaaattgaccgacacctcctcgtgtaacgtgagcagctc 2100
Db 2052 CTTGGAAGCCCTCTGGCTCACGAGAACTTGACCGACCTCTCTGGTGAACGTGAGCGACTC 2111
Qy 2101 gctggagatgcagtgcttgggtggcggagcgacgcgcccaagcatcgtgtgtacaaga 2160
Db 2112 GCTGGAGATGCAAGTGCCTGGTGGCCGAGCGCACGCCGCCAGCATCGTGTGTGTACAAGA 2171
Qy 2161 cgagagcctgctggaggaagaaagcttggagtcgacttggcgagactccaaccagaagctcag 2220
Db 2172 CCAGAGGCTGTCTGGAGGAAAAGTCTGGAGTCACTTTGGCGGACTCCAACCAAGAACTGAG 2231
Qy 2221 catccagcgtgtgcgagggaggaatgcgggacgctatctgtgcagcgtgtgcaaacgcca 2280
Db 2232 CATCCAGCCGTCGCGAGGAGGATCGCGGACCGCTATCTGTGCAGCGTGTGCAACGCCAA 2291
Qy 2281 gggcgtgctcaactcctccgcagcgtggccgtgaaagcctccgaggataaaggcagcat 2340
Db 2292 GGGCTGCGTCAACTCTCCGCCAGCGTGCCCTGGAAGGCTCCGAGGATAAAGGGCAGCAT 2351
Qy 2341 ggagatcgtgataccttctcgtgtaccggggtcactcgtctctctctctctcctcctct 2400
Db 2352 GGAGATCGTGATCCTTGTGCGGTACCGGCGTCACTGCTGTCTTCTTCTGGGTCTCTCTCT 2411
Qy 2401 cctcatcttctgttaacatgagggagggccgcccacgcagacatacaagagggggtactcctgtc 2460
Db 2412 CCTCATCTTCTTAACATGAGGAGGCGCGCCACACGACACATCAAGACGGGCTACTCTGTC 2471
Qy 2461 catcatcatgacccccggggaggtgcccctcgtgagggagcaatgcgaataacctctcctaaga 2520
Db 2472 CATCATATGGAAACCCGGGGAGGTGCTCTTGAGGAGCAATCGGAATACCTTCTCTACGA 2531
Qy 2521 tgccagcagctgggaattccccccgagagcggtgcacctgggggagagtgcctcgggtacgg 2580
Db 2532 TGCCAGCCAGTGGGAATTCCCCCGAGAGCGGCTGCACCTGGGGACAGTGCCTCGGCTACGG 2591
Qy 2581 cgccttcggggaaggtgggtggaagcctcgccttcgggcatccacaaggcgagcagctgtga 2640
Db 2592 CGCCTTCGGGAAGGTGGTGGAAAGCCTTCGCGCTTTCGGCATCCACAAAGGCGACAGCTGTGA 2651
Qy 2641 caccctggccgtgaaaaatgctgaaagagggcgccacggccagcgagcaccgcgctgat 2700
Db 2652 CACCGTGGCCGTGANAATGCTGAAGAGGGCGCCACGCGCAGCGAGCAGCCGCGCTGAT 2711
Qy 2701 gtcgagctcgaagatcctcatcacaatcggaacacacacacacgttggtaaacctcctcgg 2760
Db 2712 GTCGGAGCTCAAGATCCTCATTCACATCGGCAACCCACCTCAACGTGGTCAACCTCCTCGG 2771
Qy 2761 ggcgtgaccaagcgccagggcccccctcatggtgatcgtggagttctcgaagtaacggcaa 2820
Db 2772 GCGGTGCACCAAGCCGCGAGGCCCCCTCATGGTGATCTGTGGAGTTCTCAAGTACGGCAA 2831
Qy 2821 cctctcccaactcctcgcgcgccaagcgagccttcagccccctcgcgcggaagactctcc 2880
Db 2832 CCTCTCCAACCTTCCTGCGGCCCAACGGGACGCCCTTACGCCCTCGCGCGGAGAACTCTCC 2891
Qy 2881 cgagcagcgcggaagccttccgcgcctatggtgagctcgcacaggtcgtgatacgagggcgcc 2940
Db 2892 CGAGCAGCGCGACGCTTCCCGCCCATGCTGTGAGCTCGCCAGGCTGGATCGGAGCGGCC 2951
Qy 2941 ggggagcagcacaggttctctcgcgcggttctcgaagaccgagggcgagggagcg 3000
Db 2952 GGGGAGCAGCGACAGGGTCTCTTCGCGCGGTTCCTCGGAAGACCAGGCGGAGCGAGCGCG 3011
Qy 3001 ggcctctccagaccagaagcgtgaggaacctgtggcgtgagccgctgacacatggaagatct 3060
Db 3012 GCGTCTCCAGACCAAGAAGCTGAGGACCTGTGGCTGAGCCCGCTGACCATTGAAGATCT 3071
Qy 3061 tgcctgctacagcttccaggttggccagaggtgaggttctcgtgcttccccgaagtgcatt 3120
Db 3072 TCTCTGCTTACAGCTTCCAGGTGGCCAGAGGATGGAGTTCTCTGGCTTCCCCAAGTGCAT 3131

QY 541 ggtgctatggccagacgagcagaggtggtgtggtgatgacccgagcggtgctgtctc 600
|||||
Db 1484 GGTGCTGTGCCAGACAGGGCAGAGGTGGTGGGATGACCGCGGGGCATGCTCGTGT 1543
QY 601 cagcgaactgtcgaagtgccctgTaccctgcaagtgcagagaccacacctggggaaccagga 660
|||||
Db 1544 CAGGCCACTGCTCAGCATGCCCTGTACCTTGCAGTGGAGACCACCTGGGGAGACCAGGA 1603
QY 661 ctctcttccaaccccttcttggtgacatcacaggcaacgaagctcttatgacatccagct 720
|||||
Db 1604 CTTCCTTTTCCAACCCCTTCTGTTGTCACATCACAGGCAAGAGCTCTATGACATCCAGCT 1663
QY 721 gttgcccaggaagtgcgtgagctgctgtgtagggagaaagctgctctaaactgcaacctg 780
|||||
Db 1664 GTTGGCCAGGAAGTGCCTGAGAGTGTGTGTAGGGGAAGACTGCTCTGAACCTGCACCGT 1723
QY 781 gtgggtgagtttaactcaaggtgtcaaccttgaactggactacccagggaagcagagcaga 840
|||||
Db 1724 GTGGCTGTAGTTTAACTCAGCTGTCACTTTTGACTGGGACTACCCAGGGAAGCAGCGAGA 1783
QY 841 qcgggttaagtgggtgccgagcagcagctcccagagagacccacacagaactctccagcat 900
|||||
Db 1784 GCGGGTAAAGTGGGTGCCCGAGGAGCGCTCCCAGCAGACCCACACAGAACTCTTCCAGCAT 1843
QY 901 cctgaccatccacaagtcagcagcagcagcagcctggctgctgtgtgcaaggcccaacaa 960
|||||
Db 1844 CCTCACCATTCCAAACGTCAGCCAGCAGCAGACTTGGCTCGTATGTGTGCNAGGCCAACAA 1903
QY 961 cggcatcagcagatttcgggagagcaccagggtcattgtgcatgaaaaatcccttcacag 1020
|||||
Db 1904 CGGCATCCACCGATTTTCGGGAGAGCACCGAGGTCAATGTGTCATGATAAAATCCCTTTCATCAG 1963
QY 1021 cgtcgagtggtctcaaggaccctcctgtgagggccagcagcagagcagcagctagtgaagct 1080
|||||
Db 1964 CGTCGAGTGGCTCAAGGACCCTCTCTGGAGGCCACGGCAGGAGACAGCTGGTGAAGCT 2023
QY 1081 gccgtgaagctggcagctgtaccccccgcgcaggttccagtggtcacaagatggaaagcc 1140
|||||
Db 2024 GCCCGTGAAGCTGGCAGCGTACCCCGCCCGCCGAGTTCCAGTGTACAAGGTGGAAGGC 2083
QY 1141 actgtcgggcgcacagtcacatgccctggtgctcaaggagtgacagaggtcagagc 1200
|||||
Db 2084 ACTGTCCGGCGCCACAGTCCACATGCCCTGGTGTCTCAAGGAGGTGACAGAGGCCAGCAC 2143
QY 1201 aggcactacacccctgcgcctgtggaactcgcctgtgcctgagcgcgcaacatcagct 1260
|||||
Db 2144 AGGCACCTACACCTTCGCCCTGTGGAACATCCGCTGTGCGCTCAGCGCGCAACATCAGCCT 2203
QY 1261 ggaagctggtggtgaaagtgtcccccccccagatatacagaaaggagggcctctccccagcat 1320
|||||
Db 2204 GGAGCTGGTGGTGAATGTGCCCCCCCCAGATACATGAGAAGAGGCCCTCTCTCCCCAGCAT 2263
QY 1321 ctactcagctcacagcgcagcagccctcaccctgacagcgtactacgggtgcccctgcctct 1380
|||||
Db 2264 CTACTCGGTGACAGCGCGCCAGGCCCTCACTTCACGCGCTACGGGGTGCCTCTGCCCTCT 2323
QY 1381 cagcatccagtggtcactggcggccctggacacccctgcaagatggttgcccagctagctc 1440
|||||
Db 2324 CAGCATCCAGTGCATGGGGGCCCTTGGACACCTCTGCAGATGTTTGCACCAGGTAGTCT 2383
QY 1441 ccggcgggcagcagcaagacctcatgccacagtgccgtgactggagggcggtgaccac 1500
|||||
Db 2384 CCGCGCGCGCGCAGCAGCAAGACCTCATGCCACAGTGCCTGTACTGGAGGGCGGTGACCCAC 2443
QY 1501 gcaggatccgtgaaccccatcgagagcctggacacctgagaccgaagtttgtggagggaaa 1560
|||||
Db 2444 GCAGGATGCGGTGAACCCCATCGAGAGCTTGGACACCTCGACCGAGTTTGTGGAGGGAAA 2503
QY 1561 gaataagactgtagcaagctggtatccagaaatgcacaagctgtctgcccatacaagtg 1620
|||||
Db 2504 GAATAAGACTGTGAGCAAGCTGGTGATCCAGAAATGCCAACGTGTCTGCCCATGTACAAGTG 2563
QY 1621 tgtggtctccacaaggtgggccaagatgagcggctcatctctcta tgtgaaccacct 1680

Db 2564 TGTGCTCTCCAAACAAGGTGGCCAGGATAGCGGCTCATCTTCTATGTGACCACCAT 2623
QY 1681 ccccgacgcttccaccatcgaaatccaagccatcccgagagctactagagggccagccggt 1740
|||||
Db 2624 CCCCAGACGGCTTCACCATCATCCNAGCCATCCGAGGAGCTACTAGAGGGCCAGCCGCT 2683
QY 1741 gctctgagctgccaaagccagcagctacaagtacagcaatctgctgglaccgectcaa 1800
|||||
Db 2684 GCTCTGAGCTGCCAAGCCGACAGGTACAAAGTACGAGCATCTGCGCTGTTACCGCTCAA 2743
QY 1801 cctgtccacgctgcacgatgcgcacaggaacccgcttctgctcgactgcaaaaagctgca 1860
|||||
Db 2744 CTTGTCCACGCTGCACGATGCCACGGAAACCCGCTTCTGCTCGACTGCAAGAACGTGCA 2803
QY 1861 tctgttgcgcaacccctctggccgagcagcctggagaggttggcacctggggcgccgaagc 1920
|||||
Db 2804 TCTGTTGCGCCACCCCTCTTGCCGCCGACGCTGAGGAGGTGGCACCTTGGGGCGCCACGC 2863
QY 1921 cagcgtcagcctgagtatccccccgctgcgcccagcaagcagggccactatgtgtgca 1980
|||||
Db 2864 CACGCTCAGCCTGAGTATCCCCCGCTCGCGCCGACGACACGAGGCGCCACTATGTGTGCA 2923
QY 1981 agtgaagaccgagcagcagcatgaagcactgccacaagaagtacctgtcgtgcagc 2040
|||||
Db 2924 AGTGCNAGACCAGCGCAGCCATGACNAGCCTGCCACNAGAAAGTACCTGCTCGTGCAGGC 2983
QY 2041 cctggaagccccctcggtctacgcagaacttgaccctcctggtagcgtgagcgaactc 2100
|||||
Db 2984 CCTGGAAGCCCTCGGCTCACGAGAACTTGACCGACCTCTCTGGTGAACGTGAGCGACTC 3043
QY 2101 gctggagatgagtgctgtgtgagcggagcagcagccccagcatcggtgtgtaacaaga 2160
|||||
Db 3044 GCTGAGATGCAAGTGTCTGGTGGCGGAGCGCACGCGCCACGATCGTGTGTGTAACAAGA 3103
QY 2161 cgagaggtcgtcggaggaaaagtctggagtcgacttggcgagctcccaaccagaaagctgag 2220
Db 3104 CGAGAGGCTGCTGGAGGAAAGTCTTGGAGTGCACTTGGCGGACTCCAACCAAGACTCGAG 3163
QY 2221 catcagcgtgtgcgcgagagaggaatgcgggagcgtctatctgtgcagcgtgtgcaagccaa 2280
|||||
Db 3164 CATCCAGCCGCTGCGCAGGAGGATCGCGGAGCGCTATCTGTGCAGCGTGTGCAACGCCAA 3223
QY 2281 gggctgctcactcctccgagcgtgtgcgtgaaagctccgaggtccagaggaagggcagcat 2340
|||||
Db 3224 GGGCTGCGTCAACTCTCCGCCAGCGTGGCCGTGGAAGGCTCCGAGGATAAGGGCAGCAT 3283
QY 2341 ggagatcgtgactcctgtgtggtaccggcgctcactcgtctcttctctgtgggtcctcctct 2400
Db 3284 GGAGATCGTGTATCTTGTTCGGTACCGCGGTCTATCGCTGTCTTCTTCTGGGTCTCTCTCT 3343
QY 2401 cctcatcttctgtaacatgagagggccggccccacgcagacatcaagagcgggtacctgtc 2460
|||||
Db 3344 CCTCATCTTCTGTAACATGAGGAGCGCGCCACGCAGACATCAAGACGGGCTACCTGTC 3403
QY 2461 catcatcatgaaccccgaggaggtccctctggagaggaatgcgaataacctgtctacga 2520
Db 3404 CATCATCATGACCCCGGGAGGTGCTCTGTGAGGAGCAATGCGAATACCTGTCTCTACGA 3463
QY 2521 tgccagccagtggggaattccccccgagagcgtgcacacctggggagagtgctcggtctacgg 2580
Db 3464 TGCCAGCCAGTGGGAATTTCCCCCGAGAGCGGCTGCACCTGGGGAGAGTGTCTCGGCTACGG 3523
QY 2581 ggccttcgggaaggtggtgtggaagcctccgcttctggccatccacaagggcagcagctgta 2640
Db 3524 CGCCTTCGGGAAGGTGGTGGAAAGCCTCCGCTTTTGGCATCCACNAGGGCAGCAGCTGTGA 3583
QY 2641 cacggtgcccgtgaaaaatgctgaaagagggcgccacggccaagcagcagcccgcgctgag 2700
Db 3584 CACCGTGGCCGTGAAAAATGCTGAAGAGGGGCCACGCGCCACGCGAGCACCCCGCGCTGAT 3643
QY 2701 gtcggagctcaagaacctcatctcagatcgcgaacacctcaacgtgtgtcaacctcctcgg 2760
|||||

QY 121 caggagagagtcacacgtccatcaacacccggtgacagcctgtccatctcctgcaggggaca 180
DB 123 caccgagaggtccacacgtccatcaacacccggtgacagcctgtccatctcctgcaggggaca 182
QY 181 gcacccctcagtgggcttggccagagctcaggagcgcagcagccacccgagagacaagga 240
DB 183 gcacccctcagtgggcttggccagagctcaggagcgcagcagccacccgagagacaagga 242
QY 241 cagcagagacacgggggtgtgcgagactcgcgagggcacagagcgcagggcctactgcaa 300
NB 243 cagcagagacacgggggtgtgcgagactcgcgagggcacagagcgcagggcctactgcaa 302
QY 301 ggtgttctgtcacagagtacatcccaacagcacagcagcagtaagtcgtactacaa 360
DB 303 ggtgttctgtcacagaggtacatgccaacgacacaggcagtaagtcgtactacaa 362
QY 361 gtacataaggcgcgatcagagggcacacgcccgcagctcctacgtgtctgtgagaga 420
NB 363 glacataaggcgcgatcagagggcacacgcccgcagctcctacgtgtctgtgagaga 422
QY 421 ctlttgagcagcattcatacaagcctgcacgctcttgggtcaacaggaagacccat 480
DB 423 ctlttgagcagcattcatacaagcctgcacgctcttgggtcaacaggaagacccat 482
QY 481 gtgggtgcctctgtctgtgtccatccccgcctcaatgtcaacgtcgctcgcgaaagctc 540
DB 483 gtgggtgcctctgtctgtgtccatccccgcctcaatgtcaacgtcgctcgcgaaagctc 542
QY 541 ggtgtctgtggccagacggcgagaggtggtgtggatgacggcggggcatgctgtgtc 600
DB 543 ggtgtctgtggccagacggcgagaggtggtgtggatgacggcggggcatgctgtgtc 602
QY 601 cagcgcactgtcacaga tgcctgttacctgcagtcgcgagacacactggggagaccagga 660
DB 603 cagcgcactgtcacaga tgcctgttacctgcagtcgcgagacacactggggagaccagga 662
QY 661 ctltcctltccaaaccccttctgtgtgcacatcacaggcaacgagctctatgacatccagct 720
DB 663 ctltcctltccaaaccccttctgtgtgcacatcacaggcaacgagctctatgacatccagct 722
QY 721 gttgccaggaagtcgctggagctgctgtgtgaggagagagcttggtctaaactgcacgt 780
DB 723 gttgccaggaagtcgctggagctgctgtgtgaggagagagcttggtctaaactgcacgt 782
QY 781 gtgggtcaggttcaactcaggtgtcaactttgactgggactacccaaggagacagcaga 840
DB 783 gtgggtcaggttcaactcaggtgtcaactttgactgggactacccaaggagacagcaga 842
QY 841 gcgggataagtgggtgccgagcgcgcctcccagcagacccacacagaaactctccagct 900
DB 843 gcgggtaagtgggtgccgagcgcgcctcccacagacccacacagaaactctccagct 902
QY 901 cctgcacatccacaacgtcagccagcacgacctgggctcgtatgtgtgcaaggccaacaa 960
DB 903 cctgcacatccacaacgtcagccagcacgacctgggctcgtatgtgtgcaaggccaacaa 962
QY 961 cggatcccagcatttcgggagagcaccgagatcattgtgcataagaaatccccttcatag 1020
DB 963 cggatcccagcatttcgggagagcaccgaggtca tgtgcataaaaa tccccttcatag 1022
QY 1021 cgtcaggtggctcaaaaggaccatcctgtagggccacgagcagagacgagctggtgaagct 1080
DB 1023 cgtcaggtggctcaaaaggaccatcctgtagggccacgagcagagacgagctggtgaagct 1082
QY 1081 gcccgtgaagcttggaagctaccccccccagttccagtgtgtacaaagga tggaaagcc 1140
DB 1083 gcccgtgaagcttggaagctaccccccccagttccagtgtgtacaaagga tggaaagcc 1142
QY 1141 actgtccggggccacag tccacatgcccctgtgtctcaagaggtgacagagccagcagc 1200
DB 1143 actgtccggggccacag tccacatgcccctgtgtctcaagaggtgacagagccagcagc 1202
QY 1201 aggcacctacacccctcgccctgtggaactccgctgtggtgctgagggcgaacatcagct 1260

DB 1203 aggcacctacacccctcgccctgtggaactccgctgtggtgctgagcgcaacatcagct 1262
QY 1261 ggaagctgggtggaatgtccccccagatacatagaaagagccctcctccccagcat 1320
DB 1263 ggaagctgggtggaatgtgtccccccagatacatagaaagagccctcctccccagcat 1322
QY 1321 ctactcgctcacagcgcagccctcactcagcggctcagcgggtgcccctgcctct 1380
DB 1323 ctactcgctcacagcgcagccctcactcagcggctcagcgggtgcccctgcctct 1382
QY 1381 cagcatccagtgagcactggcgcccttgacacccctgcgaagatgtttgccacgctagctct 1440
DB 1383 cagcatccagtgagcactggcgcccttggaacccctgcgaagatgtttgccacgctagctct 1442
QY 1441 cggggcgcgccagcagcaagactcatgccacagtgccctgactgagagggcgtgaaccac 1500
DB 1443 cggggcgcgccagcagcaagactcatgccacagtgccctgactgagagggcggtgaaccac 1502
QY 1501 gcaggatgcccgtgaaccccatcgagagcctggacacctggacccgagtttctgtgagggaaa 1560
DB 1503 gcaggatgcccgtgaaccccatcgagagcctggacacctggacccgagtttctgtgagggaaa 1562
QY 1561 gaataagactgtgagcaagctggtgatccagaatgccaaactgtctgtccatgtacaaagtg 1620
DB 1563 gaataagactgtgagcaagctggtgatccagaatgccaaactgtctgtccatgtacaaagtg 1622
QY 1621 tgtgtgtctccaaaggtggtggccagatgagcggctcactctacttctatgtgaaccacat 1680
DB 1623 tgtgtgtctccaaaggtggtggccagatgagcggctcactctacttctatgtgaaccacat 1682
QY 1681 ccccgacggcttcaacatcgaa tccaaagccatcccagagactactagaggggccagcccggt 1740
DB 1683 ccccgacggcttcaacatcgaa tccaaagccatcccagagactactagaggggccagcccggt 1742
QY 1741 gctcctgagctccaaagccagacagctaaagtaacagatctgcgctggttacccgctcaa 1800
DB 1743 gctcctgagctccaaagccagacagctaaagtaacagatctgcgctggttacccgctcaa 1802
QY 1801 cctgtccacgctgcgcga tgcgcacgggaacccgcttctgtcgcactgcgaagaaagctgca 1860
DB 1803 cctgtccacgctgcgcga tgcgcacgggaacccgcttctgtcgcactgcgaagaaagctgca 1862
QY 1861 tctgttcgcacccctctggccgcagcctggagaggttggcacctggggcgccacgc 1920
DB 1863 tctgttcgcacccctctggccgcagcctggagaggttggcacctggggcgccacgc 1922
QY 1921 cagctcagctcagatctcccccgctcgcccgagcacagggcccaactatgtgtgcga 1980
DB 1923 cagctcagctcagatctcccccgctcgcccgagcacagggcccaactatgtgtgcga 1982
QY 1981 agtcaagacccggcgagccatgcaaacactgcccacagaagtacctgtcgttcagggc 2040
DB 1983 agtcaagacccggcgagccatgcaaacactgcccacagaagtacctgtcgttcagggc 2042
QY 2041 cctggaagccctcggctcagcagaaacttaccagacctcctgtgtgaacgtgagcgatcc 2100
DB 2043 cctggaagccctcggctcagcagaaacttaccagacctcctgtgtgaacgtgagcgatcc 2102
QY 2101 gctggagatgagtgcttgggtggccgagcgcagcgcacgcctcgtgtgtacaaaga 2160
DB 2103 gctggagatgagtgcttgggtggccgagcgcagcgcacgcctcgtgtgtacaaaga 2162
QY 2161 cgagaggtcgtggagggaaaagtctggagtcgacttggcggaactccaaccaggaagctgag 2220
DB 2163 cgagaggtcgtggagggaaaagtctggagtcgacttggcggaactccaaccaggaagctgag 2222
QY 2221 catccagcgcgtgcgcgagggaggtgcgggacgtatctgtgcagcgtgtgtcaacgcgcaa 2280
DB 2223 catccagcgcgtgcgcgagggaggtgcgggacgtatctgtgcagcgtgtgtcagacccaa 2282
QY 2281 gggctcgcgtcaactcctcccgcagcgtggccgtggaaggtcccagagataaaggacat 2340

Db 2283 gggctgctgtaactctctccgcagcgctggccgtggaaggctccgaggaataaggcgagcat 2342
Qy 2341 ggaagatcgtgatacctctgctcggtaccgaggatcatcgctgtctctctctctctctctctct 2400
Db 2343 ggaagatcgtgatacctctgctcggtaccgaggatcatcgctgtctctctctctctctctct 2402
Qy 2401 cctcatctctctgtaacatagagagagccgcccacgcagacatcaagagagcggtactctgctc 2460
Db 2403 cctcatctctctgtaacatagagagagccgcccacgcagacatcaagagagcggtactctgctc 2462
Qy 2461 catcatcatggaaccccgaggaggtgctctctggagagagcaatgcgaatacctgtctctacga 2520
Db 2463 catcatcatggaaccccgaggaggtgctctctggagagagcaatgcgaatacctgtctctacga 2522
Qy 2521 tgcagcagctgggaatccccccagagcgctgcacctgggagagtgctcgcgtacagc 2580
Db 2523 tgcagcagctgggaatccccccagagcgctgcacctgggagagtgctcgcgtacagc 2582
Qy 2581 cgccttcgggaaggctggtagagcctccgctcttcggcatccacagggcagcagctgtga 2640
Db 2583 cgccttcgggaaggctggtagagcctccgctcttcggcatccacagggcagcagctgtga 2642
Qy 2641 caccgtgcccgtgaaatgctgaaagagggcgccacggccagagcagcagcgcgcgtgat 2700
Db 2643 caccgtgcccgtgaaatgctgaaagagggcgccacggccagagcagcagcgcgcgtgat 2702
Qy 2701 gtcggagctcaagatcctcatctcacatcggcaacacacctcaacgtggtcaacctctcccg 2760
Db 2703 gtcggagctcaagatcctcatctcacatcggcaacacacctcaacgtggtcaacctctcccg 2762
Qy 2761 ggcgtgacacaaagccgcaaggcccccctcatggtgatcgtggagttctgcaagtagcgaac 2820
Db 2763 ggcgtgacacaaagccgcaaggcccccctcatggtgatcgtggagttctgcaagtagcgaac 2822
Qy 2821 cctctccaaactctctgcgcgccaagcggagcgctctcaagccctgcgcgaagaagatctcc 2880
Db 2823 cctctccaaactctctgcgcgccaagcggagcgctctcaagccctgcgcggaagaagatctcc 2882
Qy 2881 cgagcagcgcgagcgtctccgcgcataggtagagctcgccagggctgatacggaagcgcc 2940
Db 2883 cgagcagcgcgagcgtctccgcgcataggtagagctcgccagggctgatacggaagcgcc 2942
Qy 2941 ggggagcagcagcagaggtccctctcgcgcggttctcgaagacagagcgagcgagcgagcg 3000
Db 2943 ggggagcagcagcagaggtccctctcgcgcggttctcgaagacagagcgagcgagcgagcg 3002
Qy 3001 ggccttccagaccaaagaagctgagagcctgtgctgagcccgctgacccatggaagatct 3060
Db 3003 ggccttccagaccaaagaagctgagagcctgtgctgagcccgctgacccatggaagatct 3062
Qy 3061 tgctgtctacagcttcaggtggccagagggatggagttcctggcttcccgaaagtgcac 3120
Db 3063 tgctgtctacagcttcaggtggccagagggatggagttcctggcttcccgaaagtgcac 3122
Qy 3121 ccacagagacgtggtctcgcgaacatctcgtctcgaagaagcagcagtggtgaagatctg 3180
Db 3123 ccacagagacgtggtctcgcgaacatctcgtctcgaagaagcagcagtggtgaagatctg 3182
Qy 3181 tgactttggccttgcccgggacatctacaaagacccctgactacgtccgcaaggcgagctgc 3240
Db 3183 tgactttggccttgcccgggacatctacaaagaccccgactacgtccgcaaggcgagctgc 3242
Qy 3241 ccggctgcccctgaagtggatggagccctgaaagcatcttcgacaaaggtgtacaccacgca 3300
Db 3243 ccggctgcccctgaagtggatggagccctgaaagcatcttcgacaaaggtgtacaccacgca 3302
Qy 3301 gagtgcagtggtgctcttggtggtgctctctctggagagatctctctctctctctctctctcc 3360
Db 3303 gagtgcagtggtgctcttggtggtgctctctctgggagagatctctctctctctctctctcc 3362
Qy 3361 gtacccttggtgtcagatcaatgagaggttctgcccagcggtgagagacgagcagagagat 3420
Db 3363 gtacccttggtgtcagatcaatgagaggttctgcccagcggtgagagacgagcagagagat 3422

Qy 3421 gaggccccggagctggccactcccgccatacgcgcgcatcatgctgaactgctggtccgg 3480
Db 3423 gaggccccggagctggccactcccgccatacgcgcgcatcatgctgaactgctggtccgg 3482
Qy 3481 agaccccaaggcgagacctgcatctcggagctggtgagagatcctggggagacctgctcca 3540
Db 3483 agaccccaaggcgagacctgcatctcggagctggtgagagatcctggggagacctgctcca 3542
Qy 3541 gggcagggggcctcgaagaggaaggaggtctgcatggccccgcgcagctctcagagctc 3600
Db 3543 gggcagggggcctcgaagaggaaggaggtctgcatggccccgcgcagctctcagagctc 3602
Qy 3601 agaagaggggaagctcttcgcaggtgtccacatggtcccatggtccctacacatcgtccaggtcagcgc 3660
Db 3603 agaagagggagcctctcgcaggtgtccacatggtcccatggtccctacacatcgtccaggtcagcgc 3662
Qy 3661 tgagagcagcccgccaagcctgagccacagcctgagccagctgagccaggtattacaaactgggt 3720
Db 3663 tgagagcagcccgccaagcctgagccacagcctgagccagctgagccaggtattacaaactgggt 3722
Qy 3721 gtcccttcccgggtgctgctggccagaggggctgagacccgctggttccctccaggaagaaagc 3780
Db 3723 gtcccttcccgggtgctgctggccagaggggctgagacccgctggttccctccaggaagaaagc 3782
Qy 3781 atttgaggaattcccatgaccccaacagcctacaaaggctctgtggaacacacagacaga 3840
Db 3783 atttgaggaattcccatgaccccaacagcctacaaaggctctgtggaacacacagacaga 3842
Qy 3841 cagtggagtggtgctgctgcccgcgagggaggttgagcagatagagcagcgatagacaga 3900
Db 3843 cagtggagtggtgctgctgcccgcgagggaggttgagcagatagagcagcgatagacaga 3902
Qy 3901 aagcggcttcagctgtataaggacctggccagaatgtggtctgacaggggacacacctga 3960
Db 3903 aagcggcttcagctgtataaggacctggccagaatgtggtctgacaggggacacacctga 3962
Qy 3961 ctcccaaggagcgcgcgcgctgagcgggggcgccagcgggggcgagggagggcaggtgttttaca 4020
Db 3963 ctcccaaggagcgcgcgcgctgagcgggggcgccagcgggggcgagggagggcaggtgttttaca 4022
Qy 4021 cagcagtgatggggagctgctcgagccaaagcagggagggagggagggagggagggagggaggg 4080
Db 4023 cagcagtgatggggagctgctcgagccaaagcagggagggagggagggagggagggagggaggg 4082
Qy 4081 cgtgactttcttcacagacaaagcgtactaa 4111
Db 4083 cgtgactttcttcacagacaaagcgtactaa 4113

RESULT 25

PCT-US99-08079-1

; Sequence 1, Application PC/TUS9908079

; GENERAL INFORMATION:

; APPLICANT: Northwest Biotherapeutics, Inc.

; TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS AND TREATMENT OF METASTATIC

; TITLE OF INVENTION: PROSTATE TUMORS

; FILE REFERENCE: 8511-025-228

; CURRENT APPLICATION NUMBER: PCT/US99/08079

; CURRENT FILING DATE: 1999-04-13

; NUMBER OF SEQ ID NOS: 16

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1

; LENGTH: 4450

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (22) .. (3915)

PCT-US99-08079-1

Query Match

77.8%; Score 3198; DB 1; Length 4450;

Db 2103 gctggagatgcagtgcttggtggccggagcgacacgcccagcatcgtgtgtacaaaga 2162
Qy 2161 cgaagagctgctggaggaagaaagtcgaatcgacttgcgagactcccaacacgaagctgag 2220
Db 2163 cgaagagctgctggaggaagaaagtcgagtcgacttgcgagactcccaacacgaagctgag 2222
Qy 2221 catccagcgtgcgcggagaggatgcgggacgtatctgtgcagcgtgtgtcaacgcaa 2280
Db 2223 catccagcgtgcgcggagaggatgcgcggaccgtatctgtgcagcgtgtgtcaaccccaa 2282
Qy 2281 qgagtcgctcaactcctccgcagcgtggccgtggaaggtccgaagataagagcagcat 2340
Db 2283 ggcgtcgctcaactcctccgcagcgtggccgtggaaggtccgaagataagagcagcat 2342
Qy 2341 qgagtcgctcaactcctccgcagcgtggccgtggaaggtccgaagataagagcagcat 2400
Db 2343 ggaagtcgctcaactcctccgcagcgtggccgtggaaggtccgaagataagagcagcat 2402
Qy 2401 cctcatctctgttaacatgagaggccgcgcacgcagacatcaagacgggctacactgtc 2460
Db 2403 cctcatctctgttaacatgagaggccgcgcacgcagacatcaagacgggctacactgtc 2462
Qy 2461 catcatcatgaaccccgagggtgcctcttgagaggaacaatgcgaatcactgtcctacga 2520
Db 2463 catcatcatgaaccccgagggtgcctcttgagaggaacaatgcgaatcactgtcctacga 2522
Qy 2521 tgcagcagtggaattcccccgagagcggtgcacttgggagagtgctcgcgtacagc 2580
Db 2523 tgcagcagtggaattcccccgagagcggtgcacttgggagagtgctcgcgtacagc 2582
Qy 2581 cgccttcgggaagggtgtggaagcctcgcgtttcggcatcccaaggggcagcagctgtga 2640
Db 2583 cgccttcgggaagggtgtggaagcctcgcgtttcggcatcccaaggggcagcagctgtga 2642
Qy 2641 caccgtgcgcgtgaaatgctgaaagggcgccacggccagagacacgcgcgtcgtat 2700
Db 2643 caccgtgcgcgtgaaatgctgaaagggcgccacggccagagacacgcgcgtcgtat 2702
Qy 2701 qlcgaagctcaagatcctcatcattcacatcgggcaaccactcaacgtgtgcaacctctcgg 2760
Db 2703 gtcggagctcaagatcctcatcattcacatcgggcaaccactcaacgtgtgcaacctctcgg 2762
Qy 2761 ggcgtgcaccaagccgagggccctctcatgttgatcgttggaattctgcaagtacggcaa 2820
Db 2763 ggcgtgcaccaagccgagggccctctcatgttgatcgttggaattctgcaagtacggcaa 2822
Qy 2821 cctctcaactctcgtgcgcgaagcgggacgcttcagccctcagccctgcgcggagagctcc 2880
Db 2823 cctctcaactctcgtgcgcgaagcgggacgcttcagccctcgcgcggagagctcc 2882
Qy 2881 cgaagcgcggagcgtctccgcgcctggttgagctcgcaggtggtgagggcgcc 2940
Db 2883 cgaagcgcggagcgtctccgcgcctggttgagctcgcaggtggtgagggcgcc 2942
Qy 2941 ggggagcagcagcaggggtctcttcgcgcgttctcgaagcagcagggcgagcagggcg 3000
Db 2943 ggggagcagcagcaggggtctcttcgcgcgttctcgaagcagcagggcgagcagggcg 3002
Qy 3001 ggccttcagaccagaagcgtgagacgtgtgctgagcccgctgacctggaagatct 3060
Db 3003 ggccttcagaccagaagcgtgagacgtgtgctgagcccgctgacctggaagatct 3062
Qy 3061 tgtctctacagctccaggtggccagaggatggagttccttgcctcccgcaaaagtgc 3120
Db 3063 tgtctctacagctccaggtggccagaggatggagttccttgcctcccgcaaaagtgc 3122
Qy 3121 ccacagagaccttggctcggaaacttctcgttcggaagcgacgtgtgaaagatctg 3180
Db 3123 ccacagagaccttggctcggaaacttctcgttcggaagcgacgtgtgaaagatctg 3182
Qy 3181 tgaacttggccttgcgcgggacatctacaaagacctgactacgtccgcaagggcagtg 3240
Db 3183 tgaacttggccttgcgcgggacatctacaaagacctgactacgtccgcaagggcagtg 3242

Qy 3241 ccggtgctccccctgaagtggatggccccctgaaagcatcttcgacaaggtgtacaccgca 3300
Db 3243 ccggtgctccccctgaagtggatggccccctgaaagcatcttcgacaaggtgtacaccgca 3302
Qy 3301 gagtgcagcgtgtggtccctttggggtgctctctctggaagatctctctctggtgggctcccc 3360
Db 3303 gagtgcagcgtgtggtccctttggggtgctctctctggaagatctctctctggtgggctcccc 3362
Qy 3361 gtacccttggggtgcagatcaatgagaggttctgcacgcggtgagagacgcacaaagat 3420
Db 3363 gtacccttggggtgcagatcaatgagaggttctgcacgcggtgagagacgcacaaagat 3422
Qy 3421 gagggtccccgaggtggccactcccgcacatcacgcgcgtcatctgtgaactgctggtccgg 3480
Db 3423 gagggtccccgaggtggccactcccgcacatcacgcgcgtcatctgtgaactgctggtccgg 3482
Qy 3481 agaccctcaagcagacactgcattctcgagctggtagagatccttgggggacctgtccca 3540
Db 3483 agaccctcaagcagacactgcattctcgagctggtagagatccttgggggacctgtccca 3542
Qy 3541 gggcagggggcctgcaagagaaagaggtctcgtatggcccccgagcgtctcagagctc 3600
Db 3543 gggcagggggcctgcaagagaaagaggtctcgtatggcccccgagcgtctcagagctc 3602
Qy 3601 agaagaggggcagcttctcgcaggtgtccaccatggccctacacatcgcccaggtcgacgc 3660
Db 3603 agaagaggggcagcttctcgcaggtgtccaccatggccctacacatcgcccaggtcgacgc 3662
Qy 3661 tgaggacagcccccagcctgcagcgcgcacacgccttggccgaggtattacaaactgggt 3720
Db 3663 tgaggacagcccccagcctgcagcgcgcacacgccttggccgaggtattacaaactgggt 3722
Qy 3721 gtcccttcccgggtgctgcgcagagggtgagacccgtggttccctcagaggtgaagac 3780
Db 3723 gtcccttcccgggtgctgcgcagagggtgagacccgtggttccctcagaggtgaagac 3782
Qy 3781 atttgaggaaattcccatgaccccaacgcctacaaaggctctgtggacaaccagacaga 3840
Db 3783 atttgaggaaattcccatgaccccaacgcctacaaaggctctgtggacaaccagacaga 3842
Qy 3841 cagtgggatgggtgctggcctcggaggtttgagcagatagagagcagcatagacaaga 3900
Db 3843 cagtgggatgggtgctggcctcggaggtttgagcagatagagagcagcatagacaaga 3902
Qy 3901 aagcggcttcag 3912
Db 3903 aagcggcttcag 3914

RESULT 27

US-60-167-943-103
; Sequence 103, Application US/60167943
; GENERAL INFORMATION:
; APPLICANT: Hodgson, David M. Jones, Anissa L.
; APPLICANT: Lincoln, Stephen E. Yu, Jimmy Y.
; APPLICANT: Russo, Frank D. Greenawalt, Lila B.
; APPLICANT: Spito, Peter A. Panzer, Scott R.
; APPLICANT: Banville, Steve C. Roseberry, Ann M.
; APPLICANT: Bratcher, Shawn R. Wright, Rachel J.
; APPLICANT: Dufour, Gerard E. Chen, Wensheng
; APPLICANT: Cohen, Howard J. Liu, Tommy
; APPLICANT: Rosen, Bruce Yap, Pierre E.
; APPLICANT: Shah, Purvi Amshey, Stefan
; APPLICANT: Chalup, Michael S. Fong, Willy Tuen
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: RECEPTOR MOLECULES
; FILE REFERENCE: PT-0093 P
; CURRENT APPLICATION NUMBER: US/60167,943
; CURRENT FILING DATE: 1999-11-29
; NUMBER OF SEQ. ID NOS: 244
; SOFTWARE: PERL Program
; SEQ. ID NO 103

: FILE REFERENCE: GX-0019-1 P									
: CURRENT APPLICATION NUMBER: US/60/324,185									
: CURRENT FILING DATE: 2001-09-21									
: NUMBER OF SEQ ID NOS: 35862									
: SOFTWARE: PERL Program									
: SEQ ID NO 4274									
: LENGTH: 4459									
: TYPE: DNA									
: ORGANISM: Homo sapiens									
: FEATURE:									
: NAME/KEY: misc_feature									
: OTHER INFORMATION: Incyte ID No: 1082992.1									
: NAME/KEY: unsure									
: LOCATION: 2402-2421									
: OTHER INFORMATION: a, t, c, g, or other									
US-60-324-185-4274									
Query Match 62.6%; Score 2573; DB 71; Length 4459;									
Best Local Similarity 99.4%; Pred. No. 0;									
Matches 3673; Conservative 0; Mismatches 22; Indels 0; Gaps									
Qy	218	gcgcagccaccggagacaaaggacagcagagacacggggtggtcgagactgcgagggc	277						
Db	229	gcgcagccaccggagacaaaggacagcagagacacggggtggtcgagactgcgagggc	288						
Qy	278	acagacccagggccctactcgaagggtgtctctgcacagagtcacatgccaacgacaca	337						
Db	289	acagacccagggccctactcgaagggtgtctctgcacagagtcacatgccaacgacaca	348						
Qy	338	ggcagctcacgtctgctactacaagtacataaaggcagcgcacgcagagcaccacgcccgc	397						
Db	349	ggcagctcacgtctgctactacaagtacataaaggcagcgcacgcagagcaccacgcccgc	408						
Qy	398	agctctcacgtctgtgagagactttgagcagccatttcatacaagcctgacacgtc	457						
Db	409	agctctcacgtctgtgagagactttgagcagccatttcatacaagcctgacacgtc	468						
Qy	458	ttggtcaacaaggagacgcacatgtgggtgcacctgtctggttcacatcccgcctcaat	517						
Db	469	ttggtcaacaaggagacgcacatgtgggtgcacctgtctggttcacatcccgcctcaat	528						
Qy	518	gtcacgtcgctctgcaaaagctcgggtgctgtggccagcggcagagggtgtgtgggat	577						
Db	529	gtcacgtcgctctgcaaaagctcgggtgctgtggccagcggcagagggtgtgtgggat	588						
Qy	578	gaccggcggggcagtcctgtgtccacgcacatgctgcacagatgccctgtacctgcagtc	637						
Db	589	gaccggcggggcagtcctgtgtccacgcacatgctgcacagatgccctgtacctgcagtc	648						
Qy	638	gagacacactggygagaccagagacttcctttccaaccccttccctggtgcacatcacaggc	697						
Db	649	gagacacactggygagaccagagacttcctttccaaccccttccctggtgcacatcacaggc	708						
Qy	698	aacgagctctatgacatccagctgtgtgccaggaagtcgcctgagactcgttgtagggag	757						
Db	709	aacgagctctatgacatccagctgtgtgccaggaagtcgcctgagactcgttgtagggag	768						
Qy	758	aagctggctgaactgcaccgtgtgggctgagtttaactcaagggtcacctttgactgg	817						
Db	769	aagctggctgaactgcaccgtgtgggctgagtttaactcaagggtcacctttgactgg	828						
Qy	818	gactaccaggaagcagcagacgggttaagtgggtgtcccgagcagcgcgtccccagcag	877						
Db	829	gactaccaggaagcagcagacgggttaagtgggtgtcccgagcagcgcgtccccagcag	888						
Qy	878	accacacagaactctccagcatccttgaccatcccaatcccaacgctcagcagcagcactggc	937						
Db	889	accacacagaactctccagcatccttgaccatcccaacgctcagcagcagcactggc	948						
Qy	938	tcgatatgtgtcaaggccaacaacggcattccagcgtatttcggagagcaccagagtcatt	997						
Db	949	tcgatatgtgtcaaggccaacaacggcattccagcgtatttcggagagcaccagagtcatt	1008						

; FEATURE:									
; NAME/KEY: unsure									
; LOCATION: 2402-2421, 2907, 3602									
; OTHER INFORMATION: a, t, c, g, or other									
US-60-172-373-15763									
Query Match 58.1%; Score 2390; DB 56; Length 4462;									
Best Local Similarity 100.0%; Pred. No. 0;									
Matches 2390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1	ccacgcgcagcggccggagatgcagcggggcgccgcgtgctgcgtgcgactgtgctctg	60						
Db	12	ccacgcgcagcggccggagatgcagcggggcgccgcgtgctgcgtgcgactgtggtctg	71						
QY	61	ctcggaactcttgagcggcctggtgagtggtggtactccatgacccccccacacctgaacat	120						
Db	72	ctcggaactcttgagcggcctggtgagtggtggtactccatgacccccccacacctgaacat	131						
QY	121	cacggaggagtacacgtcatcagaccggtagacgcctgacgcctgtccatctctgcaggggaca	180						
Db	132	cacggaggagtacacgtcatcagaccggtagacgcctgtccatctctgcaggggaca	191						
QY	181	gaacccccctgagtggtctggccagagctcaaggaggccacgcaccccgagacaagga	240						
Db	192	gsacccccctgagtggtctggccagagctcagggagcgcagcgcacccggagacaagga	251						
QY	241	cagcgaggacacgggggtggtgcgagactgcgagggcacagacgcgcagccctactgcac	300						
Db	252	cagcgaggacacgggggtggtgcgagactgcgagggcacagacgcgcagccctactgcac	311						
QY	301	gggtgtgctgtgcagaggtacatgccaacgacacaggcagctactgtctgtactacaa	360						
Db	312	gggtgtgctgtgcagaggtacatgccaacgacacaggcagctactgtctgtactacaa	371						
QY	361	gtacatcaaggcacgcacagagccacacgcgcgcacgtcctactcagttctgtgagaa	420						
Db	372	gtacatcaaggcacgcacagagccacacgcgcgcacgtcctactcagttctgtgagaa	431						
QY	421	ctttgagcagccattcatcaacaagcctgacacgctcttggccaacagaaagacgccat	480						
Db	432	ctttgagcagccattcatcaacaagcctgacacgctcttggccaacagaaagacgccat	491						
QY	481	gtgggtgacctgtcgtgttccatccccggcctcaatgtcaagctgcgtgcgtcgaagctc	540						
Db	492	gtgggtgacctgtcgtgttccatccccggcctcaatgtcaagctgcgtgcgtcgaagctc	551						
QY	541	gtgtcgtgtggccagacggcgagaggtggtgtgggatgaccggcgaggcgcatgtctgtc	600						
Db	552	gtgtcgtgtggccagacggcgagaggtggtgtgggatgaccggcgaggcgcatgtctgtc	611						
QY	601	cacgcactgtgcacgagtgcctgttacctgcagtcgcagacacacctggggagaccagga	660						
Db	612	cacgcactgtgcacgagtgcctgttacctgcagtcgcagacacacctggggagaccagga	671						
QY	661	cttcctttccaaaccccttctggtgcacatcacaggcaacgactctatgacatccagct	720						
Db	672	cttcctttccaaaccccttctggtgcacatcacaggcaacgactctatgacatccagct	731						
QY	721	gttgccacgaagctcgtggagctggtgtaggggagagctgtggtcctgaactgcacct	780						
Db	732	gttgccacgaagctcgtggagctggtgtaggggagagctgtggtcctgaactgcacct	791						
QY	781	gtgggtgagtttaactcagggtgtacacctttgactgggactaccagggaagcaggcaga	840						
Db	792	gtgggtgagtttaactcagggtgtacacctttgactgggactaccagggaagcaggcaga	851						
QY	841	gcgggtaagtgggtgcccgagcagcgtcccgagacacccacacagaactctcagcat	900						
Db	852	gcgggtaagtgggtgcccgagcagcgtcccgagacacccacacagaactctcagcat	911						
QY	901	ctcgacattccacaagctcagcagcagcagcctgggctcgtatgtgtgcaaggccaacaa	960						
Db	992	agtgcgaagaccggcgagcccatgacaagcactgcacaagaagtacctgtcgtgtgcaggc	2051						

Db	912	cctgaccattccacaacgtcagcgcagcagcctgggctcgtatgtgtgcaaggccaacaa	971
QY	961	cggcatccagcagatttcgggagagacccagagtcattgtgcatgaaaaatcccttcacag	1020
Db	972	cggcatccagcagatttcgggagagacccagagtcattgtgcatgaaaaatcccttcacag	1031
QY	1021	cgtcagtggtctcaaaaggaccatccttgaggccacggcgagagacgagctggtgaagct	1080
Db	1032	cgtcagtggtctcaaaaggaccatccttgaggccacggcgagagacgagctggtgaagct	1091
QY	1081	gcccgtgaagctggcagcgttaccccccgcgcagttccagttcagtggtacaagga	1140
Db	1092	gcccgtgaagctggcagcgttaccccccgcgcagttccagttcagtggtacaagga	1151
QY	1141	actgtcccgggcccacagtcacatgccctggtgtcctcaagaggtgacagagccagcac	1200
Db	1152	actgtcccgggcccacagtcacatgccctggtgtcctcaagaggtgacagagccagcac	1211
QY	1201	aggcacctacacccctgcctctgtgaaactccgcctgctggcctgagggcgcaacatcagct	1260
Db	1212	aggcacctacacccctgcctctgtgaaactccgcctgctggcctgagggcgcaacatcagct	1271
QY	1261	ggagctggtgtgaaatgtgccccccacagatacatagaaaggaggcctctctccccagcat	1320
Db	1272	ggagctggtgtgaaatgtgccccccacagatacatagaaaggaggcctctctccccagcat	1331
QY	1321	ctactcgggtcacagccgcagccctcacctgcacgcctacgggtgcccctgcctct	1380
Db	1332	ctactcgggtcacagccgcagccctcacctgcacgcctacgggtgcccctgcctct	1391
QY	1381	cagcatccagtggcactggcgccctgaaacccctgaaacccctgaaagatggttgcaccagctagct	1440
Db	1392	cagcatccagtggcactggcgccctgaaacccctgaaacccctgaaagatggttgcaccagctagct	1451
QY	1441	ccggcgggcgagcagcagaagacacctcatgccacagtgcgcgtgactgagggcggtgaccac	1500
Db	1452	ccggcgggcgagcagcagaagacacctcatgccacagtgcgcgtgactgagggcggtgaccac	1511
QY	1501	gcagatgcggtgaaaccccatcgagagctgcgacccctggaccgagtttctgagaggaaa	1560
Db	1512	gcagatgcggtgaaaccccatcgagagctgcgacccctggaccgagtttctgagaggaaa	1571
QY	1561	gaataagacttgacaagctggtgatccagaatgccaaactgctctgcattgcataagtg	1620
Db	1572	gaataagacttgacaagctggtgatccagaatgccaaactgctctgcattgcataagtg	1631
QY	1621	tgtgtcttccaaaggtggcgccagatgagcggtcctcattctacttctgtgaccacat	1680
Db	1632	tgtgtcttccaaaggtggcgccagatgagcggtcctcattctacttctgtgaccacat	1691
QY	1681	ccccgacggcttcaccatcgaaatccaaagcattccgagagctactagaggggccagccggt	1740
Db	1692	ccccgacggcttcaccatcgaaatccaaagcattccgagagctactagaggggccagccggt	1751
QY	1741	gctcctgagctgcgaagcgcgacagctaaagtacagacatctgcgctggtaccgctcaa	1800
Db	1752	gctcctgagctgcgaagcgcgacagctaaagtacagacatctgcgctggtaccgctcaa	1811
QY	1801	ectgtccacgctgcacgatgcgcacggaaacccgctctgctcgcactcaagaacgtgca	1860
Db	1812	cctgtccacgctgcacgatgcgcacggaaacccgctctgctcgcactcaagaacgtgca	1871
QY	1861	tctgttccacccctctggccgcagcctggagaggtggcacctggggcgccgacgc	1920
Db	1872	tctgttccacccctctggccgcagcctggagaggtggcacctggggcgccgacgc	1931
QY	1921	cacgctcagctgagta	1980
Db	1932	cacgctcagctgagta	1991
QY	1981	agtgcgaagaccggcgacacatgacaagcactgcacaagaagtacctgtcgtgtgcaggc	2040
Db	1992	agtgcgaagaccggcgacacatgacaagcactgcacaagaagtacctgtcgtgtgcaggc	2051

10

QY	2041	ctctggaagccctcggtcacgcagaaacttgaccgacctctctgtgaaacgtgagcgactc	2100
Db	2052	ctctggaagccctcggtcacgcagaaacttgaccgacctctctgtgaaacgtgagcgactc	2111
QY	2101	gctggaagatcagtgcttggtgcccgagacgcacgcgcccagcatcgtgtgtacaaga	2160
Db	2112	gctggaagatcagtgcttggtgcccgagacgcacgcgcccagcatcgtgtgtacaaga	2171
QY	2161	cgagaggctgctgagggaaaagtcctggagtcgacttggcgactccaaaccagaagctgag	2220
Db	2172	cgagaggctgctgagggaaaagtcctggagtcgacttggcgactccaaaccagaagctgag	2231
QY	2221	catccaacgcgctgcgcgagagagatcggagacgcgtatctgtgcagcgtgtgcaacgccaa	2280
Db	2232	catccaacgcgctgcgcgagagagatcggagacgcgtatctgtgcagcgtgtgcaacgccaa	2291
QY	2281	gggctgcgtcaactctctccgcagcgtggccctggaaagctccagagataagggcagcat	2340
Db	2292	gggctgcgtcaactctctccgcagcgtggccctggaaagctccagagataagggcagcat	2351
QY	2341	ggagatcgtgatcctctgctcggtaaccggcgcacgcgtctcttctctggg	2390
Db	2352	ggagatcgtgatcctctgctcggtaaccggcgcacgcgtctcttctctggg	2401
RESULT 30			
US-60-209-009-455			
; Sequence 455, Application US/60209009			
; GENERAL INFORMATION:			
; APPLICANT: Faris, Mary			
; APPLICANT: Pearson, Cecelia I.			
; TITLE OF INVENTION: GENES EXPRESSED IN PROSTATE CANCER			
; FILE REFERENCE: PA-0027 P			
; CURRENT APPLICATION NUMBER: US/60/209,009			
; CURRENT FILING DATE: 2000-06-01			
; NUMBER OF SEQ ID NOS: 501			
; SOFTWARE: PERL Program			
; SEQ ID NO 455			
; LENGTH: 3277			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
; FEATURE:			
; NAME/KEY: misc_feature			
; OTHER INFORMATION: Incyte ID No: 1084493.6			
US-60-209-009-455			

Query Match	30.4%	Score 1248;	DB 59;	Length 3277;
Best Local Similarity	99.7%	Pred. NO. 0;		
Matches 1588; Conservative		0; Mismatches	2; Indels	2; Gaps

Qy	2522	gcaagccagtgggaaattccccgcagagcgctgcacctgggagagtgctcggtacggc	2581
Db	1	gcaagccagtgggaaattccccgcagagcgctgcacctgggagagtgctcggtacggc	60
Qy	2582	gccttcgggaagtggtggaagcctccgcttcgcattccacaagggcagcagctgcac	2641
Db	61	gccttcgggaagtggtggaagcctccgcttcgcattccacaagggcagcagctgcac	120
Qy	2642	accgtggccgtgaaaaatgctgaaagaggcgccacggyccagcgagcaccgcgcgtgatg	2701
Db	121	accgtggccgtgaaaaatgctgaaagaggcgccacggyccagcgagcgcgcgtgatg	180
Qy	2702	tcggagctcaagatcctctattcacatcggaaccacacctccaacgltgggtcaacctctcggg	2761
Db	181	tcggagctcaagatcctctattcacatcggaaccacacctccaacgltgggtcaacctctcggg	240
Qy	2762	gcgtgaccaaacgcccgcaggcccccct-catggtgatedtgaggtcttcgcaagtacggcaa	2820
Db	241	gcgtgaccaaacgcccgcaggcccccctgcattggtgatedtgaggtcttcgcaagtacggcaa	300
Qy	2821	cctctccaactctctgcgcgcccaagcgggg-cgccttcagcccctgcgcgaagaaatctc	2879

[illegible]

Db	1381	aaagcggttcacgctgataagggacctggccagaatgtggctgtgacaggggacacccctg	1440
Qy	3960	actcccaaggagggcgggcgccctgagcgggggggcccgagagggccaggtgttttaca	4019
Db	1441	actcccaaggagggcgggcgccctgagcgggggggcccgagagggccaggtgttttaca	1500
Qy	4020	acagcgagtagtggggagctgtcgagcccaagcgagaggagaccactgctccccctgtgcc	4079
Db	1501	acagcgagtagtggggagctgtcgagcccaagcgagaggagaccactgctccccctgtgcc	1560
Qy	4080	gcgtgactttcttcacagacacagctactaa	4111
Db	1561	gcgtgactttcttcacagacacagctactaa	1592
RESULT 31			
US-60-213-360-951			
: Sequence 951, Application US/60213360			
: GENERAL INFORMATION:			
: APPLICANT: Morris, MacDonald			
: APPLICANT: Lal, Preeti			
: APPLICANT: Diep, Dinh			
: TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using			
: TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide Polymor			
: FILE REFERENCE: GX-0014 P			
: CURRENT APPLICATION NUMBER: US/60/213,360			
: CURRENT FILING DATE: 2000-06-21			
: NUMBER OF SEQ ID NOS: 8347			
: SOFTWARE: PERL Program			
: SEQ ID NO 951			
: LENGTH: 3277			
: TYPE: DNA			
: ORGANISM: Homo sapiens			
: NAME/KEY: misc_feature			
: OTHER INFORMATION: Incyte ID No: 1084493.6			
US-60-213-360-951			
Query Match 30.4%; Score 1248; DB 60; Length 3277;			
Best Local Similarity 99.7%; Pred. No. 0;			
Matches 1588; Conservative 0; Mismatches 2; Indels 2; Gaps 2;			
Qy	2522	gccagccagtgggaattcccccgagagcgctgcacctggaggagagtgctcggtacggc	2581
Db	1	gccagccagtgggaattcccccgagagcgctgcacctggaggagagtgctcggtacggc	60
Qy	2582	gccttcgggaagggtgtggaagcctccgctttcggcatcccaaggcgagcgagctgtgac	2641
Db	61	gccttcgggaagggtgtggaagcctccgctttcggcatcccaaggcgagcgagctgtgac	120
Qy	2642	accgtgcccgtgaaatgctgaaaggcgccacggccagcgagcacccgcgctgatg	2701
Db	121	accgtgcccgtgaaatgctgaaaggcgccacggccagcgagcacccgcgctgatg	180
Qy	2702	tcggagctcaagatctctcattcacatcgcaacacccctcaacgtgtgaacctctcggg	2761
Db	181	tcggagctcaagatctctcattcacatcgcaacacccctcaacgtgtgaacctctcggg	240
Qy	2762	gcgtgcaccaagcccgaggccccctt-catggtgatcgtggagttctcgaatcagcgcaa	2820
Db	241	gcgtgcaccaagcccgaggcccccttgcattgctgatcgtggagttctcgaatcagcgcaa	300
Qy	2821	ctctctccaaactctctgcgcgccaagcgga-cgcttcagccccctgcgcggaagaagtc	2879
Db	301	ctctctccaaactctctgcgcgccaagcggaacgcgcttcagccccctgcgcggaagaagtc	360
Qy	2880	ccgagcagcgagcgctcccgcccatggtgagactcgcaaggtggtgagcgagcgccg	2939
Db	361	ccgagcagcgagcgctcccgcccatggtgagactcgcaaggtggtgagcgagcgccg	420
Qy	2940	cggggagcagcgacagggtccctcttcgcgcggttcttcgaagaccgagggcgagcgaggc	2999

Db	421	cggggagcagcgacagggtccctcttcgcgcggttcttcgaagaccgaggcgagcgaggc	480
Qy	3000	gggcttctccacacaaagaagctgaggacctgtgctgagccccgctgacctggaagatc	3059
Db	481	gggcttctccacacaaagaagctgaggacctgtgctgagccccgctgacctggaagatc	540
Qy	3060	ttgtctgtcacagcttccaggctggccagagggatggagttctctgcttcccgaaagtgc	3119
Db	541	ttgtctgtcacagcttccaggctggccagagggatggagttctctgcttcccgaaagtgc	600
Qy	3120	tcacagagacctggtgctcggaaattctctgctcgaaagcgacgtgggtgaagatct	3179
Db	601	tcacagagacctggtgctcggaaattctctgctcgaaagcgacgtgggtgaagatct	660
Qy	3180	gtgactttggccttggccgggacatctacaaagaccctgacctacgtccgcaaggcagtg	3239
Db	661	gtgactttggccttggccgggacatctacaaagaccctgacctacgtccgcaaggcagtg	720
Qy	3240	cccggctgcccctgaagtggatggccccctgaaagcatcttcgacaagggtgtacacacgc	3299
Db	721	cccggctgcccctgaagtggatggccccctgaaagcatcttcgacaagggtgtacacacgc	780
Qy	3300	agagtgacgtgtggtctcttgggggtgcttctctggtggaatcttctctggtgggctccc	3359
Db	781	agagtgacgtgtggtctcttgggggtgcttctctggtggaatcttctctggtgggctccc	840
Qy	3360	cgtaccttgggtgcagatcaatgagagttctgccagcgctgagagcgacgcaaga	3419
Db	841	cgtaccttgggtgcagatcaatgagagttctgccagcgctgagagcgacgcaaga	900
Qy	3420	tgaggggcccggagctggccactcccgccatcacgcccgcgcatcatgctgaactggtccg	3479
Db	901	tgaggggcccggagctggccactcccgccatcacgcccgcgcatcatgctgaactggtccg	960
Qy	3480	gagaccccaaggcgagacctgcattctcgagagctggtgagagatctctggtgggacctgc	3539
Db	961	gagaccccaaggcgagacctgcattctcgagagctggtgagagatctctggtgggacctgc	1020
Qy	3540	aggggcaggggcgctgcaaggagaggggtctgcatggcccccgcgagctctcagagct	3599
Db	1021	aggggcaggggcgctgcaaggagaggggtctgcatggcccccgcgagctctcagagct	1080
Qy	3600	cagaagaggagcttctcgaggtgtccacatggccctacacatcgccccagggctgacg	3659
Db	1081	cagaagaggagcttctcgaggtgtccacatggccctacacatcgccccagggctgacg	1140
Qy	3660	ctgaggacagcccgcacagcctgcagcgccacagcctggtggccaggtattacaactggg	3719
Db	1141	ctgaggacagcccgcacagcctgcagcgccacagcctggtggccaggtattacaactggg	1200
Qy	3720	tgctcttcccggttgctggccagaggggtgagacccgtggttctccaggaatgaaga	3779
Db	1201	tgctcttcccggttgctggccagaggggtgagacccgtggttctccaggaatgaaga	1260
Qy	3780	catttgaggaattccccatgacctacacacacgacacacacacacacacacacacacac	3839
Db	1261	catttgaggaattccccatgacctacacacacgacacacacacacacacacacacacac	1320
Qy	3840	acagtggagatggtgctgctcgagaggtttgagcagatagagagcaggtatgacacag	3899
Db	1321	acagtggagatggtgctgctcgagaggtttgagcagatagagagcaggtatgacacag	1380
Qy	3900	aaagcgggttcagctgtaaaagacctggccagaatgtggctgtgacagggcacacccctg	3959
Db	1381	aaagcgggttcagctgtaaaagacctggccagaatgtggctgtgacagggcacacccctg	1440
Qy	3960	actcccaaggagggcgcgccgctgagcgggggccccaggaggccaggtgttttaca	4019
Db	1441	actcccaaggagggcgcgcgccgctgagcgggggccccaggaggccaggtgttttaca	1500
Qy	4020	acagcgagtagtggggagctgtcgagcccaagcgagaggagaccactgctccccctgtgcc	4079

Db 1501 acagcagtagtattgaggagcgtcggagccaagcgaggagaccactgctccccgtctgcc 1560

Qy 4080 gcgtgaattcttcacagacaacagctactaa 4111
|||||

Db 1561 gcgtgaattcttcacagacaacagctactaa 1592

RESULT 32

```

US-60-324-185-4300
: Sequence 4300, Application US/60324185
: GENERAL INFORMATION:
: APPLICANT: Morris, MacDonald
: APPLICANT: Lal, Preeti
: APPLICANT: Deep, Dinh
: TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING
: TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE
: TITLE OF INVENTION: POLYMORPHISMS IDENTIFIED THEREBY
: FILE REFERENCE: GX-0019-1 P
: CURRENT APPLICATION NUMBER: US/60/324,185
: CURRENT FILING DATE: 2001-09-21
: NUMBER OF SEQ ID NOS: 35862
: SOFTWARE: PERL Program
: SEQ ID NO 4300
: LENGTH: 3277
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: OTHER INFORMATION: Incyte ID No: 1084493.6
US-60-324-185-4300

```

Query Match	30.4%;	Score 1248;	DB 71;	Length 3277;
Best Local Similarity	99.7%;	Pred. No. 0;		
Matches 1588; Conservative	0;	Mismatches	2;	Indels
2; Gaps				
QY	2522	gcacgcaagtggaaattcccccagagagcgctgcacctggggagagagtctcgggtacagc	2581	
Db	1	gcacgcaagtggaaattcccccagagagcgctgcacctggggagagagtctcgggtacagc	60	
QY	2582	gccttcgggaagtggtggaaagcttcgcttctcgcatcccaagggcagcagctgtgac	2641	
Db	61	gccttcgggaagtggtggaaagcttcgcttctcgcatcccaagggcagcagctgtgac	120	
QY	2642	accgtggccgtgaaatgctgaaagaggcgccacgcccagcagcaccgcgcgctgatg	2701	
Db	121	accgtggccgtgaaatgctgaaagaggcgccacgcccagcagcagcgcgcgctgatg	180	
QY	2702	tcggagctcaagatctctattcacatcggaacaccctccaacgtggtcaacctcctcggg	2761	
Db	181	tcggagctcaagatctctattcacatcggaacaccctccaacgtggtcaacctcctcggg	240	
QY	2762	gcgtgacaaagccgcagggcccccct-catgtgatctgtagttctgcaagtacggcaa	2820	
Db	241	gcgtgacaaagccgcagggcccccctgatggtatcgtagttctgcaagtacggcaa	300	
QY	2821	cccttccaacttctcgcgcgaagcgga-cgccttcagccccgcgcgagaagcttc	2879	
Db	301	cccttccaacttctcgcgcgaagcgga-cgccttcagccccgcgcgagaagcttc	360	
QY	2880	ccgagcagcgcggaagccttcgcgcacatggtggagctccgcaggtcgagcgcgcc	2939	
Db	361	ccgagcagcgcggaagccttcgcgcacatggtggagctccgcaggtcgagcgcgcc	420	
QY	2940	cgggagagcagacagggcttccttcgcgcaggttctcaagaccgagggcgagcgagc	2999	
Db	421	cgggagagcagacagggcttccttcgcgcaggttctcaagaccgagggcgagcgagc	480	
QY	3000	gggcttctccagaccaaagagctgagacccttgcttgagccccctaacatggaatc	3059	
Db	481	gggcttctccagaccaaagagctgagacccttgcttgagccccctaacatggaatc	540	
QY	3060	tgtctgtctacagcttcacggtggcgacgaggaaggagttcctggcttcccgaagtgca	3119	

RESULT 33

Query Match	23.1%	Score 950;	DB 6;	Length 6026;
Best Local Similarity	99.9%;	Pred. No. 0;		
Matches 1000;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
QY 2869	ggagaagtctccgagacgacgagcgtcttcgcgcgcattgtgagctgcgccaggtcgtga	2928		
DB 2924	GGAGAAGTCTCCCGAGCAGCGCGACGCTTCCGCGCCATGGTGGAGCTGCCAGGCTGCA	2865		
QY 2929	tcggaggcgccgcggggagcagcgacagggctccctcttcgcgcggtttctcgaagaccgaggg	2988		
DB 2864	TCGGAGCGCGCGGGGACGACAGAGGTCTCTTCGCGCGGTTCCTCGAAGACCGGAGGG	2805		
QY 2989	cggaagcgagcgggcgtctctccagaccagaagctgaggacctgtggtcagccgcctaac	3048		
DB 2804	CGGAGCGAGCGCGGCTTCTCCAGACCAAGAGCTGAGGACCTGTGGCTGAGGCCGCTGAC	2745		
QY 3049	csigagaagatctgtctgtctacagcttcacaggtggccagagggatggagttctctggcttc	3108		
DB 2744	CATGGAAGATCTGTCTGCTACAGCTTCCAGGTGGCCAGAGGGATGGAGTTCCTGGCTTC	2695		
QY 3109	ccgaagaagtgcattcacagagacacctgctcgtcgcgaacattctcgtctcgtcggaaagcgacgt	3168		

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genetech)
CURRENT APPLICATION DATA:
FILING DATE: US/08/446, 648
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/222616
FILING DATE: 04-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40, 378
REFERENCE/DOCKET NUMBER: P0821P3PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 6827 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-08-446-648-17

Query Match 23.1%; Score 950; DB 8; Length 6827;
Best Local Similarity 99.9%; Pred. No. 0;

Matches 1000; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2869 ggagaagtctccagacgagcgagcgttcgagccatggtgagctccagagctga 2928
DB 2924 GGAAGATCTCCGACACGCGGGACGCTTCGCGCATGGTGGAGCTGCCAGGCTGA 2865
QY 2929 tcggagggcgccgggagcagcgacaggggtcctcttcgcgcggttctcgaagaccgaggg 2988
DB 2864 TCGGAGCGCGCGGGAGCAGGACAGAGGCTCTCTTCGCGCGGTTCCTCAAGACCGAGGG 2805
QY 2989 cgagcgagcggggtctccagaccagaaagactgagagcctgtggtgagccgctgac 3048
DB 2804 CGGAGCGAGCGGGGCTTCTCCAGACCAGAAAGCTGAGGACCTTGGCTGAGCCGCTGAC 2745
QY 3049 catggaagatcttctgtctgtacagcttcnaggtggccagagggatggagttcctggtctc 3108
DB 2744 CATGGAAGATCTTGTCTGTACAGCTTCCAGCTGCGCAGGTGCGCAGAGGATGAGTTCCTGCTC 2685
QY 3109 ccgaaagtcatccacagagacactggctgtcctcggaacattctgctcggaaagcgactg 3168
DB 2684 CCGAAAGTGCATCCACAGAGACCTGGCTGCTCGGAACATTCCTGTCGGAAGCGACGT 2625
QY 3169 ggtgaagatctgtgactttggccttggccgggagacatctacaagaccctgactacgtccg 3228
DB 2624 GGTGAAGATCTGTGACTTTGGCTTGGCCGTCGCCGGGACATCTACAAGACCCCGACTACGTCGG 2565
QY 3229 caaggcgagtcgccggctccctgaagtggatggccccctgaaagcatcttcgacaaggt 3288
DB 2564 CAAGGCGAGTCGCGCTGCCCTCAAGTGATGCGCCCTGAAAGCATCTTCGACAAAGGT 2505
QY 3289 gtacaccacgagatgacgtgtgtctctttgggtgtctctctctctctctctctctctctct 3348
DB 2504 GTACACACGACGAGATGAGCTGTGGTGTCTCTTGGGTGCTCTCTCTGGAGATCTTCTCTCTCT 2445
QY 3349 gggggcctcccgtagccttgggtgcaataatgaggagtctctccagcggtgagaga 3408
DB 2444 GGGGGCTCTCCCGTACCTTGGGGTGCATATCAATGAGGAGTTCCTCCAGCGGCTGAGAGA 2385
QY 3409 cgggcaaggatgagggccccggagctggccactcccgccatccagcccatcatctgaa 3468
DB 2384 CGGCAAGGATGAGGGCCCCGGAGCTGGCCACTCCCGCCATACCGCCGATCATGCTGAA 2325
QY 3469 ctgctggtccggagagaccccaaggcgagagacctgcatctctcgtgagctggtggagatccctggg 3528

DB 2324 CTCCTGGTCCGGAGACCCCAAGCGGAGACCTGCATTTCTCGGAGCTGGTGGAGATCCTGGG 2265
QY 3529 ggaactgtctccagggcaggggctcgaagagaaagagaggtctcgtatggcccgccgag 3588
DB 2264 GGACCTGTCCAGGCGAGGGGCTTCAAGAGGAAGAGGAGGTCTGCATGGCCCCCGGAG 2205
QY 3589 ctctcagagctcagaagaggggagcttctcgcaggtgtccaccatggccctacacatcgc 3648
DB 2204 CTCTCAGAGCTCAGAAAGAGGGGAGCTTCTCGCAGGTGTCCACCATGGCCCTACACATCGC 2145
QY 3649 ccaggtcagctgagacagagcccgcccaagcctcagagcgccacagcctggcccgccaggtla 3708
DB 2144 CCAGGCTGACGCTGAGGACAGCCCGCCCAAGCCTGCGAGCGCCACAGCCTGGCCCGCAGGTA 2085
QY 3709 ttacaactgggtgtctcttcccggtgctggtggtccagaggggctgagacccgtggttctctc 3768
DB 2084 TTACAACCTGGGTGTCTTTTCCCGGGTGCTTGGCCAGAGGGGCTGAGACCCGTGGTTCCTC 2025
QY 3769 caggatgaagacatttgaggaattcccccatgaccccaacgacctacaaggtctctgtgga 3828
DB 2024 CAGGATGAAGACATTTGAGGAATTCCTCCATGACCCCAAGACCTACAAAGGCTCTCTGGA 1965
QY 3829 caaccagacagacagtggatggtgctggtcctcgaggaagt 3869
DB 1964 CAACCAGACAGACAGTGGATGGTCTGCTGCGCTCGGAGGAGT 1924

RESULT 35

US-08-770-449-17/c
; Sequence 17, Application US/08770449
; GENERAL INFORMATION:
; APPLICANT: Bennett, Brian D.
; APPLICANT: Goeddel, David
; APPLICANT: Lee, James M.
; APPLICANT: Matthews, William
; APPLICANT: Tsai, Siao Ping
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genetech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770.449
; FILING DATE: 20-Dec-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/00586
; FILING DATE: 22-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/826935
; FILING DATE: 22-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/222616
; FILING DATE: 04-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40, 378
; REFERENCE/DOCKET NUMBER: P0821P2D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168

; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6827 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
US-08-770-449-17

Query Match 23.1%; Score 950; DB 11; Length 6827;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1000; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2869 ggagaagtctccagacagcagcagcgttccgcgcacatggtgagagctcgcagagctgga 2928
Db 2924 GGAGAAGTCTCCCGAGCAGCGCGGAGCGCTTCCGCGCATGGTGGAGCTCGCCAGGCTGA 2865

Qy 2929 tcggagagcggcgggagcagcagcaggggtctctcttcgcgcggttctcgaagaccgaggg 2988
Db 2864 TCGGAGGCGCGCGGAGCAGCGACAGGCTCTTCCGCGCGTCTTCGGAAGACCGAGCG 2805

Qy 2989 cggagcagcggcggcgtctctccagacaaagcagcagcctgaggacctggtgagcccgctgac 3048
Db 2804 CGGAGCGAGCGCGGCTCTCCAGACCAAGAGCTGAGGAGCTGTGGCTGAGCCCGCTGAC 2745

Qy 3049 catggaagatctgtctgtacagcttcaggtgcccagaggaatgagattcctggtcttc 3108
Db 2744 CATGGAAGATCTGTCTGTCTACAGCTTCCAGGTGGCCAGAGGATGGATTCCTGGCTTC 2685

Qy 3109 ccgaaagtgcatccacagagacctggtctcgcggaacattctctgtcggaaagcagcgt 3168
Db 2684 CCGAAAGTGCAATCCACAGAGACCTGGCTGCTCGGAACATTCTCTCTCGGAAGCGACGT 2625

Qy 3169 ggtgaagatctgtaacttggccttccgcgggacatctcacaagaccctgactacgtccg 3228
Db 2624 GGTGAAGATCTGTGACTTTGGCCTTCCCGGGACATCTACAAAGACCCCGACTACGTCCG 2565

Qy 3229 caagggcagtgcccggtcgcctgaagtggatggatggccctgaagcatcttcgaagat 3288
Db 2564 CAAGGCGAGTGCCCGCTGCCCTGAAGTGGATGGCGCCCTGAAAGCATCTTCGACAAGGT 2505

Qy 3289 gtacacacagcagagtgaagtgtggttccttgggtgtctctcttggagatctctctct 3348
Db 2504 GTACACACGACAGTGAAGTGTGTGTCCTTTGGGTGCTTCTCTGGAGATCTTCTCTCT 2445

Qy 3349 gggggcctcccgatccctggggtgcagatcaatgagagatctgcacgcgctcagaga 3408
Db 2444 GGGGGCTCCCCGTACCCGTGGGTGCAGATCAATGAGAGATTCTGCGACGCGCTGAGAGA 2385

Qy 3409 cggcacaaggatgagggcccgagctggccactccgcacacacgcgcgcgcgcgcgcgcgc 3468
Db 2384 CGGCACAAGGATGAGGGCCCGGAGCTGGCCACTCCCGCCATACGCCGCTCATCTGAA 2325

Qy 3469 ctgctggtccggagaccacaaaggcagacactgcattctcggagctgggtgagatcctggg 3528
Db 2324 CTGCTGCTCCGGAGACCCCAAGCCGAGACCTGCATCTCTCGAGCTGCTGGAGATCTCTGG 2265

Qy 3529 ggacctctccagggcagggcctcgaagagaaagagaggtctgcatggcccccgag 3588
Db 2264 GGACCTGCTCCAGGCGAGGGGCTGCAAGAGAAAGAGAGGTCTGCATGGCCCCCGCGAG 2205

Qy 3589 ctctcagagctcagaagaggcagcttctcgcaggtgttcacacatggccctacacatcgc 3648
Db 2204 CTCTCAGAGCTCAGAAGAGGCGAGCTTCTCGCAGGTGTCCACCATGGCCCTACACATCGC 2145

Qy 3649 ccagctgacgctgagacagcccgccaaagcctgcagcgcacacagcctgcccagagta 3708
Db 2144 CCAGGCTGACGCTGAGGAGACGGCCGCAAGCCTGCAGCGCCACAGACCTGGCCGCCAGGTA 2085

Qy 3709 ttacaactgggtgtctcttctcccggtgtgcttggccagaggggctgagaccgtggttctc 3768
Db 2084 TTACAACCTGGGTGTCTCTTCTCCCGGTGCTTGCCACAGAGGGGCTGAGACCGGTTCCTC 2025

Qy 3769 caggatgaagacatttgaggaaattcccatgaccaccaagcactacaaaggctctgtgga 3828
Db 2024 CAGGATGAAGACATTTGAGGAATTTCCCATGACCCCAAGCAGCTACAAAGGCTCTGTGA 1965

Qy 3829 caaccagacagacagtggtgctgctggcctcgagagagt 3869
Db 1964 CAACACAGACAGACGTGGATGGTCTGCTCGCCTCGGAGGAGT 1924

RESULT 36
US-09-982-610-17/c
; Sequence 17, Application US/09982610
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; Bennett, Brian D.
; Goeddel, David
; Lee, James M.
; Matthews, William
; Tsai, Siao Ping
; Wood, William I.
; TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/982,610
; FILING DATE: 17-Oct-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/446,648
; FILING DATE: 1996-MAY-23
; APPLICATION NUMBER: 08/222616
; FILING DATE: 04-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0821P3PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6827 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-982-610-17

Query Match 23.1%; Score 950; DB 36; Length 6827;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1000; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2869 ggagaagtctcccgagcagcgcgcgccttccgcgcacatggtgagctcgcagagctgga 2928
Db 2924 GGAGAAGTCTCCCGAGCAGCGCGGAGCGCTTCCGCGCATGGTGGAGCTCGCCAGGCTGA 2865

Qy 2929 tcggagagcggcgggagcagcagcaggggtctcttctcgcgcggttctcgaagaccgaggg 2988
Db 2864 TCGGAGGCGCGCGGAGCAGCGAGGCTCTCTTCCGCGGCTTCTCGAAGACCGAGG 2805

```

;
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 575
; TYPE: DNA
; ORGANISM: HUMAN
US-60-213-847-55

Query Match      10.7%; Score 440; DB 60; Length 575;
Best Local Similarity 100.0%; Pred. No. 5e-199;
Matches 440; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2989 cggagcagcggggtcttccagaccagaagctgagacctgtggtgagcccgctgac 3048
      |||||||
DB 2804 CGGAGCGAGCGGGCTTCTCCAGACCAAGAAGCTGAGGACCTGTGGCTGAGCCCGCTGAC 2745

QY 3049 catggaagatctgtgtctacagcttccagtggtccagagagtgagtgcttccgcttc 3108
      |||||||
DB 2744 CATGGAAGATCTGTGTCTACAGCTTCCAGGTGGCCAGAGGATGAGTTCCTGGCTTC 2685

QY 3109 cgaagagtcattccacagagacctgctgctcggaaacattcgtctcggaagcagct 3168
      |||||||
DB 2684 CGGAAGTGCATCCACAGAGACCTGGCTCTCGGAACATTCCTGCGAAGGACGCT 2625

QY 3169 ggtgaagatctgtgacttggccttggccgggagacattacaaagaccctgactacgctccg 3228
      |||||||
DB 2624 GGTGAAGATCTGTGACTTGGCCTGGCCGGGACATCTACAAAGACCCGACTAGCTCCG 2565

QY 3229 caaggcagtgccggctgcccctgaagtggatggccctgaaagcatctcttgacaaagt 3288
      |||||||
DB 2564 CAAGGCGAGTGGCCGCTGCCCTGAAAGTGGATGGGCCCTGAAGACATCTTCCACAAGGT 2505

QY 3289 gtacaccagcagagtgagctgtgcttggggtgcttctctgggagcttctctctct 3348
      |||||||
DB 2504 GTACACCAGCAGAGTGAGCTGTGGTCTTCTGGGTGCTTCTCTGGAGATCTTCTCTCT 2445

QY 3349 gggggcctcccgctacccctgggtgcagatcaatgaggagttcttccagcggctgagaga 3408
      |||||||
DB 2444 GGGGGCTCTCCCGTACCTTGGGGTGCAGATCAATGAGGAGTTCTGCCAGCGCTCAGAGA 2385

QY 3409 cggcacaagatgagggcccccggagctggccactcccgccatccagccgcatcgtgaa 3468
      |||||||
DB 2384 CGGCACAAAGATGAGGGCCCCGGAGCTGGCCACTCCCGCATACACCGCCGATCATGCTGAA 2325

QY 3469 ctgctggtccgagagaccccaaggcagagacctgctctcggagctggtggaatcctggg 3528
      |||||||
DB 2324 CTGCTGCTCGGAGACCCCAAGCCGAGACCTGCTCATTTCTGGAGCTGTGTGGAGATCCTGG 2265

QY 3529 ggaactgtctccggcaggggctcgaagaggaagagaggttctgcatggtgcccgcgcag 3588
      |||||||
DB 2264 GGACCTGTCTCCAGGGCAGGGGCTGCAAGAGGAGAGAGGAGTCTGCATGTGCCCGCCGCGAG 2205

QY 3589 ctctcagagctcagaagagggcagcttctcgcagtggttccaccattgcccctacacatgc 3648
      |||||||
DB 2204 CTCTCAGACCTCAGAAGAGGGGAGCTTCTTCGAGAGTGTCCACATGGCCCTTACACATGCG 2145

QY 3649 ccagctgagcgtgagcagagcccgccagcctgagcgccacagcctgagcagcctgagcagta 3708
      |||||||
DB 2144 CCAGGCTGACGCTGAGGACAGCCCGCCAGCCTGCAGGCCACACACCTTGGCGCCGAGGTA 2085

QY 3709 ttacaactgggtgtctcttccgggtgctggtggtggtggtggtggtggtggtggtggtggt 3768
      |||||||
DB 2084 TTACAACCTGGGTGTCTTCTCCCGGTGCTTGGCCAGAGGGGCTGAGACCCCGTGTCTCTC 2025

QY 3769 caggatgaagacatttgaggaattcccatgaccccaacgacctcaaaagcctctgtgga 3828
      |||||||
DB 2024 CAGGATGAAGACATTTGAGGAATTTCCCATGATACCCCAACGACCTTACAAAGGCTCTGTGGA 1965

QY 3829 caaccagacagacagtggatggtggtggtggtggtggtggtggtggtggtggtggtggtggt 3869
      |||||||
DB 1964 CAACCAGACAGACATGGGATGCTGCTGGCCTCGGAGGAGT 1924

RESULT 37
US-60-213-847-55
; Sequence 55, Application US/60213847
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS OF THE
; TITLE OF INVENTION: SER/THR AND TYR FAMILY OF KINASES, NUCLEIC ACID MOLECULES
; FILE REFERENCE: CL000704
; CURRENT FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 1824
```

```

;
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 575
; TYPE: DNA
; ORGANISM: HUMAN
US-60-213-847-55

Query Match      10.7%; Score 440; DB 60; Length 575;
Best Local Similarity 100.0%; Pred. No. 5e-199;
Matches 440; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3672 cgcgaagcctcagcgccacagcctggtggtccaggtattacaactggtgtcccttccc 3731
      |||||||
DB 32 cgcgaagcctcagcgccacagcctggtggtccaggtattacaactggtgtcccttccc 91

QY 3732 ggtgctggtcagaggggctgagacccgtggttctccaggtatgaagacatttgaggat 3791
      |||||||
DB 92 ggtgctggtcagaggggctgagacccgtggttctccaggtatgaagacatttgaggat 151

QY 3792 tccccatgaccccaacgacctacaaggtctgtggaacaacagacagacagcagtggtg 3851
      |||||||
DB 152 tccccatgaccccaacgacctacaaggtctgtggaacaacagacagcagtggtg 211

QY 3852 tgcgtggtcctcgagaggtttgagcagatagagcagcagcagcagcagcagcagcagc 3911
      |||||||
DB 212 tgcgtggtcctcgagaggtttgagcagatagagcagcagcagcagcagcagcagcagc 271

QY 3912 gctgtaaaggacctggccagaatgtggtgagcagcagcagcagcagcagcagcagcag 3971
      |||||||
DB 272 gctgtaaaggacctggccagaatgtggtgagcagcagcagcagcagcagcagcagcag 331

QY 3972 ggcggcggtcctgagcgggggggggggggggggggggggggggggggggggggggggg 4031
      |||||||
DB 332 ggcggcggtcctgagcgggggggggggggggggggggggggggggggggggggggggg 391

QY 4032 gggagctgctggagcgaagcagagagagcagcagcagcagcagcagcagcagcagcag 4091
      |||||||
DB 392 gggagctgctggagcgaagcagagagagagagagagagagagagagagagagagagag 451

QY 4092 tcacagacaacagctactaa 4111
      |||||||
DB 452 tcacagacaacagctactaa 471

RESULT 38
US-60-213-178-1247
; Sequence 1247, Application US/60213178
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL000689
; CURRENT FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 1425
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1247
; LENGTH: 415
; TYPE: DNA
; ORGANISM: Human
US-60-213-178-1247

Query Match      9.8%; Score 401; DB 60; Length 415;
Best Local Similarity 100.0%; Pred. No. 2.4e-180;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3114 agtgcattccacagagacctggtgctgctggaacattctgctggaagcagcagtggtga 3173
      |||||||
DB 15 agtgcattccacagagacctggtgctgctggaacattctgctggaagcagcagtggtga 74
```

QY 3174 agatctgtgactttggccttgcgcggagacatctacaaagaccctgactaogtccgcgaag 3233
Db 75 agatctgtgactttggccttgcgcggagacatctacaaagaccctgactaogtccgcgaag 134
QY 3234 gcagtgccggctgcgcctgaagtgaatggccctgaagcatcttcgacaaggtatata 3293
Db 135 gcagtgccggctgcgcctgaagtgaatggccctgaagcatcttcgacaaggtatata 194
QY 3294 ccacgcagagtgactgtgtgtcttctgggggtgtcttctctgggagatcttctctctgggg 3353
Db 195 ccacgcagagtgactgtgtgtcttctgggggtgtcttctctgggagatcttctctctgggg 254
QY 3354 cctcccgcctaccctggggtgcagatcaatgagaggttctgcacggctgagagacgca 3413
Db 255 cctcccgcctaccctggggtgcagatcaatgagaggttctgcacggctgagagacgca 314
QY 3414 caaggtatggggcccgaggctggccactcccgccatcacgcgcacatctgctgaactgct 3473
Db 315 caaggtatggggcccgaggctggccactcccgccatcacgcgcacatctgctgaactgct 374
QY 3474 ggtccggagaccccaaggcgagacctgcattcttcggagctg 3514
Db 375 ggtccggagaccccaaggcgagacctgcattcttcggagctg 415

RESULT 39

US-09-716-953-1245
; Sequence 1245, Application US/09716953
; GENERAL INFORMATION:
; APPLICANT: Gearing, David P.
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: McCarthy, Sean
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 1600.2044-001
; CURRENT APPLICATION NUMBER: US/09/716,953
; CURRENT FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: 60/167,413
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 2620
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1245
; LENGTH: 535
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(535)
; OTHER INFORMATION: n = A,T,C or G
US-09-716-953-1245

Query Match 9.4%; Score 388; DB 28; Length 535;
Best Local Similarity 99.8%; Pred. No. 4e-174;
Matches 438; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3281 gacaaaggtgtacacacgcagagtgactgtgtgtcttctgggggtgtctctcggagatc 3340
Db 15 gacaaaggtgtacacacgcagagtgactgtgtgtcttctgggggtgtctctcggagatc 74
QY 3341 ttctctctgggggctcccgctaccctgggtgcagatcaatgagagttcttgcgcagcgg 3400
Db 75 ttctctctgggggctcccgctaccctgggtgcagatcaatgagagttcttgcgcagcgg 134
QY 3401 ctgagagacggcacaaagatgagggcccgagctggccactccgcatacgcgcgcatc 3460
Db 135 ctgagagacggcacaaagatgagggcccgagctggccactccgcatacgcgcgcatc 194
QY 3461 atgctgaactgtctgctcggagaccccaaggcgagacctgcattctcggagctggtgag 3520
Db 195 atgctgaactgtctgctcggagaccccaaggcgagacctgcattctcggagctggtgag 254
QY 3521 atctctgggggacctgctccagggcgagggcctgctgcaagagagagaggtctgcatggcc 3580

Db 255 atctctgggggacctgctccagggcgagggcctgcaagagagagaggtctgcatggcc 314
QY 3581 ccgcgcagctctcagagctcacaagagggcagcttctcgcaggtgtccaccatggcccta 3640
Db 315 ccgcgcagctctcagagctcacaagagggcagcttctcgcaggtgtccaccatggcccta 374
QY 3641 cacatcgcccgagctgacgctgagacagcccgcccaagcctgcagcgccacagcctggcc 3700
Db 375 cacatcgcccgagctgacgctgagacagcccgcccaagcctgcagcgccacagcctggcc 434
QY 3701 gccaggtattacaactggg 3719
Db 435 gccaggtattacaactggg 453

RESULT 40

US-60-172-373-15761
; Sequence 15761, Application US/60172373
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preeti
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
; TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide Poly
; FILE REFERENCE: GX-0006 P
; CURRENT APPLICATION NUMBER: US/60/172,373
; CURRENT FILING DATE: 1999-12-16
; NUMBER OF SEQ ID NOS: 25,772
; SOFTWARE: PERL Program
; SEQ ID NO 15761
; LENGTH: 1575
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 902563.1
US-60-172-373-15761

Query Match 8.3%; Score 340; DB 56; Length 1575;
Best Local Similarity 100.0%; Pred. No. 3.7e-151;
Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3772 gatgaagacatttgagggaattcccatgaccccaacgacctacaaaggtctctggacaa 3831
Db 1 gatgaagacatttgagggaattcccatgaccccaacgacctacaaaggtctctggacaa 60
QY 3832 ccagacagacagtgaggatggtgctggtcctcgagaggtttgagcagatagagagcaggca 3891
Db 61 ccagacagacagtgaggatggtgctggtcctcgagaggtttgagcagatagagagcaggca 120
QY 3892 tagacaagaaagcgcttcagctgttaaaggacctggccagaaatgtggctgtgaccaggc 3951
Db 121 tagacaagaaagcgcttcagctgttaaaggacctgtaaaggacctggccagaaatgtggctgtgaccaggc 180
QY 3952 acacctgactcccaagggagggcggtggcctgagcggggcccgagagagccagggt 4011
Db 181 acacctgactcccaagggagggcggtggcctgagcggggcccgagagagccagggt 240
QY 4012 gttttacaacagcagtgatgggagctgtcgagagccagcgagagagccactgtcccc 4071
Db 241 gttttacaacagcagtgatgggagctgtcgagagccagcgagagagagccactgtcccc 300
QY 4072 gctgcccgcgtgactttcttcacagacaacagctactaa 4111
Db 301 gctgcccgcgtgactttcttcacagacaacagctactaa 340

RESULT 41

US-60-213-847-1271
; Sequence 1271, Application US/60213847
; GENERAL INFORMATION:

APPLICANT: Beasley, Ellen
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS OF THE
SER/THR AND TYR FAMILY OF KINASES, NUCLEIC ACID MOLECULES
ENCODING THESE HUMAN KINASE PROTEINS, AND USES THEREOF
FILE REFERENCE: CL000704
CURRENT APPLICATION NUMBER: US/60/213,847
CURRENT FILING DATE: 2000-06-23
NUMBER OF SEQ ID NOS: 1824
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO: 1271
LENGTH: 340
TYPE: DNA
ORGANISM: HUMAN
US-60-213-847-1271

Query Match 8.2%; Score 339; DB 60; Length 340;
Best Local Similarity 100.0%; Pred. No. 1.2e-150;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3723 ccttcccggtgctgctgaggggctgagaccctgagccctggttctccagatgaagacat 3782
Db 2 ccttcccggtgctgctgaggggctgagaccctggttctccagatgaagacat 61
QY 3783 tlgaggaattcccatgaccccaacgacctacaaggtctgtgacaaacagacagaca 3842
Db 62 tlgaggaattcccatgaccccaacgacctacaaggtctgtgacaaacagacagaca 121
QY 3843 gtggagtggtgctgctgagggaggtttgagcagatagagagcagcagatagacaagaa 3902
Db 122 gtggagtggtgctgctgagggaggtttgagcagatagagagcagcagatagacaagaa 181
QY 3903 gcggcttcagctgtaaaggacctgcccagaaatgtggtgtgacaggggcaccctgact 3962
Db 182 gcggcttcagctgtaaaggacctgcccagaaatgtggtgtgacaggggcaccctgact 241
QY 3963 cccaaggagagcggcggcctgagcgggggcccagagagccaggtgttttacaaca 4022
Db 242 cccaaggagagcggcggcctgagcggggggcccagagagccaggtgttttacaaca 301
QY 4023 gcgagtaggggagctgtcgagagcagcagcagaggagacc 4061
Db 302 gcgagtaggggagctgtcgagagcagcagcagaggagacc 340

RESULT 42
US-60-184-770-470
Sequence 470, Application US/60184770
GENERAL INFORMATION:
APPLICANT: Hodgson, David M. Jones, Anissa L.
APPLICANT: Lincoln, Stephen E. Yu, Jimmy Y.
APPLICANT: Russo, Frank D. Greenawalt, Lila B.
APPLICANT: Spiro, Peter A. Panzer, Scott R.
APPLICANT: Banville, Steve C. Roseberry, Ann M.
APPLICANT: Bratcher, Shawn R. Wright, Rachel J.
APPLICANT: Dufour, Gerard E. Chen, Wensheng
APPLICANT: Cohen, Howard J. Liu, Tommy
APPLICANT: Rosen, Bruce Yap, Pierre E.
APPLICANT: Shah, Purvi
APPLICANT: Chalup, Michael S. Amshery, Stefan
APPLICANT: Hillman, Jennifer L. Fong, Willy Tuen
TITLE OF INVENTION: RECEPTOR MOLECULES
FILE REFERENCE: PT-0117 P
CURRENT APPLICATION NUMBER: US/60/184,770
CURRENT FILING DATE: 2000-02-24
NUMBER OF SEQ ID NOS: 1461
SOFTWARE: PERL Program
SEQ ID NO 470
LENGTH: 724
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature

OTHER INFORMATION: Incyte ID No: 1083172.1
US-60-184-770-470

Query Match 7.5%; Score 310; DB 57; Length 724;
Best Local Similarity 100.0%; Pred. No. 8.7e-137;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3602 gaagaggcagcttctcgagggtgtccaccatgcccctacacatcgcacaggtgacgt 3661
Db 1 gaagaggcagcttctcgagggtgtccaccatgcccctacacatcgcacaggtgacgt 60
QY 3662 gaggacagccgcgaagcctgcagcgcacagcctgcccaggtattacaactgggtg 3721
Db 61 gaggacagccgcgaagcctgcagcgcacagcctgcccaggtattacaactgggtg 120
QY 3722 tcttcccggtgctgctgaggggctgagaccctggttctccagatgaagaca 3781
Db 121 tcttcccggtgctgctgaggggctgagaccctggttctccagatgaagaca 180
QY 3782 ttgaggaattcccatgaccccaacgacctacaaggtctgtggacaaccagacagac 3841
Db 181 ttgaggaattcccatgaccccaacgacctacaaggtctgtggacaaccagacagac 240
QY 3842 agtggagtggtgctgctgaggggagtttgagcagatagagagcaggtatagacaaga 3901
Db 241 agtggagtggtgctgctgaggggagtttgagcagatagagagcaggtatagacaaga 300
QY 3902 agcggcttca 3911
Db 301 agcggcttca 310

RESULT 43
US-09-823-241-233
Sequence 233, Application US/09823241
GENERAL INFORMATION:
APPLICANT: Gearing, David P.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.2075-001
CURRENT APPLICATION NUMBER: US/09/823,241
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: US 60/193,434
PRIOR FILING DATE: 2000-03-30
NUMBER OF SEQ ID NOS: 10028
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 233
LENGTH: 576
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)-(576)
OTHER INFORMATION: n = A,T,C or G
US-09-823-241-233

Query Match 7.5%; Score 309; DB 31; Length 576;
Best Local Similarity 99.7%; Pred. No. 2.6e-136;
Matches 359; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3553 gcaagaggagaggtgtgtgcatggcccgagctctcagagctcagaagaggcag 3612
Db 10 gcaagaggagaggtgtgtgcatggcccgagctctcagagctcagaagaggcag 69
QY 3613 ctctcgcaggtgtccaccatgcccctacacatcgcacaggtgacgtgagagacccc 3672
Db 70 ctctcgcaggtgtccaccatgcccctacacatcgcacaggtgacgtgagagacccc 129
QY 3673 gccaaagcctgagcgcacagcctggcccgaggtattacaactggttcttcccg 3732
Db 3732 gccaaagcctgagcgcacagcctggcccgaggtattacaactggttcttcccg 3732

TITLE OF INVENTION:	THEREOF
NUMBER OF SEQUENCES:	20
CORRESPONDENCE NO.:	

COMPUTER READABLE FORM:

OPERATING SYSTEM: IBM PC compatible

CURRENT APPLICATION #1.0

FILING DATE: 08/08/90, 710

APPLICATION DATA:

RIOR APPLICATION DATE: 14-NOV-1994

FILING DATE: 09-11-2008
FILING NUMBER: 08/25

APPLICATION NUMBER: 07/058 053

NAME: Cass
AGENT INFORMATION:

REFERENCE/DOCKET NUMBER: 38,152

TELEPHONE: 312/474-6300

INFORMATION FOR: 25-3856

LENGTH: 4795

TRANDEDNESS: single

C'DNA

DECLARATION:

Y Match

Local Similarity 100.0%; Score 4111; DB 3; Length 4795;
 Res 4111; Conservativeness

[illegible]

1 CCACGGCGAGCGCGCGGCGGCGCGCTGTGCTGCGACTGLGCTCTG 60

61 cctgggactcctggaggccctaatcctcctgggagcggggcgccgctgctggcactgtggcctctg 60

61 CCCTGGACTCTCTGACGGCTGCTCAGCTGACCTGACAT 120

21 carqaygaqtacacqtcactcagaccgaccttgaaacat 120

21 CACGGAGGACTCACACCTCATCGACACCCCTTTCATCCTGCAGCGGCCA 180

11 gcacccctcgcagtgaggcttgacagagctt
|||||
|||||gcacacccggtgacagccctgtccatctctcttcaggggaca 180

GCACCCCTTCAGTGGGCTTGCCACCACCA

1 cagcqaaggaacaggggggtagtgcagacat-
|||||
-ccacagagctcaggagcgccagccaccggagacaagga 240

1 CACCGAGGACACGGGGGTGGTGGCAGACTm22 |||||

gggtgttgctgctgcagaggtacatcaaa-
-cctgacatgccagggcacagagccaggccctactgcac 300

...ccacgcacaggaclctgclacaa 360

1381 CAGCATCCAGTGGCACTGGCGGCCCTGGACACCCCTGCAAGATGTTTGCCCACTGTTAGTCT 1440
QY 1441 ccggcgccgagcagcaayacctcatgcccacagtgccctgactgagagggcggtgaccac 1500
Db 1441 CGGGCGCGCGAGCAGCAAGACCTCATGCCACAGATGCCGTGACTGGAGGGCGGTGACCCAC 1500
QY 1501 gcaagatgcccgtgaaaccccatcgagagcctggaacccctggagccgagtttgtagagggaaa 1560
Db 1501 GCAGGATGCGGTGAACCCCATCGAGAGCCTGGACACCTGGACCGGAGTTTGTGGAGGGAAA 1560
QY 1561 gaataaagactgtagcaagctggtgataccagaatgccaaacgtagtctgcatatatacaagtg 1620
Db 1561 GAATAAGACTGTGAGCAAGCTGTGATCCAGAAATGCCAAGTGTCTGTGCCATCTACAAAGTG 1620
QY 1621 tgtatgcttccaaagtgtagcagagatgagcggtcatctacttctatatacaaccacat 1680
Db 1621 TGTGTGCTCTCAACAAGGTGGGCTAGGATGAGGGGCTCATCTACTTCTATGTGACCACTAT 1680
QY 1681 cccgagagcttcaacatccgaalccaaagccatccagagagcttcttctgactgacaacaqtura 1740
Db 1681 CCGCGAGCGCTTACCATCGAATCCAAGCCATCCGAGGAGCTACTAGAGGCGTAGCGGCT 1740
QY 1741 gclcttgagctgccaaagccagacgclauaaytlacagaaclclqngcltqgcllqarqlcaaa 1800
Db 1741 GCTTCCTGAGCTGCCAAGCCAGAGCTTACAAGTACGAGCATCTCCGGTGTGTAPCGCTCAA 1800
QY 1801 cctgtccacgctgcacgatyccacgggaacccgcttcttctgactgacaacaqtura 1860
Db 1801 CTTTGCACGCTGCAGCATGCCACUGGAACCCGCTTCTGCTCGACTGCAAGAAGCTGCA 1860
QY 1861 tctgttcgcacacccctctggccgcagcctggaggaagtgggcacctggagcgccacgic 1920
Db 1861 TCTTTTGGCCACCCCTCTGUCGCCAGCCTGGAGGAGGTGGCACCTGGGGCGCGCACGC 1920
QY 1921 cagcgclcaagcttgagtaatcccccggctcgccgcgagcaagagggccactatgtagcga 1980
Db 1921 CAGCCTCAGGCTGAGTATCCCCCGCTCGCGCCGAGCACGAGGGCCACTATGTGTGCCA 1980
QY 1981 anttgaagaccggcgagccatgacaaycacttccacaagaagtaaccttctgactgacgic 2040
Db 1981 ACTGCAAGACCGCGCAGCCATGACAAGCACTGCCACAGAAGTACCTGTCTCGGTGACGC 2040
QY 2041 cclqgaagcccttnggctcaacrajaacttggccacclctctgggtgaaagctgagagctc 2100
Db 2041 CTTGGAAGCCCTTCGGCTCACGCAGAACTTGACCGACCTTCTTGGTGAAGCTGAGCGACTC 2100
QY 2101 gclqgaagatcaagtgacttggtagcagagcagcagcccaacalclqatatacaaaa 2160
Db 2101 GCTGGAGATGCACTGTTGGTGGCCGAGCGCACCGGCCCCAGCATCGTGTGTACAAAAG 2160
QY 2161 cnagaagclgcltggagaagaaagcltggagtcgacttggcggacltccaaaccagaagcltag 2220
Db 2161 CGAGAGGCTTCTCGAGAGAAACTTGGAGTGGACTTGGTGGACTCCACCCAGAACCTGAG 2220
QY 2221 catccagcgctgtagcagaggaatgtaggagcglatcltgtcagcgtgtatcaacgcaaa 2280
Db 2221 CATCCAGCGCTCGCGGAGGAGATGCGGAGCGCTATCTGTGCAAGCTGTGCAAGGCCAA 2280
QY 2281 gggctgcataactcctccgcagagtgagcgtgaaagctccgaggaalaaagagagcat 2340
Db 2281 GGGCTCGGTCAACTCTCTCCCGCAGCGTGGCCGTGGAAGGCTCCGAGGATTAAGGGGAGCAT 2340
QY 2341 ggaagclclqatclcttgttcqgtagcggcgclcatcgcgtgtcttcttctgtggtcctcctcct 2400
Db 2341 GGAGATCGTGATCTTGTGCGTACCGCGCTCATCGCTGTCTTCTTGTGGTCTCTCTCT 2400
QY 2401 cctcatctctgatacatgagagggcgccgcccacgcagacatacaagacaggttaactgtc 2460
Db 2401 CCTCATCTTCTGTAACTATGAGGAGCGCGCCACGACAGACATCAAGACCGGCTTACCTGTC 2460
QY 2461 calcatcalggagcccgaggagtgccctctgaggaagaaalacuyaataacttctclacua 2520
Db 2461 CATCATCATGGAGCCCGGGAGGTGCTCTTGGAGGAGCAATGCGAATACCTCTCTTACCA 2520

QY 2521 tgcagaccagtgaggaaattccccccgagagcggtgcacactggggagagtgctcggtacag 2580
Db 2521 TGCCAGCCAGTGGGAATTTCCCCCGAGAGCGGCTGCACCTGGGGAGAGTGTCTCGGCTACGG 2580
QY 2581 qcctctcggaaggtgggtggaagcctccgcttctggacatccacaagggcagcagctgtga 2640
Db 2581 CGCTTCTGGGAAGGTGGTGGGAAGCTCCGCTTTCGGCATCCACAAGGCGCAGCAGCTGTGA 2640
QY 2641 caccgtgcccgtgaaaaatgctgaaagagggcgccacggccagcgagcaccgcgcgtgat 2700
Db 2641 CACCGTGGCCGTGAAATGCTGAAAGAGGGCGCCACGCCAGCAGCACCGCCGCTGAT 2700
QY 2701 gtcgagagctcaagatccctcatctcacatcggaacacacactcaacgtgggtcaacctctcg 2760
Db 2701 GTCGAGGCTCAAGATCTCTCATTTACATTCGGCAACCACTCAACGTGTGTCAACCTCTCGG 2760
QY 2761 ggcgtgcaccacacccgagggccccctcatgttgatctgtagtctctgcaagtacggcaa 2820
Db 2761 GGCGTGCCACCAGCGCCAGGGGCCCTCATGTGTATCTGGAGTTCTGCAAGTACGGCAA 2820
QY 2821 cctctccaaactcttgcgcgcaagcgagcgcttcagccccctgcgcggagaagtclcc 2880
Db 2821 COTCTCCAACCTTTCCTGCGCGCCCAAGCGGAGCGCTTCAAGCCCTGCGCGGAGAAGTCTCC 2880
QY 2881 cgagcagcgagacgttccgcgccatggtgagctcgcaggtcgagctggatcgagagcgcc 2940
Db 2881 CGAGCAGCGCGGACGCTTCCGGGCCATGTTGGAGCTCGCCAGGCTGGATCGGAGCGGCC 2940
QY 2941 ggggagcagcagaggttctcttcgcgcggttctcgaagaccgagggcgagcgagggcg 3000
Db 2941 GGGGAGCAGCGCAGGGTCTCTTCCGCGGTTCTTCGAAGACCCGAGGCGGAGCGAGCGC 3000
QY 3001 ggccttccagaccaagaagctgagacctgtggctgagccccctgacatlggaagatclt 3060
Db 3001 GGCCTTCCAGACCAGAAGCTGAGGACCTGTGGCTGAGCCCCCTGACCATTGAAGATCT 3060
QY 3061 tctctgtacagcttccaggtggccagaggtgagttctctggcttccccgaaagtgc 3120
Db 3061 TGCTGCTACAGCTTCCAGGTGGCGCAGAGGATGAGTTCTTGGCTTCCCGAAAGTGCAT 3120
QY 3121 ccaagagacctggctgctcggaacattctgctgclcgaaagcgagctgggtgaagatctg 3180
Db 3121 CCACAGAGACCTTGGCTGCTCGCAACATTTCTGTGTCGAAAGCGACCTGCTGAAGATCTG 3180
QY 3181 tgacttgaccttgcscgggacatctacaagacctgaclacgtcccgaagggcagtg 3240
Db 3181 TGACTTTGGCTTGGCCGGACATCTACAAGACCCCTGACTACGTCCCGCAAGGCGCAGTGC 3240
QY 3241 ccggtgccccctgaagtggatggccccctgaaagcatcttcgacaagggtgtacaccagca 3300
Db 3241 CCGGCTGCCCTGAAAGTGGATGGCCCTTGAAGCATCTTCGACAAGGTGTACACCAGCA 3300
QY 3301 gagtgaagtgtagtcttgggggtctctctggagatcttctctctgggggcctcccc 3360
Db 3301 GAGTGACGTGTGTCTTGGGGTGTCTCTCTGGAGAGATCTTCTCTCTGGGGCTCCCC 3360
QY 3361 gtacctgggtgagatcaatgaggaatctlgccagcgctgagagcgccacaagat 3420
Db 3361 GTACCCTGGGGTGAGATCAATGAGAGTCTTCCAGCGGCTTGAGAGACGGCACAAGAT 3420
QY 3421 gaggccccgagctggcactccccccatccgcgcacatcgcgcacatclgtgaaactgtgtccgg 3480
Db 3421 GAGGCCCCGGAGCTGGCCACTCCGCCCATACGCCGCATCATGCTGAACCTGCTGTGCCG 3480
QY 3481 agaccccaagcgagacctgcattctcgagctggtagatctctgggggaacctgtctcca 3540
Db 3481 AGACCCCAAGCGAGACCTGCAATTTCTCGAGCTGTGTGAGATCTCTTGGGGACCTCTCTCCA 3540
QY 3541 gggcagggcctcaagaggaagagaggtctgcatggccccgcagctctcagagctc 3600
Db 3541 GGGCAGGGGCTTGCAAGAGGAAGAGGAGGTGTGCATGCCCCCGCGCAGCTCTCTAGAGCTC 3600

|||||
Db 841 CGGGCTAAGTGGGTGCCCGAGCCAGCGTCCACAGACAGACCACACAGAACTTCTCCAGCAT 900
Qy cctgaccaaccacaacylccagccagcacagcctgggctcgtatgtgtcgaagggcraacaa 960
Db CTTGACCATCCACAAAGCTACGCCAGCACAGCTGGCGCTCGTATGTGTGCAAGGCCAACAA 960
Qy rnycatccagcyallccgggagagcacagagtlcatlgtlcatgaaalccctlcalcag 1020
Db CGGCATCCAGCGATTTTCGGGAGAGACCGAGGTCAATTGTGATGAAATCCCTTCATCAG 1020
Qy cttcagylqgcllcaaaagaccatctctggagggccacqccagagacagctlqglqaagct 1080
Db CTTCCAGTGGCTCAANGGACCCATCTCGAGGCCACAGGCCAGAGACGAGCTGGTCAAGCT 1080
Qy rrccllqaaqlqgcagcglacccccccgcgcgaatlccagtlqglacaagqalqaaaggg 1140
Db r'ccctGAAGCTGGCAGCGTACCGCCCGCCGACGTTCAGTGGTACAAAGGATGGAAGGC 1140
Qy actatlcyyggccacagtlccacalgccttqgtlgtcgaagagtlgacagagccaaac 1200
Db ACTTCCGGGGCCACAGATCCACATGCCCTGTGTCTCAAGGAGGTGACAGAGGCGAGCAC 1200
Qy aygcaactacacccctgccttqgtgaactccgctgctgctgagggcaycaucaacagcct 1260
Db AGGCACCTACACCCCTGCCCTGTGGAACCTGCCCTGCTGCGCTGAGGCCUCAACATCAGCCT 1260
Qy gtagctggllqaaatgtgccccccacagatacalqagagagagcctcctcccccaycal 1320
Db GGAGTGGTGGTGAATGTGCCCGCCACAGATACATGAGAAGGAGGCGCTCTCCGCCAGCAT 1320
Qy ctactlcgcgtccacagcccgagccctcaactgcacgucctacgggylgccccgtcct 1380
Db CTACTTCGGCTACACGCCCGCAGGCCCTCACCTGACAGGCCCTACGGGGTGCCTGCTCT 1380
Qy cagcatccagtggcactggcgccctggacacccctgcaagatgtttgcccaycgtagtct 1440
Db CAGCATTCAGTGGCATCGCGGCCCTTGACACACCCTGCAAGATGTTTGGCCAGCGTAGTCT 1440
Qy ccggcgccggcagcagaagacctcatgccacagtlgcctgactgagggcggtaccac 1500
Db CCGGCGCGCGGACAGCAGAACCTCATGCCACAGTGGCGCTGACTGAGGGCGGTGACCAC 1500
Qy cgaggatgccgtgaaccccatlcgagagcctggacaacctggaccaggtlgtlqgauggaaa 1560
Db GCAGGATGCCGTGAACCCCATCGAGCGCTCGACACCTTGACCCGAGTTGTGAGGJAAA 1560
Qy gaataaactcglagcaagctgtgtalcccaaatgccaaactgtctgccaatgtacaagt 1620
Db GAAATGAAGACTGTGAGCAAGCTGGTGTATCCAGAAATGCCAAGCTGTCTGCATGTACAAGTG 1620
Qy tqtggtctccaagaagtggccagatgagcgctcatctactctatglgacacacat 1680
Db TGTGTCTCCAACAAGTGGGCCAGGATGAGCGGCTCATCTACTTCTATGTGACACCACAT 1680
Qy ccccgacggcttcaacatlcaaatccaaagccatccgagagctactagaggccagccggt 1740
Db CCCCAGCGCTTCCATTCGAATCCAGCCATCCGAGGAGCTACTAGAGGCCAGCCGGT 1740
Qy gclctgagctgcgaagccagagctacaagtaagagcatctgagctgggtaccgcctcaa 1800
Db GCTCTGAGCTGCCAAGCCGACAGCTACAAGTACGAGCATCTGCGCTGTGTACCGCCTCAA 1800
Qy cctgtlccacgctgacgatgcgcaaggaacccctctctgctgacttcaagaagcgtqca 1860
Db CTTGTCCAGCTTGCAGATGCGCAGCGGAACCGGCTTCTGCTCGACTGCAAGAAGTGCA 1860
Qy tctgttgcacccctctgycgcgcagccttgagagagtggtgacacctgggcgcgcacgc 1920
Db TCTGTTCGCCACCCCTCTGGCGCCAGCCTTGAGAGGTGGCACCTGGGGCGGCCACGC 1920
Qy cagctcagcctagatatacccccgctgcgcgcagccagcagagggccactatglgtqca 1980
Db |||||

Db 1921 CACGCTCAGCTGAGTATCCCGCGCTGCGCGCCGAGCAGAGGGCCACTATGTGTGCCGA 1980
Qy agtgaagaacggcgcgagccatgacaagcactgccacaagaagtacctgtcggtgaagc 2040
Db AGTCAAGACGGCGCAGCCATGACAAGCATGCGCAAGAAGTACCTGTGTGTCGAGGC 2040
Qy cctgaagccctcgctcagcagaactlgaccgacctcctgctgactgacgtlgaagcagctc 2100
Db CCTGGAAGCCCTCGGCTACGCAGAACTTGACCGACCTCTCTGTTGAACGTGACGACTC 2100
Qy gctgagatcagtlgcttgggtggcgagcgacgcgcccagcaclgltgltggtlacaaga 2160
Db GCTGAGATGCAGTGCTTGTGTGGCGGAGCGACCGCCCGAGCATCTGTGTGTTACAAGA 2160
Qy cgaagagctgctgagagaaaagtctggagtcgacttggcgactlccaaaccagaagctgag 2220
Db CGAGAGCTGCTGGAGGAAAGTCTGGAGTGCAGTTGGCGACTTCCAACCAAGAAAGCTGAG 2220
Qy catcagcggtgcgagagagagatgcggaagcgtalctgtgaagcgtlglgaacgcgcaa 2280
Db CATCCAGCGCTGGCGAGGAGGATGGGGACGCTATCTGTGCAGCGTGTGCAACGCCAA 2280
Qy gggtcggtcaactcctccgcccagcgtggcggtggaaggtccgaggaataagggcagcat 2340
Db GGGCTGCGTCAACTCTCCGCCAGCGTGGCGTGGCAAGGCTCCGAGGATAAGGGCAGCAT 2340
Qy ggagatcgtaactctgtcggtaccggcgtaactgctgtctcttctlgtgggtlccctcct 2400
Db GGAGATCGTATCTTGTGCGTACCGCGCTATCGCTGTCTTCTTCTGGGTCTCTCTCT 2400
Qy cctcatctctgtaaactgagagcgccgcccagcagacataagcgaggtacctgtc 2460
Db CCTCATCTTCTGTAACTAGGAGCGCGGCCACCGACATCAAGACGGCTACCTGTCT 2460
Qy catcatcatggacccccgggaggtgctctctggaggaacaaatgcgaaatctctgtcctacga 2520
Db CATCATGACGCCCGGGAGTGCCTCTGCAAGGCAATGCGAATACCTGTCTCTACGA 2520
Qy tgcagcagtggaatctcccccgagagcggtcgaactgggagagactgctcggactcag 2580
Db TGCCAGCGAGTGGGAAATTCCTCCCGAGAGCGGCTGCACCTGGGGAGAGTGTCTGGCTACGG 2580
Qy cgctctggggaagtgggtggaagcctcgcttctgggcatccacaagggcagcagctgta 2640
Db CGCCTTCGGGAAGTGGTGGAAAGCTTCGCTTTCGGCATCCACAAGGGCAGCAGCTGTGA 2640
Qy caccgtggcggtgaaatgctgaaagggcgccacggcgagcgagcagcagcgcgctgat 2700
Db CACGCTGGCGGTGAAATGCTGAAAGAGGGCGCCACGGCCAGCGAGGACCCCGCGCTGAT 2700
Qy gtcgagctcaagatcctcatcacatcggcaaccactcaactggtcaacctcctcgg 2760
Db GTCGGAGCTCAAGATCTCTATTCATCTGGCAACCACTCAACGTGTGTCACCTCTCTCGG 2760
Qy ggctgtcaccaagcgagggccccctcatggtgactggtgagttctgcaagtacggcaa 2820
Db GGCGTGCAACCAAGCGCAGGGCCCCCTCATGTGTGATCTGTGAGTTCGTCAAGTACGGCAA 2820
Qy cctctcaactcctcgcgccaaagcgagccttcagccccctgcgcgagagaagttctcc 2880
Db CCTCTCAACTTCTTGGCGCGCAAGCGGAGCGCTTTCAGCCCCCTGCGCGGAGAAAGTCTCC 2880
Qy cgaagcagcgagccttccgcccattggtgagctccagctcgcagagctgdatcggagcgagcc 2940
Db CGAGCAGCGGAGCGCTTTCGCGGCCATGTTGGAGCTCGCCAGGCTGGATCGAGAGCGGCC 2940
Qy ggggagcagcagaggtctcttcgcgcgcttctcgaagcagcgagggcgagcgagcg 3000
Db GGGGAGCAGCAGAGGTCTCTTTCGCGCGCTTCTTCCGAAGACCGAGGGCGGAGCGGCG 3000
Qy ggtcttccagaccagaagctgagggacctgtggtcagccccctgacctggaagatct 3060
Db GGCTTCTCCAGACCAAGAAGCTGAGGACCTGTGGCTGAGCCCGCTGACCATGGAAGATCT 3060

Db 2461 CATCATATGAGCCCGGAGAGTGGCTCTGGAGGAGCAATGCCAATACCTGTCTCCACGA 2520
Qy 2521 tgcacgcagctggaatctcccccagagcggctgacccctggggagagtgcttcgggtacag 2580
Db 2521 TGGCAGCCAGTGGGAATCTCCCGCGAGAGCGGCTGGACCTGGGGAGAGTCTCGGCTACGG 2580
Qy 2581 cggctctgggdaaqtgggtgaagcctcctgcctcttcgcatcacaaagggcagcagctgtga 2640
Db 2581 CGGCTTCCGGGAGAGTGTGTAAGCCTCCGCTTTCCGGCATCCACAAGGGCAGCAGCTGTGA 2640
Qy 2641 caccgtggcgtgaaatcctgaaaggggcacgcggcagcagcagcagcagcagcagcagcagc 2700
Db 2641 CACCGTGGCCGTGAATGCTGAAGAGGGCGCCAGCGCCAGCGAGCGAGCGCGCGCTGAT 2700
Qy 2701 qtcqquctcaagatctcctacatcggcaaccacccctcaacgttggtcaacrcctctcag 2760
Db 2701 GTCGAGCTCAAGATCTTCATTCACATCGCGCAACCACCTCAACGTGGTCAACCTCTCTCG 2760
Qy 2761 qccqfgraccaagccgagggccctcctcatggtgagtcgtgagctctctcaaatcagcga 2820
Db 2761 GGGCTGCTACCAACGCGCAGGGCGCCCTCATTTGCTGATCTGTGAGCTTCTGCAAGTACGGCA 2820
Qy 2821 cctctcraactctctcgcgcgcgaagcggacgccttcaacccctcgcgcgaagaatctcc 2880
Db 2821 CCTCTCCAGCTTCTGCGCGCTCAAGCGGAGCGGCTTTCAGCCCTTGCCTGGAGAGTCTCC 2880
Qy 2881 caagcaacgcgcgcctctcgcgcgaagcggagctcggagctcggagctcggagctcggagct 2940
Db 2881 CGAGCAGCGCGAGCTTCTCGCGCCATGCTGTGAGCTCGCCAGCTGGATCGAGCGGCC 2940
Qy 2941 qgggagcagcagaggtctctctcgcgcggttctcgaagaccgagcggagcggagcggag 3000
Db 2941 GGGGAGCAGCGAGAGGTCTCTTTCCGCGCTTCTCGAGACCCAGCGCGAGTCGAGGGCG 3000
Qy 3001 ggcctctcagaccaaagcctgaagacctctgctgagccctgaacatgaaatct 3060
Db 3001 GGCTTCTCCAGACCAAGAGCTGAGGACCTGTGGCTGAGCCCTGACCATGGAAGATCT 3060
Qy 3061 lqctctacagctctcagctggcgcagagagatggagctctcagctctcgcgaagctgcat 3120
Db 3061 TGCTCTGTCTACAGCTTCCAGGTGCCAGAGGATGGAGTTCTCGCTTCCGGAAGTGCAT 3120
Qy 3121 crucagagacctggctgctcgggaacatctctgctcggaaagcagcgtggtgaagatctg 3180
Db 3121 CCACAGAGACTTGGCTGCTCGGAACATTTCTGCTGCGGAAGGAGCTGTGTAAGATCTG 3180
Qy 3181 tgaclttggccttgcccgggacatctacaaagccctgaactacgtccgcaagcagctgc 3240
Db 3181 TGACTTTGGCTTTGCCCGGACATCTACAAAGACCTGACTACTCTCGCAAGGGCAGTGC 3240
Qy 3241 ccggctgcccctgaagtggatggccctgaaagcatcttcgacaagatgttacacacgca 3300
Db 3241 CCGGCTGCCCTCAAGTGGATGGCCCTGAAAGCATCTTCGACAAGGTGTACACCACGA 3300
Qy 3301 gautgagctgctctcttggtgctctctgagagatctctctgagggcctccc 3360
Db 3301 GAGTGAAGCTGTGGTCTTTGGGGTGCTTCTCTGGGAGATCTTCTCTCTGGGGCTCCCC 3360
Qy 3361 gtaccctgggtgcagatcaatgagagttcttcgagcggctgagagcggcacaagat 3420
Db 3361 GTACCCTGGGTGCAGATCAATCAGGAGTTCTGCCAGCGCTCAGAGCGGCACAAGGAT 3420
Qy 3421 gaggggcccgagctggccactcccgccaacgcgcgcgaatctgctgaactgctggctcgg 3480
Db 3421 CAGGGCCCGGAGCTGGCCACTCCCGCCATACCGCCCATCATGCTCAACTGCTGGTCCGG 3480
Qy 3481 agaccacaagcagacacctcatctcggagctggggagatctctggggacacctgtcca 3540
Db 3481 AGACCCCAAGCGAGACCTGCATTTCTCGGAGCTGGTGGAGATCTTGGGGACCTGCTCCA 3540
Qy 3511 ggcgcagggcctcgaagagagagagatctcagatggcccgccgcagctctcaagctc 3600

Db 3541 GGGCAGGGGCCCTGCAAGAGGAAGAGAGGCTTGCATGGCCCCCGCCAGCTCTCAGAGCTC 3600
Qy 3601 aagaagggcagctctcgcaggtgtccaccatggccctacacatcgcccaggtcgacgc 3660
Db 3601 AGAAGAGGGCAGCTTCTCGCAGGTGTCCACCATGGCCCTACACATCGCCAGGCTGACGC 3660
Qy 3661 tgagagacccgcgaagcctgcagcgcacacagcctggcccgaggtattacaactgggt 3720
Db 3661 TGAGGACAGCCGCCAAGCTTCAGCGCCACAGCCTTGGCCCGCAGGTATTACAAGTGGGT 3720
Qy 3721 gtccttcccgagtgctcgcagaggggctgagaccgtggttctcctcagatgaagac 3780
Db 3721 GTCTTTCCGGGTGCTGCGCCAGAGGGGCTGAGACCCGTGGTTCTTCAGGATGAAGAC 3780
Qy 3781 attgagggaattcccccatgaccccaacgacctacaaaggctctgtggcaaccagacaga 3840
Db 3781 ATTTGAGGAATTTCCCCATGACCCCAACGACCTACAAAGGCTCTGTGGACAACACAGAGA 3840
Qy 3841 cagtgagatggctgctggcctcgaggagtttgagcagatagagagcagcagcatagacaaga 3900
Db 3841 CAGTGGGATGGTGTGGCTTCGGAGGAGTTTGAGCAGATAGAGAGCAGCATAGACAAGA 3900
Qy 3901 aagcggttcag 3912
Db 3901 AAGCGGCTTCAG 3912

RESULT 5
US-08-795-430-1
; Sequence 1, Application US/08795430
; Patent No. 6130071
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; APPLICANT: Joukov, Vladimir
; TITLE OF INVENTION: Vascular Endothelial Growth Factor C (VEGF-C)
; TITLE OF INVENTION: Protein and Gene, Mutants Thereof, and Uses Thereof
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,430
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FI96/00427
; FILING DATE: 01-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/671,573
; FILING DATE: 28-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/601,132
; FILING DATE: 14-FEB-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/585,895
; FILING DATE: 12-JAN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/510,133
; FILING DATE: 01-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/340,011
; FILING DATE: 14-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Gass, David A.

QY 1441 ccqgqgcygcaqcaagacctcatgccacagtgccgtlaactlgaaggcgglgaccac 1500
DB 1452 CCGCGCGGGCAGCAGCAAGACCTCATGCCACAGTCCCGTACTGAGAGGGCGGTACACAC 1511
QY 1501 gcagagatgccgtgaaccaccaatcgagagcctggacacctggaccaggttctggyaggga 1560
DB 1512 GCAGGATGCCGTGAACCCCATCGAGAGCTTGACACACCTGGACCGAGTTTGTGGAGGAAA 1571
QY 1561 gaataagactgtgaqcaagcttggtgatccaaatgccaacgtgtctgccatgtaacaagt 1620
DB 1572 GAATAAGACTGTGACCAAGCTTGGTATCCAAATGCCAAACCTGTCTGCCATGTACAAGTG 1631
QY 1621 tgtgtlctccaacaagggtggccaggatgagcgctcatctacttctatgtatgtacacacat 1680
DB 1642 TGTGTCTCCAAACAGGTGGCCAGGATGACGGCTCATCTTCTATGTGACCACTAT 1691
QY 1681 ccccaqaygcttlcaccatlcgaatccaagccatccgagagatctatagaggccagccggt 1740
DB 1692 CCCCCAGCGGCTTCACCATTCGAATGCCAAGCCATCCGAGGAGCTACTAGAGGGCCAGCCGT 1751
QY 1741 gctcttgaqcltqccaagccagactacaagtacgagcatctgcgcttggtaccgctcaa 1800
DB 1752 GCTCTGAGCTGCCAAGCCGACACTACAAGTACGAGCATCTGCCCTGGTACCCTCCAA 1811
QY 1801 cctlgccaacqclgacacgatgacgacgggaaccccgcttctgtctgacLgcaaaacqLqca 1860
DB 1812 CTTCTCCACCTGTCACAGTGCACATGCCACCGGMACCCTCTTCTGCTCAGCTCCAAAGACGTGCA 1871
QY 1861 tctgttcgcacacccctctggccgcagaccttgagagagtggtggaacctggcgqgcccacgc 1920
DB 1872 TCTGTTCGCCACCCCTCTGGCCGCCACGCTTGGAGGAGTGGCACCTGGGGCGTGCACGC 1931
QY 1921 cactgcagcctgagtalcccccgctgcgqcccgagcacgagggccactatgtgtcga 1980
DB 1932 CACGCTCAGCCTGAGTATCCCGCGCTCGCGCCGACGACGAGGGGCCACTATGTGTCGA 1991
QY 1981 agtcaagacccgcgaagccatgaacaagcactgccaagaagtacctgtcgtgycaggc 2040
DB 1992 AGTCAAGACCCGCGCAGCCATGACAAGCACATGCCACAAGAAGTATCTGCTGGTGCAGGC 2051
QY 2041 cctggaagccctcgggtcaacgagaactlgaccagacctccttgtgaactgagcagactc 2100
DB 2052 CTTGGAAGCCCTCGCGCTACGCAAGACTTTCACCGACCTCTGCTGTAACCTGAGCGACTC 2111
QY 2101 gctgaagatgcagtgtctgtgtgcccgaagcgcgcagcccgacatcgtgtgtacaaga 2160
DB 2112 GCTGGAGATGCAGTGTGTGTGGCCGAGCGCACCGCCCGCAGCATCTGTGTGGTACAAAGA 2171
QY 2161 cgaagctctgtgagaaagLctgagatcgacttgcggaactcaaaccaagactgaag 2220
DB 2172 CGAGAGCTCTGGAGGAAGTCTGGAGTTCGACTTGGCGGACTTCCAAACGAGAAGCTGAG 2231
QY 2221 catcagcgcgtgcgagagagatgcggagcgtatctgtgcagcgtgtgcaacqcaa 2280
DB 2232 CATCACGCGCTGCGCGAGGAGGATGCGGACGCTATCTGTGACGCTGTGCAACGCTCAA 2291
QY 2281 gggctgcgtcaactctcgcgcagcgttgccgttggaaggtccgagataagggcagcat 2340
DB 2292 GGGCTGCGTCAACTCTCTCCGCCACGCGTGGCGGTGGAGGTCCGAGGATAAAGCCAGCAT 2351
QY 2341 ggaatcgatcatcttgtcggtaccggcgtcatcgctgtctctctgtgggtctctctct 2400
DB 2352 GGAGATCGTGATCTTGTCTGGTACCGCGCTCATCGCTGTCTTCTTCTGGGTCTCTCTCT 2411
QY 2401 cctcatcttctgaacatgaggaggcggccacgcagacatacaagacgggtacctgtctc 2460
DB 2412 CCTCATCTTCTGAACATGAGAGGCGCGCCACGACAGCATCAAGACGGGCTTACCTGTC 2471
QY 2461 catcataaggaccccgggaggtgctcttgaggagcaatgcgaatacctgtctctacga 2520
DB 2472 CATCATCATGACCCCGGAGGTGCTCTTGAGGAGCAATCGGAATACCTGTCTCTACGA 2531
QY 2531 tgcacqacagtggaattcccccgagagcggtgcacctggaccctgggagagtgctcqqctarq 2580

DB 2532 TGCCAGGACAGTGGAAATTCCTCCCGAGAGCGGCTGCACCTGGGGAGAGTGTCTCGGCTACGG 2591
QY 2581 cgccttcgggaaggtggtgaaagcctcgccttctcggcataccacaagggcagcagctgtga 2640
DB 2592 CGCCTTCGGGAAGGTGGTGGNAGCTCCGCTTTCGGGATCCACANAAGGGCAGCAGCTGTGA 2651
QY 2641 caccgtgcccgtgaaatgtctgaaagggcgccacggccagcgagcaccgcgcgtgcat 2700
DB 2652 CACGCTGGCGCTGAAAATGTCTGAAAGAGGGCGCCACGCCAGCAGCAGCCGCGCTGTAT 2711
QY 2701 gtcgagactcaagatcctcatcacatcgcaaacaccactcaacgtgtglaaacclctcgg 2760
DB 2712 GTCGAGCTCAAGATCCTCATTTACATCGGCAACCACTCAACGTGGTGTCAACCTCTCTCG 2771
QY 2761 ggcgtgcaccaagcgcgagggccccctcatlggtgaatcggtgagtlctlycaagLacgycaa 2820
DB 2772 GGCGTGCACCAAGCCGAGGGCCCCCTTCATGGTTCATGCTGAGTTCCTGCAAGTACGGCAA 2831
QY 2821 cctctcaaatctcctgcgcgcgaagcgagcgctctcaagccccctgcygagagaaagLctcc 2880
DB 2832 CTTCTCCAAGTTCTTCGCGGCCAAGCGGGACGCTTTCAGCCCCCTGCGCGAGAGTCTCC 2891
QY 2881 cgagcagcgcgagccttccgcgccatggtgagctcgcagagcttgatcggagggcgcc 2940
DB 2892 CGAGCAGCGGAGCTTCCGCCCATGTGTGGAGCTCGCCAGGCTGGATCGGAGGGCGCC 2951
QY 2941 ggggagcagcagaggtcctcttcgcgcgttctcgaaagccgagggcgagcgagcgagcg 3000
DB 2952 GGGGAGCAGGCACAGGTCTCTTTCGCGCGTTCCTGCAAGACCGAGGGCGACGAGGCG 3011
QY 3001 ggccttctcaagacaaagaagctgagagcctgtggtcgagcccgctgacacatggaagatct 3060
DB 3012 GGCCTTCTCCAGACAAGAGCTGAGGACCTGTGGCTTGAGCCCCCTGACCATGGAAGATCT 3071
QY 3061 tgtctctacagcttccaggtggccagaggaLggagttctctgagcttcccgaagLgcat 3120
DB 3072 TGTCTGCTACAGCTTCAGGTGGCCAGAGGGATGGAGTTCTTGGCTTCCGAAAGTGCAT 3131
QY 3121 ccaagagacctggctgctcggaacatctgtctgtcggaagcgagcgtgggtgaagatLctg 3180
DB 3132 CCACAGAGACCTGGCTGCTCGGAACATTTCTGCTGCGAAAGCAGCTGTGTAAGATCTG 3191
QY 3181 tgacttggccttgcccgggacatctacaagaacctgactcgtccgcaagggcgagtc 3240
DB 3192 TGACTTTGGCTTGCCCGGACATCTACAAAGACCTGACTACTGCCGCAAGGGCAGTGC 3251
QY 3241 ccgctgccccctgaagtggatggccccctgaaagcatcttcgaaggtgtacaccacgca 3300
DB 3252 CCGCTTGCCCTCAAGTGGATGCCCTCGAAAGCATCTTCGACAAAGGTCTACACACGCA 3311
QY 3301 gagtgaagtggttgccttgggggtgcttctctgggagatcttctctctgggggctctccc 3360
DB 3312 GAGTGACGTGTGTGCTCTTTGGGTGCTTCTCTGGGAGATCTTCTCTCTGGGGCTCTCC 3371
QY 3361 gLaccctgggtgcaagatcaatgagaggtcttcgcagcggtgagagagcgacaaagat 3420
DB 3372 GTACCTCTGGGTGCAGATCAATGAGAGTTCGCCACGGCTGAGAGACGGCACAAAGAT 3431
QY 3421 gaggcccccgagctggccactccccgcaatacgccgcatctatgtaactgtgtgtccgg 3480
DB 3432 GAGGGCCCCGAGCTGGCCACTCCCGCATACGCCCATCTGCTGAACTGTGTGTCTCC 3491
QY 3481 aqaccccaagcgagacctgcatctcgaggtggtgagatLccttgggggaacctgtctcca 3540
DB 3492 AGACCCCAAGCGAGACCTTGCAATTCGAGAGTGGTGGAGATCTCTGGGGACTCTCTCCA 3551
QY 3541 gggcggggcttcgaagaggaagaggtctgtcatgcccccgccagcactctcagagctc 3600
DB 3552 GGGCAGGGCCCTGCAAGAGGAAGAGAGGTCTGCAATGGCCCCCGCGCAGCTCTCTCAGAGCTC 3611
QY 3601 agaagaggcgagcttctcgaggtgtccaccatggccctacacatcgcgccaggtcgagc 3660

[illegible]

```

RESULT      7
PCT-US95-04228-31
: Sequence 31, Application PC/TUS9504228
: GENERAL INFORMATION:
: APPLICANT: Genentech, Inc.
: APPLICANT: Bennett, Brian D.
: APPLICANT: Goeddel, David
: APPLICANT: Lee, James M.
: APPLICANT: Matthews, William
: APPLICANT: Tsai, Siao Ping
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: PROTEIN TYROSINE KINASE ACONIST ANTIODIES
: NUMBER OF SEQUENCES: 45
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 460 Point San Bruno Blvd
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: patin (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US95/04228
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/222616
: FILING DATE: 04-APR-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Wendy M. Lee
: REGISTRATION NUMBER: 00,000
: REFERENCE/DOCKET NUMBER: 821P3PCT
: TELEPHONE: 415/225-1994
: TELEFAX: 415/952-9881
: TELEX: 910/371-7168
: INFORMATION FOR SEQ ID NO: 31:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 4425 bases
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: PCT-US95-04228-31

```

Query Match 95.2%; Score 3912; DB 5; Length 4425;

QY 661 cttcccttccaaaccccttctggtgcacatcacaggcaacgagctctatgacatccagct 720
|||||
Db 1604 CTTCTTTTCCAAACCCCTTCTGTGTGCACATCACAGCAACGAGCTCTATGACATCAAGCT 1663

QY 721 gttgccagaagtgctgagctgctggtgtaggggagaaagctggctcctgaaactgcacagct 780
|||||
Db 1664 GTTGCCACGAAAGTCGCTGCAGCTGCTGTGTACGGGAGAACTGGTCTGAACCTGCACCGT 1723

QY 781 gtagggctgaagtttaactcaagtggtcucctlltgactggagactcccagggaagcagaga 840
|||||
Db 1724 GTGGGCTGAGTTTAACTCAAGGTGTACCTTTTACCTTGTGACCTACCCAGGGGAAGCAGGCAGA 1783

QY 841 gcuqggtaagtggggtgcctcagcagctccccagcagjactcacacagaactcctccagat 900
|||||
Db 1784 GCGGGGTAAAGTGGGTGCCCGACGAGCTCCACGACAGCCACACAGAACTCTCCAGGAT 1843

QY 901 rrtgacratccacaacgctcagcagcaagcctgggctcctatgtgtcgaauqccaaaca 960
|||||
Db 1844 CTTGACCATCCACAACGCTCAGCCAGCAGACCTGGGCTCGTATGTGTGCAAGGCCAACAA 1903

QY 961 cuqcatccagcagatttcagggaagcagcagagctcaattgtgcatgaaaaatccctlculcaq 1020
|||||
Db 1904 CCGCATCCACCGATTTCCGGAGAGCAGCCAGGCTGTGATGTGCAATGCAATTCCTTCATCAG 1963

QY 1021 cgtcagtggtctcaaggaacccatccttgaaqccacgagagcagagcagclggtgaagct 1080
|||||
Db 1964 CCTCGAGTGGCTCAAGGACCCATCTCGAGGCCACGCGAGGAGCAGAGCTGGTGAAGCT 2023

QY 1081 gccgtgaaagctggcagcgtaccccccccccagcttccagtggtacaaggatgaaagc 1140
|||||
Db 2024 GCCCGTGAAGCTGGGAGGCTAGCCCCCCCCAGTTCCAGTGGTACAAGGATGGAAGGC 2083

QY 1141 actgcccgggcagcagctcacatgcctcgtggtcctaagagagtgacagagccagcac 1200
|||||
Db 2084 ACTGTCCGGGCCACACATGCTCACAATGCCCCCTGTGCTCAAGAGAGGTGACAGAGGCGCAGCAC 2143

QY 1201 aggcacctlacacctcgcctctggaactccqclgctggcctgagggcgaacatcagcct 1260
|||||
Db 2144 AGGCACCTTACACCCCTCGCCCTGTGGAACCTCGCTGCTGGCCGTGAGGCGCAACATCAGGCT 2203

QY 1261 gtagctggtggtgtaagtgcctcccccagatatatgaaagagagcctcctccccagcat 1320
|||||
Db 2204 GGAGCTGTGTGTGAATGTGCCCCCCCCAGATACATCAGAAGAGGCTCTCTCCCCACAGCAT 2263

QY 1321 ctactccgtgcacagccagcagcctcaactgcagcctcagcgtctacugggtgcccctgacctct 1380
|||||
Db 2264 CTACTCGCTCAGACCCGCCAGGCCCTCACCCTGCACGGGCTTACCGGGGTGCCCCCTGCCCTCT 2323

QY 1381 cagcatccagtggcactggcgcctggacacccctgcaagatgtttgcccagcgtagtct 1440
|||||
Db 2324 CAGCATCCAGTGGACATGGCGGCCCTGGACACCCCTTGCAAGATGTTTGCCACAGCTAGTCT 2383

QY 1441 ccggcggcggcagcagaagacctcatgcaacagtgcctgactggaggggcgtgacccac 1500
|||||
Db 2384 CCGCGGGGGCAGCAGCAAGACCTCATGCCACAGTGGCGGTGACTGGAGGGCGGTGACCCAC 2443

QY 1501 gcaggaatgcctgaaccccatcggagagcctggacacctgacccagttctgcccattgacaagtq 1560
|||||
Db 2444 GCAGGATGCCGTGAACCCATCGAGAGCCTGGACACCTTGACCCAGTGTGTGGAGGGAAA 2503

QY 1561 gaataagactgtgagcaagctggtgatccagaatgccaaagctgctgcccattgacaagtq 1620
|||||
Db 2504 GAATAAGACTGTGAGCAAGCTGGTGATCCAGATGCCAACGCTGCTGCCATGTACAACTG 2563

QY 1621 tgtggttccaaagagtgggcagaagtgagcggcctacttacttctatgtgaccacct 1680
|||||
Db 2564 TGTGGTCTCCAACAAGGTGGGCCAGGATGAGCGGCTCATCTACTTCTATGTGACCCACAT 2623

QY 1681 cccgcagcgtcttaccatcgaaatccagccatccgaggaactactagagggccagccggt 1740
|||||
Db 2624 CCCCAGCGGCTTACCATTCAATCCAACCCATCCGAGGAGCTACTCAGAGGGCCAGCCGCT 2683

QY 1741 gctcctgagctgccagccgacagctlacaagtacgagcactcgtgcgtggtaaccgcctlcaa 1800
|||||

Db 2684 GCTCTGAGCTGCCAAGCCGACAGCTACAAGTACGAGCATCTGCCTGCTACCGCCTCAA 2743

QY 1801 cctgtccacgctgcacagatgcacgaggaacccgcttctgctcagctgcaagaacgctgca 1860
|||||
Db 2744 CCTGTCCACGCTGCAAGATGCGCACGGGAACCCGCTTCTGCTCAGCTGCAAGAAGCTGCA 2803

QY 1861 tctgttcgcaacccctctggccgacgctgagagagtggtgacacctggggcgccacgc 1920
|||||
Db 2804 TCTGTTCCCCACCCCTCTGGCCGCGCAGCTGGAGAGGTGGCACCCTGGGGCGCCGACGC 2863

QY 1921 cagcgtcaagctgagatctccccccgctgcgcccagcagcagagggccactatgctgtcgca 1980
|||||
Db 2864 CACGCTCAAGCTGAGTATTCCTCCCGCTGCGCCGCGAGCACGAGGGCCCACTATGTGTGCGA 2923

QY 1981 agtgcaagaccgcgagcagcctgacaagcactgccaagaagtacacttgtcgtgctgcaaggc 2040
|||||
Db 2924 AGTGCAAGACCGCGCACCCATGACAAGACTGCCACAAGAAGTACCTGTGCGGTGACAGC 2983

QY 2041 cctggaagccctcggtctcacgcagaacttgaccgacctcctcgtgtaacgtgagcagctc 2100
|||||
Db 2984 CCTGGAAGCCCTCGGCTCACCGCAGAACTTGACCCGACCTCTCTGCTGAACGTGACGGACTC 3043

QY 2101 gctggagatgcagtgcttggtggtggtggtggtggtggtggtggtggtggtggtggtggt 2160
|||||
Db 3044 GCTGGAGATGCAGTGTCTGTGTGGCCGGAGCGCACGCGCCAGCATCGTGTGTTACAAAGA 3103

QY 2161 cgagagcgtcgtgaggaagctctgagtcgagtcgacttgagcagctcctcagcagagctgag 2220
|||||
Db 3104 CGAGAGCTGCTGGAGGANAAGTCTGGAGTGCAGTTGGCGACTCCCAACAGAAAGCTGAG 3163

QY 2221 catccagcgtgctgagagaggaatgcgggaacgctactctgtgagcgtgctgcaacgcaaa 2280
|||||
Db 3164 CATCCAGCGCTGCGCGAGGAGGATCGGGAGGCTATCTGTGACGCTGTGCAACGCCAA 3223

QY 2281 ggggtggtcactcctccgcccagctggtggtggtggtggtggtggtggtggtggtggtggt 2340
|||||
Db 3224 GGGTGGGTCAACTCTCCGCCAGCGTGGCGTGGAAAGGCTCCGAGGATTAAGGGCAGCAT 3283

QY 2341 ggagatcgtgactcctcgtggtaccggcgtcactcgtcgtcgtcgtcgtcgtcgtcgtcgtc 2400
|||||
Db 3284 GGAGATCGTGCATCTTGTGCGGTACCGGCGTCTATCGCTGTCTTCTTCTGGGTCTCTCTCT 3343

QY 2401 cctcatctctgtaactgagggagcggcccgacgagacatcaagacgggctacctgtc 2460
|||||
Db 3344 CCTCATCTTCTGTAACATGAGGAGCGCGCCACGACAGATCAAGACGGCTTACCTGTCT 3403

QY 2461 catcatcatgaccccgaggagtgctcctctgaggaggacaaatgcgaataactcgttctacga 2520
|||||
Db 3404 CATCATCATGGACCCCGGGAGGTGGCTCTGGAGGAGCAATGCGAATACCTGTCTCTACGA 3463

QY 2521 tgcagccagtgggaaattccccccgagagcggctgcacctggggagagtgctcgggctacgg 2580
|||||
Db 3464 TGCCAGCCAGTGGGAATTTCCCCCGAGAGCGGCTGCACTGGGGAGAGTGTCTGGCTACGG 3523

QY 2581 cgcttcgggaaagtggtggaagcctccgcttctgcaatccacaaggcagcagctgctga 2640
|||||
Db 3524 CGCCTTTCGGGAAGTGGTGGAAAGCTCCGCTTTTCGGCATCCACAAGGGCAGCAGCTGTGA 3583

QY 2641 caccgtggccgtgaaagtctgaaagaggcgccacggccagcagcagcagcagcagcagcagc 2700
|||||
Db 3584 CACCGTGGCGGTGAANAATGCTGAAGAGGGCGCCACGGCCAGCGAGCACCGCGCGCTGAT 3643

QY 2701 gtcggagctcaagatcctcatctcaatcggaacacctcaagctggttcaactcctcgtg 2760
|||||
Db 3644 GTCGGAGCTCAAGATCCTTATTCATCGCGCAACCACTCAACAGTGGTGTCAACTCTCTCGG 3703

QY 2761 ggcgtgaccaaagcagcagggccccctcatggtgtagctgtggagttctgcaagtacggcaaa 2820
|||||
Db 3704 GCGCTGCACAAAGCCGACGGGCCCTCATGTGTGTCGTGGAGTCTTCGAAGTACGGGCAA 3763

QY 2821 cctctccaaactcctcgtgcgcgaagcgggagccttccagccctcgtgcggagaaagtctcct 2880
|||||

Db 3764 CTCTCTCCAACTTTCCTGCGCGCCAAAGCGGACGCCCTTCAGCCCCCTGCGCGGAGAAAGTCTCC 3823
Qy cgagcagcgcgagcgtctccgcgcgcctgtagagctcagcaggtgtagtcygaagcgccgc 2940
Db 3824 CCAGCAGCGCGGACCGCTTCCGCGCCCATGCTGAGCTCGCCAGGCTGATCGGAGGCGGCC 3883
Qy 2941 ggggagcagcgacaggggtctctcttcgcgcgcgttctcgaagaccgagggcgagcgagcg 3000
Db 3884 GGGGAGCAGCGACAGGGTCTCTTCGCGCGCTTCTCGAAGACCCGAGGCGCGGAGCGG 3943
Qy 3001 ggcctctcagaacaaagcgtgaggaacctggtgtagcagcccgtagccatggaagatct 3060
Db 3944 GGTCTCTCAGACCAAGAAGCTGAGGACCTGTGGCTGAGCGCGCTGACCATGGAAGATCT 4003
Qy 3061 tgcctgctacagcttccagggtggccagaggtgaggttccctgcttcccgaaagtgc 3120
Db 4004 TGTCTGCTACAGCTTCCAGGTGGCCAGAGGATGGAGTCTCTGCTTCCCGAAGTGCAT 4063
Qy 3121 ccacagagacctggctgctcggaacattctgctcggaaagcgactgtagaatctg 3180
Db 4064 CCACAGAGACCTGGCTGCTCGGAACATTCGTCTCGAAAGCGACGCTGCTGAAGATCTG 4123
Qy 3181 tgactttggccttgcgcgggacattctcaaaagaccctgactagctccgcaaggcgagtc 3240
Db 4124 TGACTTTGGCCTTCCCGGGACATCTACAAAGACCTTGACTAGCTCCGCAAGGCGAGTGC 4183
Qy 3241 ccgctgccccctgaagtgaatggccccctgaaagcatcttcgacaaggtgtacaccacgca 3300
Db 4184 CCGCGTGGCCCCTGAGTGGATGGGCCCTGAAAGCATCTTCGACAAGGTGTACACCAGCA 4243
Qy 3301 gagtgacgtggtgcttgggtgcttctctctgggaagattctctctgggggcctccccc 3360
Db 4244 CAGTGACGTGTGGTCTTTGGGGTGCTTCTCTGGGAGATCTTCTCTGGGGGCCCTCCCC 4303
Qy 3361 glaccctgggtgtagatcaatgaggagttctccagcggtgtagagacggcacaaggat 3420
Db 4304 GTACCTGGGTGTCAGATCAATGAGGAGTCTTCCAGCGGCTGAGAGCGGCACAGGAT 4363
Qy 3421 gagggccccagagctgccactccgcgcatacgcgcacatcgtgaactgctggtccgg 3480
Db 4364 CAGGCCCCGGAGCTGGCCACTCCCGCCATACGCCGCATCATCTGAACCTGCTGTGGTCCGG 4423
Qy 3481 agaccccaaggcgagactgctattctcggagctgggtggaagatcctgggacctgctcca 3540
Db 4424 ACACCCCAAGCGAGACCTGCATTCTCGGAGCTGGTGAGATCCTGGGGACCTGCTCCA 4483
Qy 3541 gggcaggggctgcaagagaaagagggctgcatggcccccgagctctcagagctc 3600
Db 4484 GGGCAGGGGCTGCAAGAGGAAGAGGAGGTCTGCATGGCCCCCGCAGCTCTCAGAGCTC 4543
Qy 3601 agaagagggcagcttctcgcaggtgtccaccatggccctacacatcgcccaaggctgagcg 3660
Db 4544 AGAAGAGGGCAGCTTCTCGCAGGTGTCCACCATGGCCCTTACATCGCCCGAGGCTGACGC 4603
Qy 3661 tgaggacagcccgccagcgtcagcgccacagcctggcgccaggtattacaactgggt 3720
Db 4604 TGAGGACAGCCCGCAAGCCTGCAGCGCCACACGCTGGCGCCAGGTATTACAATGGGT 4663
Qy 3721 gtcctttcccggtgctggcgcaagagggctgagacccctgggttctccaggtatgaagac 3780
Db 4664 GTCTTTTCCCGGGTGCTGGCCAGAGGGGCTGAGACCCCTGGTGTCTCTCCAGGATGAAGAC 4723
Qy 3781 atttgaggaattccccatgaccccaacgacctacaaggctgtgtggaaccaagacaga 3840
Db 4724 ATTTGAGGAATTCCTCATGACCCCAACGACCTACAAGGCTCTGTGGACAAACGACAGA 4783
Qy 3841 cagtgggattggtgctggcctcgagaggttttagcagatagagacgagcatagacaaga 3900
Db 4784 CAGTGGGATGCTGCTGGCCTCGGAGGAGTTTGAGCAGATAGAGACGACGCATAGACAAGA 4843
Qy 3901 aagcggtctcag 3912
Db 4844 AAGCGGCTTCAG 4855

RESULT 9

US-08-222-616-17/c
: Sequence 17, Application US/08222616
: Patent No. 5635177
: GENERAL INFORMATION:
: APPLICANT: Bennett, Brian D.
: APPLICANT: Goeddel, David
: APPLICANT: Lee, James M.
: APPLICANT: Matthews, William
: APPLICANT: Tsai, Siao ping
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST
: TITLE OF INVENTION: ANTIBODIES
: NUMBER OF SEQUENCES: 42
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 460 Point San Bruno Blvd
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: patin (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/222.616
: FILING DATE: 4-APR-1994
: CLASSIFICATION: 530
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/US93/00586
: FILING DATE: 22-JAN-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/826935
: FILING DATE: 22-JAN-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: Lee, Wendy M.
: REGISTRATION NUMBER:
: REFERENCE/DOCKET NUMBER: 821P2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415/225-1994
: TELEFAX: 415/952-9881
: TELEX: 910/371-7168
: INFORMATION FOR SEQ ID NO: 17:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 6827 bases
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: US-08-222-616-17

Query Match 23.1%; Score 950; DB 1; Length 6827;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1000; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2869 ggagaaatctccgagcagcgagcagcgttccgcgcacatggtgagctcgcagcgctgga 2928
Db 2924 GGAGAACTCTCCCGAGCAGCGCGGACGCTTCCGCGCATGGTGGAGCTGCCAGGCTGA 2865
Qy 2929 tcggagcgccgggagcagcgagcagcgttccctctcgcgcaggttctcgaagaccgaggg 2988
Db 2864 TCGGAGCGCGCGGGGAGCAGCGCACAGGGTCTCTTCGCGCGGTCTCGAAGACCGAGGG 2805
Qy 2989 cggagcgagcggggcttctccagaccaaagaagctgagggacctggtgctgagccccgtac 3048
Db 2804 CGGAGCGAGCGGGCTTCTCCAGACCAAGAGCTGAGGACCTGTGGCTGAGCCCCGCTAC 2745
Qy 3049 catggaagatctgtctgtctacagcttccaggtgcccagagggatggagttcctgcttc 3108
|||||

